

## Swope, Sheridan

---

**From:** Swope, Sheridan  
**Sent:** Wednesday, December 10, 2003 9:28 PM  
**To:** Schreiber, David  
**Subject:** 09896522

David, Would you do me the favor of the following alignments/searches?

For 09896522

Search SID 1, SID 2, AND SID 3 against all of the sequences in the following cases:

1 2 3

✓ Tang et al  
09/488,725  
09/522,317 ← 552,317  
NO CRF

✓ Ho et al  
09/536,647

✓ Robinson et al  
09/516,448

✓ Hyseq et al  
09/235,076

Rosen et al  
PCT/US00/05988  
60/124,270 — NO CRF Do 102e  
Shift burden

Let me know if you can do it.  
TTHANKS!!!

Sheridan Swope, Ph.D.  
Patent Examiner, AU 1652,  
Recombinant Enzymes  
sheridan.swope@uspto.gov  
703-305-1696 (voice)  
703-308-3014 (FAX)  
Mailbox: CM1 Rm10D01  
Office: CM1 Rm12D12

**This Page Blank (uspto)**

1	832.4	99.8	834	2	US-09-536-647-1	Sequence 1, Appl1
2	832.4	99.8	2152	1	US-09-488-7258-7130	Sequence 7130, Ap
3	823.5	98.7	1648	3	US-09-516-448-2048	Sequence 2048, Ap
4	432.8	51.9	472	4	US-09-235-076-3039*	Sequence 3039, A
5	363.599	43.6	1310	5	PCT-US00-05988-220	Sequence 220, Appl
6	281.899	33.8	1316	1	US-09-488-7258-6367	Sequence 6367, Ap
7	221	25.5	472	4	US-09-235-076-24042	Sequence 24042, A
8	210.4	26.2	455	4	US-09-235-076-2393	Sequence 2393, A
9	126.5	15.2	470	4	US-09-235-076-9667	Sequence 9667, Ap
10	40.6	4.5	1298	5	PCT-US00-05988-682	Sequence 682, Appl
11	37.2	4.9	4134	1	US-09-488-7258-3819	Sequence 3819, Ap
12	35.8	4.3	8872	1	US-09-488-7258-6268	Sequence 6268, Ap
13	35.4	4.2	489	4	US-09-235-076-20462	Sequence 20462, Ap
14	35.2	4.2	752	3	US-09-516-448-1912	Sequence 1912, Ap
15	34.6	4.1	1404	1	US-09-488-7258-2608	Sequence 2608, Ap
16	34.4	4.1	3479	1	US-09-488-7258-3555	Sequence 3555, Ap
17	34.2	4.1	480	4	US-09-235-076-12224	Sequence 12224, A
18	34.2	4.1	2838	1	US-09-488-7258-5906	Sequence 5906, Ap
19	34.1999	4.1	5122	1	US-09-488-7258-5012	Sequence 5012, Ap
20	34	4.1	471	1	US-09-235-076-29236	Sequence 29236, Ap
21	34	4.1	1618	4	US-09-488-7258-7758	Sequence 7758, Ap
22	34	4.1	4308	1	US-09-488-7258-3800	Sequence 3800, Ap
23	34	4.1	4454	1	US-09-488-7258-6591	Sequence 6591, Ap
24	33.6	4.0	1746	1	US-09-488-7258-5104	Sequence 5104, Ap
25	33.6	4.0	2586	1	US-09-488-7258-8011	Sequence 8011, Ap
26	33	4.0	1108	1	US-09-488-7258-8980	Sequence 8980, Ap
27	33	4.0	3285	4	US-09-516-448-877	Sequence 877, Appl
28	32.8	3.9	478	4	US-09-235-076-2081	Sequence 2081, Ap

29	32.8	3.9	773	1	US-09-488-725B-9166	Sequence 9186, A
30	32.8	3.9	1573	1	US-09-488-725B-1006	Sequence 1006, A
31	32.8	3.9	4567	1	US-09-488-725B-3552	Sequence 3552, A
32	32.8	3.9	4372	1	US-09-488-725B-3745	Sequence 3745, A
33	32.8	3.9	4410	1	US-09-488-725B-3680	Sequence 3680, A
34	32.4	3.9	478	4	US-09-233-076-82	Sequence 32, A
35	32.4	3.9	1749	1	US-09-488-725B-8030	Sequence 8030, A
36	32.4	3.9	1955	1	US-09-488-725B-906	Sequence 906, A
37	32.3	3.9	547	1	US-09-488-725B-1497	Sequence 1497, A
38	32.2	3.9	585	1	US-09-488-725B-4795	Sequence 4795, A
39	31.8	3.8	463	4	US-09-233-076-4484	Sequence 2484, A
40	31.8	3.8	5103	1	US-09-488-725B-6574	Sequence 6574, A
41	31.4	3.8	493	4	US-09-233-076-22668	Sequence 22668, A
42	31.4	3.8	496	4	US-09-233-076-24688	Sequence 24688, A
43	31.4	3.8	910	1	US-09-488-725B-6522	Sequence 6522, A
44	31.4	3.8	6553	1	US-09-488-725B-6256	Sequence 6256, A
45	31	3.7	1585	1	US-09-488-725B-8299	Sequence 8299, A

## ALIGNMENTS

```

RESULT 1
US-09-536-647-1
Sequence 1, Application US/09536647
Patent No. 6579708
GENERAL INFORMATION:
APPLICANT: Ho, Yen Sen
APPLICANT: Johnson, Randall
TITLE OF INVENTION: No. 6579708e1 Human Uridine Kinasee
FILE REFERENCE: GP50020
CURRENT APPLICATION NUMBER: US/09/536,647
CURRENT FILING DATE: 2000-03-27
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 834
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (780)
US-09-536-647-1

```

Query Match	99.8%	Score 832.4	DB 2	Length 834
-------------	-------	-------------	------	------------

Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	ATGGCTTCGGGGGCGGGAGGCGAATCTGGCAGAGGCCCGGCGCGGAGGCGACCGTCCGAC	60
Db	1	ATGGCTTCGGGGGCGGGAGGCGAATCTGGCAGAGGCCCGGCGCGGAGGCGACCGTCCGAC	60
Qy	61	CAGCGGCCCTTCTCTATATAGGGGTGAGCGCGGCACTGTGCACGGGAAAGTCGACCGTGTGT	120
Db	61	CAGCGGCCCTTCTCTATATAGGGGTGAGCGCGGCACTGTGCACGGGAAAGTCGACCGTGTGT	120
Qy	121	GAGAAATCATGAGGTGTCTGGACAGAACGAGGTGAAACACCGGCAACCGGAGGTGTC	180
Db	121	GAGAAATCATGAGGTGTCTGGACAGAACGAGGTGAAACACCGGCAACCGGAGGTGTC	180
Qy	181	ATCTCTAGCCAGAGCAAGTTCTTACAAGTCTCTGACGCGACAGCAAGAGCCAGGCTTG	240
Db	181	ATCTCTAGCCAGAGCAAGTTCTTACAAGTCTCTGACGCGACAGCAAGAGCCAGGCTTG	240
Qy	241	AAAGGCACTAATTTTTCACATCCATCCATCCCTTTGATATATGATTTGATGCAACGACT	300
Db	241	AAAGGCACTAATTTTTCACATCCATCCATCCCTTTGATATATGATTTGATGCAACGACT	300
Qy	301	CTGAAGAAATCGTGGAGGGCAAAACGCTGAGAGTCCGACCTATGATTTTGTGACACAC	360
Db	301	CTGAAGAAATCGTGGAGGGCAAAACGCTGAGAGTCCGACCTATGATTTTGTGACACAC	360
Qy	361	TCAGGGTATCAGAGCAACGCTGCTTACCTCTCGGACGCTGTCTCTTTGAGGGATC	420
Db	361	TCAGGGTATCAGAGCAACGCTGCTTACCTCTCGGACGCTGTCTCTTTGAGGGATC	420

```

Db      |||TCAAAGTTACCAAGAGACCAAGGTGTCTACCTTCGACAGCTGTCTCTTTGAGGCAATC 420
Qy      |||421 TTGGTGTCTTACACGACGAGAGATCCGGACATGTTCCACCTGCGCTCTTGTGACACC 480
Db      |||421 TTGGTGTCTTACACGACGAGATCCGGACATGTTCCACCTGCGCTCTTGTGACACC 480
Qy      |||481 GACTCCCACTGACGCTGTCTCGAAGATTCTCCGGACCTGCGCGCCGAGGAGGACCTG 540
Db      |||481 GACTCCCACTGACGCTGTCTCGAAGATTCTCCGGACCTGCGCGCGCCGAGGAGGACCTG 540
Qy      |||541 GAGCAGATTCTGACGACGACATCCACCTTGTGAGGCGGCTTCGAGAGTTCTGCTG 600
Db      |||541 GAGCAGATTCTGACGACGACATCCACCTTGTGAGGCGGCTTCGAGAGTTCTGCTG 600
Qy      |||601 CCGACAAAGAGTATGCGATGTATCATCCACGAGAGTGAACAATATGTGGCATC 660
Db      |||601 CCGACAAAGAGTATGCGATGTATCATCCACGAGAGTGAACAATATGTGGCATC 660
Qy      |||661 AACCTGATCGTGCAGCAGCATTCAGAGCATTTGATGTGACATCTGCAATGACACCGA 720
Db      |||661 AACCTGATCGTGCAGCAGCATTCAGAGCATTTGATGTGACATCTGCAATGACACCGA 720
Qy      |||721 GAGAGGTTCATGAGCGGAGCTAACAAGCGACCTTTTCTGAGCGGAGGACCACTG 780
Db      |||721 GAGAGGTTCATGAGCGGAGCTAACAAGCGACCTTTTCTGAGCGGAGGACCACTG 780
Qy      |||781 ATGCTGACTCTGTGCAAAAGGTGACATTTGAGATGTCAGACAGACCCCACTGA 834
Db      |||781 ATGCTGACTCTGTGCAAAAGGTGACATTTGAGATGTCAGACAGACCCCACTGA 834

```

RESULT 2  
US-09-488-725B-7130

```

; Sequence 7130, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; PRIOR APPLICATION NUMBER: 2000-01-21
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: PC_CT_genes Version 1.01
; SEQ ID NO 7130
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: Homo sapiens

```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2153)
; OTHER INFORMATION: n = a,t,c or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (110)...(891)
; OTHER INFORMATION: similar to g1471981 in the genepept database release 114,
; US-09-488-725B-7130

```

Query Match 99.8%; Score 832.4; DB 1; Length 2152;  
Best Local Similarity 99.9%; Pred. No. 2,3e-166;  
Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;.

```

Qy      |||1 ATGCTTTCGCGGAGGCGAAGCTGCGAGAGCCCGCGCGGAGCGGACCGTCCGAC 60
Db      |||59 ATGCTTTCGCGGAGGCGAAGCTGCGAGAGCCCGCGCGGAGCGGACCGTCCGAC 118
Qy      |||61 CAGCGGCGCTTCTGTATAGGGGTGACCGGCGGACCTGCGAGCGGAAAGTGCACCGTGT 120
Db      |||119 CAGCGGCGCTTCTGTATAGGGGTGACCGGCGGACCTGCGAGCGGAAAGTGCACCGTGT 178
Qy      |||121 GAGAGATCATGAGATTGCTGAGACAAAGAGTGAACAAGCGGAGCGGAGGAGTGT 180
Db      |||179 GAGAGATCATGAGATTGCTGAGACAAAGAGTGAACAAGCGGAGCGGAGGAGTGT 238
Qy      |||181 ATCTGAGCGAGACAGATTCTAACAAGTCTGACGCGAGAGCAAGAGCTTGG 240
Db      |||239 ATCTGAGCGAGACAGATTCTAACAAGTCTGACGCGAGAGCAAGAGCTTGG 298
Qy      |||241 AAAGGACAGTAAATTTTGCATCCAGATGCTTGTATATATATTTGATGACAGACT 300
Db      |||299 AAAGGACAGTAAATTTTGCATCCAGATGCTTGTATATATATTTGATGACAGACT 358
Qy      |||301 CTGAGAGACATCTGTGAGGCGCAAAAGGTGAGAGTCCGACCTATGATTTTGTGACAC 360
Db      |||359 CTGAGAGACATCTGTGAGGCGCAAAAGGTGAGAGTCCGACCTATGATTTTGTGACAC 418
Qy      |||361 TCAGAGTTACCAAGACACAGGTGTCTACCTGCGGACCTGTTCTGTTGAGGCAATC 420
Db      |||419 TCAGAGTTACCAAGACACAGGTGTCTACCTGCGGACCTGTTCTGTTGAGGCAATC 478
Qy      |||421 TTGGTGTCTTACACGACGAGATCCGGACATGTTCCACCTGCGCTCTTGTGACACC 480
Db      |||479 TTGGTGTCTTACACGACGAGATCCGGACATGTTCCACCTGCGCTCTTGTGACACC 538
Qy      |||481 GACTCCGACGTCAAGCTGTCTCGAAGATTCTCCGGACCTGCGCGGAGGAGGACCTG 540
Db      |||539 GACTCCGACGTCAAGCTGTCTCGAAGATTCTCCGGACCTGCGCGGAGGAGGACCTG 598
Qy      |||541 GAGCAGATTCTGACGACGATCACCACTTGTGAAGCGGCTTTCGAGGAGTTCTGCTG 600
Db      |||599 GAGCAGATTCTGACGACGATCACCACTTGTGAAGCGGCTTTCGAGGAGTTCTGCTG 658
Qy      |||601 CCGACAAAGAGTATGCGATGTATCATCCACGAGAGTGAACAATATGTGGCATC 660
Db      |||659 CCGACAAAGAGTATGCGATGTATCATCCACGAGAGTGAACAATATGTGGCATC 718
Qy      |||661 AACCTGATCGTGCAGCAGCATTCAGAGCATTTGATGTGACATCTGCAATGACACCGA 720
Db      |||719 AACCTGATCGTGCAGCAGCATTCAGAGCATTTGATGTGACATCTGCAATGACACCGA 778
Qy      |||721 GAGAGGTTCATGAGCGGAGCTAACAAGCGACCTTTTCTGAGCGGAGGACCACTG 780
Db      |||779 GAGAGGTTCATGAGCGGAGCTAACAAGCGACCTTTTCTGAGCGGAGGACCACTG 838
Qy      |||781 ATGCTGACTCTGTGCAAAAGGTGACATTTGAGATGTCAGACAGACCCCACTGA 834
Db      |||839 ATGCTGACTCTGTGCAAAAGGTGACATTTGAGATGTCAGACAGACCCCACTGA 892

```

RESULT 3



US-09-516-448-2048  
 ; Sequence 2048, Application US/09516448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: **RODARON, Keith E**  
 ; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs  
 ; FILE REFERENCE: 5800-119  
 ; CURRENT APPLICATION NUMBER: US/09/516,448  
 ; CURRENT FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 2050  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2048  
 ; LENGTH: 1648  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(1648)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-516-448-2048

Query Match 98.7%; Score 823.5; DB 3; Length 1648;  
 Best Local Similarity 99.9%; Pred. No. 1,7e-164;

Matches 834; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

```

QY 1 ATGGCTTCGCGCGGAGCGAAGACTGCGAGAGCCCGCGCGGAGCGGACCGTCCGAC 60
DB 84 ATGGCTTCGCGCGGAGCGAAGACTGCGAGAGCCCGCGCGGAGCGGACCGTCCGAC 143
QY 61 CAGCGGCGCTTCTGATAGGGGTGAGCGCGGCACTGCGAGCGGAAAGTGCAGTGTGT 120
DB 144 CAGCGGCGCTTCTGATAGGGGTGAGCGCGGCACTGCGAGCGGAAAGTGCAGTGTGT 203
QY 121 GAAAGATCATGAGTGTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGC 180
DB 204 GAAAGATCATGAGTGTCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGC 263
QY 181 ATCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGC 240
DB 264 ATCTGAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGTGC 323
QY 241 AAGAGACATGATATTTGACATCCAGATGCTTTGATATGATTTGATGACAGAGACT 300
DB 324 AAGAGACATGATATTTGACATCCAGATGCTTTGATATGATTTGATGACAGAGACT 383
QY 301 CTGAAGACATCTGTGAGGGCAAAACGCTGAGAGTGCAGACTATGATTTTGTGACAC 360
DB 384 CTGAAGACATCTGTGAGGGCAAAACGCTGAGAGTGCAGACTATGATTTTGTGACAC 443
QY 361 TCAAGGTACAGAGACAGAGTGTCTACCTGCGGAGCGTGTCTGAGGGGATC 420
DB 444 TCAAGGTACAGAGACAGAGTGTCTACCTGCGGAGCGTGTCTGAGGGGATC 503
QY 421 TTGGTGTTCACGCGAGAGATCCGAGACATGTTCCAGCTGCGCTCTCTGTGACACC 480
DB 504 TTGGTGTTCACGCGAGAGATCCGAGACATGTTCCAGCTGCGCTCTCTGTGACACC 563
QY 481 GATCTCGACGTCGCGTGTCTCGAAGAGTTCCTCGGAGAGTGCAGAGAGAGAGCTG 540
DB 564 GATCTCGACGTCGCGTGTCTCGAAGAGTTCCTCGGAGAGTGCAGAGAGAGAGCTG 623
QY 541 GAGCAGATTCGAGCGAGTACACACCTTGAGAGCGGCGCTTCAGAGAGATTCGCTG 600
DB 624 GAGCAGATTCGAGCGAGTACACACCTTGAGAGCGGCGCTTCAGAGAGATTCGCTG 663
QY 601 CCGACAAGAGTA-TGCCGATGTGATCATCCACGAGAGTGTGACATATGTGTCAT 659
DB 684 CCGACAAGAGTA-TGCCGATGTGATCATCCACGAGAGTGTGACATATGTGTCAT 743
QY 660 CAACCTGATGTGACAGACATCCAGACATTTGATGATGTGACATCTGCAATGACACG 719
DB 744 CAACCTGATGTGACAGACATCCAGACATTTGATGATGTGACATCTGCAATGACACG 803
QY 720 AGAGGGGTCCAAATGGGCGAGCTACAAAGCGGACCTTTTCTGAGCGAGGAGACACCTG 779

```

```

DB 804 AGAGGGGTCCAAATGGGCGAGCTACAAAGCGGACCTTTTCTGAGCGAGGAGACACCTG 863
QY 780 GATCTGACCTCTGCGAAGAGTCACTTTGAGTGTGACAGAGAGAGAGAGAGAGAGT 834
DB 864 GATCTGACCTCTGCGAAGAGTCACTTTGAGTGTGACAGAGAGAGAGAGAGAGAGT 918

```

RESULT 4:  
 US-09-235-076-30379

; Sequence 30379, Application US/09235076

; GENERAL INFORMATION:

; APPLICANT: HySeq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/235,076

; CURRENT FILING DATE: 1999-01-20

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 30379

; LENGTH: 472

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(472)

; OTHER INFORMATION: n = A,T,C or G

US-09-235-076-30379

Query Match 51.9%; Score 432.8; DB 4; Length 472;  
 Best Local Similarity 98.2%; Pred. No. 7.6e-83;

Matches 437; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

QY 84 GAGCGGCGGACCTGCCAGCGGAGAGTGCACCGTGTGTGAGAGATCATGAGTGTGCG 143
DB 28 GTGCGTGAAGAGAGCGGAGAGAGTGCACCGTGTGTGAGAGATCATGAGTGTGCG 87
QY 144 ACAGAACAGAGTGTGAAACAGCGGCGAGGAGAGTGTGTCTTGAAGCAGAGACAGTTC 203
DB 88 ACAGAACAGAGTGTGAAACAGCGGCGAGGAGAGTGTGTCTTGAAGCAGAGACAGTTC 147
QY 204 CAAGGTCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 263
DB 148 CAAGGTCTGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
QY 264 TCCAGATGCTTTGATATGATTTGATGACAGAGACTTGTGAGAGAGAGAGAGAG 323
DB 208 TCCAGATGCTTTGATATGATTTGATGACAGAGACTTGTGAGAGAGAGAGAGAG 267
QY 324 AACGCTGAGAGTCCGACCTATGATTTTGTGACACCTCAAGGTTACAGAGACACG 383
DB 268 AACGCTGAGAGTCCGACCTATGATTTTGTGACACCTCAAGGTTACAGAGACACG 327
QY 384 GGTCTACCTCGGAGAGAGTGTCTGTTGAGAGGACATCTGTGTCTTACAGCAGAGAG 443
DB 328 GGTCTACCTCGGAGAGAGTGTCTGTTGAGAGGACATCTGTGTCTTACAGCAGAGAG 387
QY 444 CCGGAGACATGTTCCAGCTGCGCTCTTGTGACACCGACCTCCGAGCTCAGCTGTCTG 503
DB 388 CCGGAGACATGTTCCAGCTGCGCTCTTGTGACACCGACCTCCGAGCTCAGCTGTCTG 447
QY 504 AAGAGTTCTCCGAGAGAGTGTGCGCGA 528
DB 448 AAGAGTTCTCCGAGAGAGTGTGCGCGA 472

```

RESULT 5  
 PCT-US00-05988-220

; Sequence 220, Application PC/TUS0005988

; GENERAL INFORMATION:

; APPLICANT: Craig Rosen,  
 ; APPLICANT: Steve Ruben



```

OY      541 GAGAGAGATTCTGACGACAGTACAC---CACCTTGTGAAGCGGCTTCGAGGAGTTCTG 596
      |||
DB      548 GAGAGAGATTTTATCTCTCAAGTACATTACGTTTCGTAACCTCCCTTTGAGGAATTTCTG 489
OY      597 CTTCCCGACAAA-GAAGTATCCGATGTGATCATCC--ACGAGAGTGAACAATATGAT 653
DB      488 CTTCCCAACAAAGGAAGTATCTGTATGTGATCATCTCCCTTAAGAGTGCAGATTAATCCGGGT 429
OY      654 TGCCATCAACTGTATCTGTGACGACATCCA-GGACATTTCTGAATGTGATCATCTGCAAA 711
DB      428 GCCCATCAACTCTCATCTGTGACGACATCATCCAGGACATCTGTGAATGAGGCGCTCCAAA 370

RESULT 7
US-09-235-076-24042
; Sequence 24042, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: FROM VARIOUS CDNA LIBRARIES
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24042
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-24042

Query Match      26.5%; Score 221; DB 4; Length 472;
Best Local Similarity 73.0%; Prid. No. 1.4e-38;
Matches 284; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

OY      66  GCCCTTCCTGATAGGGGTGAGCGGCGGCACTGCGCGGGAAGTGCACCGTGTGTGAGA 125
DB      84  GCCCTTCTTATAGGCGTCAACGGGGGAACAGCTTAGCGGCAAGTCTTCGTGTGTGCTBA 143
OY      126 GATCATGAGTTGTGTGAGACAGAAAGAGTGGAAACAGCGGACGCGAAGTGTCTATCT 185
DB      144 GATGTGTACGTCTCTGGGGCAGAAATGAGTGGATCATGTGCCAAGACAGTGTGTATCT 203
OY      186 GAGCCAGACAGGTTTCTAACAAGTCTTGACGCGCAGAGCAAGAGGCGCAAGCCTTGAAAG 245
DB      204 GAGCCAGAGATGTCTTCTACCGTGTCTTACTCGGAGCAGAAAGGCCAAGCCCTTAAGGG 263
OY      246 ACAGTACAAATTTTGAACCATCCAGATGCTCTTTGATTAATGATTTGAAGCACAAGACTCTGA 305
DB      264 CCAATCTCAACTTTGACCAACCGGATGCTTTTGAACATTAACATCTTCAAAAACCTCAA 323
OY      306 GAACATCGTGGAGGGCAAAAAGGTGAGAGTGCACCATGATTTTGTGACACATCTCAAG 365
DB      324 AGAATATCACTGAGAGGAAAAGATGCAGATCCCGGTATATGCTTTGTCTCCATTTCCG 383
OY      366 GTTACCAAGACCAACGCTGTCTTACCTTCGCGACGATGCTTCTGTTTGAAGGACATCTTGAT 425
DB      384 GAAGAGAGAGACAATTACTGTCTTATCCGCGAGAGAGTGTGTCTTTGAAGGATCTGTGC 443
OY      426 GTTCTTACAGCCAGAGATCCGGACATGT 454
DB      444 CTCTACTCTCCAGAGGATGACGACCTGT 472

RESULT 8
US-09-235-076-23923
; Sequence 23923, Application US/09235076
; GENERAL INFORMATION:

```

```

APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/235,076
CURRENT FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 23923
LENGTH: 455
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(455)
OTHER INFORMATION: n = A,T,C or G
US-09-235-076-23923

Query Match      25.2%   Score 210.4; DB 4;   Length 455;
Best Local Similarity 72.8%;   Pred. No. 2,2e-35;
Matches 271; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

```

```

Query Match      25.2%; Score 210.4; DB 4; Length 455;
Best Local Similarity 72.8%; Pred. No. 2.2e-36;
Matches 271; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

QY 66 GCCCTTCCTGATAGGGGTGAGCGCGCGCACTGCGACGCGGAGAGTCAACCGTGTGTGAGAA 125
   |||||
Db 84 GCCCTTCCTTATAGGGGTGAGCGCGCGGAGAACAGTACGAGGGCAAGTCTTCGGTGTGTGCTAA 143
   |||||

QY 126 GATCATGAGAGTTGCTGGGACAGAACGAGGTGGAAACAGCGGACGCGAAGGTGTGATCTT 185
   |||||
Db 144 GATGTGCACTCTCGTGGGAGAGATGAGTGGACTATCGCAGAAAGCAGGTGTGATCTT 203
   |||||

QY 186 GAGCGACAGACAGGTTTCAACAAGGCTCGACGACGACAGAAAGCCAAAGCCTGAAAG 245
   |||||
Db 204 GAGCGACAGAAATGCTTCAACGCTGCTTACCTCGAGACAGAAAGCCGAAAGG 263
   |||||

QY 246 ACAGTAAATTTGACCACTCAGATGCGCTTTGATTAATGATTTGATGACAGACTTGAA 305
   |||||
Db 264 CCAATTCACTTGACCAACCGGATGCTTTGACAAATGAACTATTTCAAAAACATCA 323
   |||||

QY 306 GAACATCGTGAAGGCAAAACGTTGAGGTGCGCGACTATGATTTGTGACACTCAAG 365
   |||||
Db 324 AGAATACATGAAGGGGAAAACAGTCAGATCCCGGTATGACTTGTCTCCCATTC 383
   |||||

QY 366 GTTACCAAGAACCAACGTTGTTTACCTCGGGGACAGTGTCTGTTAAGGCACTTGT 425
   |||||
Db 384 GAAGAGAGAAACAGTTTACTGTATCCCGACAGTGTGTCTTTGAAGGATCTGGC 443
   |||||

QY 426 GTTCTACAGCA 437
   |||||
Db 444 CTTCTACTCCCA 455
   |||||

RESULT 9.
US-09-235-076--9667/c
; Sequence 9667, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235.076
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9667
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(470)
; OTHER INFORMATION: n = A,T,C or G
; US-09-235-076-9667

```

```

Query Match      15.2%; Score 126.5; DB 4; Length 470;
Best Local Similarity 57.3%; Pred. No. 7.6e-19;
Matches 246; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

QY 267 AGATGCTTTGATTAATGATTGACACAGACTCTGAGAAACATCGTGGAGGCAAAAC 326
DB 470 AGATGCTTTGATTAATGATTGACACACTTTCACCTCAAGAGAGTGAAGAGGAAAGAG 411

QY 327 GGTGAGAGTCCGACATGATTTTGTGACACACTCAAGGTACAGAGACACAGGTGGT 386
DB 410 TGTCAAGAGTCCCATTTATATCACTTCAACAGCAGCCGAGAGAGAGTGAAGAAACACT 351

QY 387 CTACCCGCGAGAGTGGTCTGTTTGGAGGAGATCTTGTTCTACAGCCAGAGAGATCCG 446
DB 350 GTATGCTGCAAGGTATCATCTTTTGAGGAGATCATGCTTTGCTGACAAAGACTGTT 291

QY 447 GGAATGTTCCACCTGCGCTCTTCGTGACACAGACTCCGAGCTGAGCTGTCTCGAG 506
DB 290 GGAAGCTCTGACATGAAGATCTTTTGTGACACAGACTCCGAGATCCGCTGGTGAAGGCG 231

QY 507 AGTTCTCCGAGAGCTGCG---CGAGGAGAGGACCTGGAGCATTTTGAACGACATAC 563
DB 230 GCTGCGCGGAGACATCATGAGCGCGCGGACATGAGGAGTGTCTCAAGAGATACAA 171

QY 564 CACCTTGATGAAGCGCGCTTCGAGAGATTCTGCTGCGCAAGAAATATGCGCATGT 623
DB 170 CAAGTTTGTCAAGCCCTCTCTTCAACCATATCACTCAAGCCCATGCGCTGGACAT 111

QY 624 GATCATCCACGAGAGTGAACATATGTTGCCATCAACCTGATCTGACAGACATCCA 683
DB 110 CGTGTGCTCCAGAGGAGGAGCGGCAACAGGTGGCATGACTGTGACAGTGTGCA 51

QY 684 GGACATTTCT 692
DB 50 CGAATTCCT 42

RESULT 10
PCT-US00-05988-682
; Sequence 682, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: PA101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 682
; LENGTH: 1298
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1294)
; OTHER INFORMATION: n equals a,t,g, or c
PCT-US00-05988-682

Query Match      4.9%; Score 40.6; DB 5; Length 1298;
Best Local Similarity 49.8%; Pred. No. 0.65;
Matches 100; Conservative 1; Mismatches 100; Indels 0; Gaps 0;

QY 375 GACCAAGGTGATTAACCTGCGAGCGTGTCTTTGAGGAGCATCTTGTGTTCTACAG 434
DB 736 GATCGAGATGAGAGACCAAGCAACGACGATGACAGAGCGGACATCCCGTGTGAGCTA 795

QY 435 CCAAGAGATCCGAGACATGTTCAACTGCGCTTCTTGTGACACGACATCCGAGTCA 494
DB 796 CAAGACTTAACCGACGCGGTCTTCTTCTGCTCCCTCAAGAGAGCGGACAAAGAGAT 855

```

```

QY 495 GCTGTCTCAAGAGTTCCTCCGAGAGCTGCGCGAGAGAGGACCTGAGCAGATTCTGAC 554
DB 856 GATCACCGGACAGCTGAGATATCCCTYAGCGCGGCGCGGTGTGAGACAGGCCCTCTA 915

QY 555 GCAGTACACCACTTCGTGAA 575
DB 916 CCAGTCTCAACCTGTGAA 936

RESULT 11
US-09-488-725B-3819/c
; Sequence 3819, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 3819
; LENGTH: 4134
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (4136)...(639)
; OTHER INFORMATION: similar to g11504026 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-3819

Query Match      4.5%; Score 37.2; DB 1; Length 4134;
Best Local Similarity 47.1%; Pred. No. 3.2;
Matches 114; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

QY 302 TGAAGAACATCGTGAGGGGAAACGTTGAGAGTGCAGACTTGAATTTGTGACACT 361
DB 1050 TGCCGTAACCTGAGGCGGCGGAGCGGTGTCTTACCCGCTGACAGAGCGCGCGGACG 991

QY 362 CAAGGTACAGAGACCAACGAGTGTCTTACCTGCGAGCGTGTCTTGTGAGGAGATCT 421
DB 990 GGTGAGAGAAATCCGAGTTGTCTCAACGATTCGAACTCGAACCTAAGAGAGGCGTCCG 931

QY 422 TGGTGTCTTACACCCAGAGAGATCCGAGACATGTTCACTGCGCTTCTTGTGACACCG 481
DB 930 AGCTGCTGTCTCATGTGAGGCGAGTGCCTTGGGCGACCTCAAGCTTCTGTGAGACAGC 871

```

Qy 482 ACTCCGACGTCTGAGAGTTCTCCGGGACGTGGCGGAGGAGGAGCTTG 541  
 Db 870 AGAGCGAGCGCAGCTTAGAGGTGCTTCTGCGACCCAGCGAGTGAAGAGCACTGG 811

Qy 542 AG 543  
 Db 810 AG 809

## RESULT 12

US-09-488-725B-6268  
 ; Sequence 6268, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: Ankura Slinku  
 ; APPLICANT: Ankura Slinku  
 ; APPLICANT: Radoje T. Drmanac  
 ; TITLE OF INVENTION: Novel Contigs Obtained  
 ; TITLE OF INVENTION: From Various Libraries  
 ; FILE REFERENCE: 784  
 ; CURRENT APPLICATION NUMBER: US/09/488,725B  
 ; CURRENT FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/034,341  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 09/045,400  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/321,214  
 ; PRIOR FILING DATE: 1999-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/131,598  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: US 09/170,294  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: US 09/179,473  
 ; PRIOR FILING DATE: 1998-10-27  
 ; PRIOR APPLICATION NUMBER: US 09/181,430  
 ; PRIOR FILING DATE: 1998-10-28  
 ; PRIOR APPLICATION NUMBER: US 09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; PRIOR APPLICATION NUMBER: US 09/234,611  
 ; PRIOR FILING DATE: 1999-01-22  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10289  
 ; SOFTWARE: pc\_ct\_genes Version 1.01  
 ; SEQ ID NO 6268  
 ; LENGTH: 8872  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(8873)  
 ; OTHER INFORMATION: n = a,t,c or g  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (170)...(5244)  
 ; OTHER INFORMATION: similar to g1212917 in the genepept database release 114,  
 ; OTHER INFORMATION: Run with FASTXY 3.3c00, default parameters  
 ; US-09-488-725B-6268

Query Match 4.3%; Score 35.8; DB 1; Length 8872;

Best Local Similarity 54.1%; Pred. No. 6; Mismatches 62; Indels 0; Gaps 0;

Qy 58 CACCAAGCGCCCTCTCTGATAGGGGTAGCGCGGCACTGCCAGCGGAAGTGCACCGTG 117  
 Db 1427 CTCACAGAGCGCATCTTTGTCGCCCGGCGGAGGAGGCGCATTTAAAGACTGAAGAA 1486  
 Qy 118 TGTGAGAGATCATGAGTTGCTGGAGACAGACGAGGTGAGACGCGGACGCGAAGGTG 177  
 Db 1487 ACAGAGAGATCATGAGTTGCTGGAGACAGACGAGGTGAGACGCGGACGCGAAGGTG 1546

Qy 178 GTGATCTTGAGCCAG 192  
 Db 1547 GCCATCCGATGAG 1561

## RESULT 13

US-09-235-076-20462  
 ; Sequence 20462, Application US/09235076  
 ; GENERAL INFORMATION:  
 ; APPLICANT: HySeq, Inc.  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 ; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
 ; FILE REFERENCE: 20411-756  
 ; CURRENT APPLICATION NUMBER: US/09/235,076  
 ; CURRENT FILING DATE: 1999-01-20  
 ; NUMBER OF SEQ ID NOS: 38054  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 20462  
 ; LENGTH: 489  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(489)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-235-076-20462

Query Match 4.2%; Score 35.4; DB 4; Length 489;

Best Local Similarity 48.7%; Pred. No. 8.2; Mismatches 96; Conservative 0; Indels 101; Gaps 0;

Qy 434 GCGAGAGATCCGGGACATGTTCCACTGCGCTTCTTGAGACACCGACTCCGAGTCA 493  
 Db 21 GGCACAGCTCAAGTCCGTGAACAAAGCATCGCACTGACGACCGACTGAGGACG 80  
 Qy 494 GGCTGTCTGAGAGTTCTCCGGGACGTGCGCGGAGGAGGACCTGAGCATTTCTGA 553  
 Db 81 GGCTGCGCTCATCGGCTGCTGAGTGTCTGAGCCAGAGGACATGACGAGTACC 140  
 Qy 554 CGCAGTACACCACTTCTGTAAGCCGCGCTTCTGAGAGTTCTGCTGCCGACAAAGT 613  
 Db 141 ATCAGAGGCGCCACTTCCCGAGATGACCTGAGAGATGTGTCGCGGCTCGAGTTCC 200  
 Qy 614 ATGCCATGTGATCATC 630  
 Db 201 TGCACCGTGAAGCATC 217

## RESULT 14

US-09-516-448-1912  
 ; Sequence 1912, Application US/09516448  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Robison, Keith E.  
 ; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs  
 ; FILE REFERENCE: 5800-119  
 ; CURRENT APPLICATION NUMBER: US/09/516,448  
 ; CURRENT FILING DATE: 2000-02-29  
 ; NUMBER OF SEQ ID NOS: 2050  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 1912  
 ; LENGTH: 752  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(752)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-516-448-1912

Query Match 4.2%; Score 35.2; DB 3; Length 752;

Best Local Similarity 49.5%; Pred. No. 8.9; Mismatches 91; Conservative 0; Indels 93; Gaps 0;



Qy 237 CTTGAAAG 244  
 Db 1854 CTTGAGG 1861

RESULT 17  
 US-09-235-076-12224

; Sequence 12224, Application US/09235076

; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.

; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED

; FILE REFERENCE: 20411-756

; CURRENT APPLICATION NUMBER: US/09/235,076

; NUMBER OF SEQ ID NOS: 38054

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 12224

; LENGTH: 480

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (1)..(480)

; OTHER INFORMATION: n = A,T,C or G

US-09-235-076-12224

Query Match 4.1%; Score 34.2; DB 4; Length 480;

Best Local Similarity 50.9%; Pred. No. 15;

Matches 81; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

Qy 424 GTGTTACAGCAGGATCCGGGACATGTTCCACCTGGCCCTTCGTGAGACCGAC 483  
 Db 92 GTGTTTCCACCAAGAGCGTCTTCTCTGCAAGTGAGAGCCCTCATTGAAAGAGAC 151  
 Qy 484 TCCGACGTGAGCGTGTCTCCAGAGATTCTCCGGACGTGCGCGAGGAGGAGCCTGGAG 543  
 Db 152 CTCAGGCTCAGGAAGAGCTGAGAGCAGCCATTGAGAGGCCCAAGGCCGGAGCTCATG 211  
 Qy 544 CAGATTCTGACGCACTACACCCACTTCGTGAAAGCCGCC 582  
 Db 212 AATAAGTCAAGGATAGAACAGCCCTGTCATGCCAGCC 250

RESULT 18

US-09-488-725B-5906/c

; Sequence 5906, Application US/09488725B

; GENERAL INFORMATION:

; APPLICANT: Yuanhua T. Tang

; APPLICANT: John Tillinghaast

; APPLICANT: Ankura Sanku

; APPLICANT: Chenghua Liu

; APPLICANT: Radoje T. Dmanac

; TITLE OF INVENTION: Novel Contigs Obtained

; FILE REFERENCE: 784

; CURRENT APPLICATION NUMBER: US/09/488,725B

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 09/004,182

; PRIOR FILING DATE: 1998-01-07

; PRIOR APPLICATION NUMBER: US 09/034,341

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 09/045,400

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: US 09/321,214

; PRIOR FILING DATE: 1999-05-26

; PRIOR APPLICATION NUMBER: US 09/131,598

; PRIOR FILING DATE: 1998-08-10

; PRIOR APPLICATION NUMBER: US 09/170,294

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: US 09/179,473

; PRIOR FILING DATE: 1998-10-27

; PRIOR APPLICATION NUMBER: US 09/181,430

; PRIOR FILING DATE: 1998-10-28

; PRIOR APPLICATION NUMBER: US 09/235,076

; PRIOR FILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: US 09/234,611

; PRIOR FILING DATE: 1999-01-22

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 10289

; SOFTWARE: Pt CT\_genes Version 1.01

; SEQ ID NO 5906

; LENGTH: 2838

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (2765)..(353)

; OTHER INFORMATION: similar to gi4995641 in the genepept database release 114,

; OTHER INFORMATION: Run with FASTY 3.3f00, default parameters

US-09-488-725B-5906

Query Match 4.1%; Score 34.2; DB 1; Length 2838;

Best Local Similarity 49.2%; Pred. No. 14;

Matches 90; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

Qy 373 GAGACACGCGTGTCTACCTCGGAGCGTGTCTGTTGAGGAGCATCTGTGTTTAC 432  
 Db 1248 GTGAGCCCTGCTGTCTACCTTATCACACGCGCTGAGCGGCAATCGAGAGACAG 1189  
 Qy 433 AGCCAGAGATCCGGAGCATGTTCCACTGCGCTCTTCTGTGACACCGACTCGAGCTC 492  
 Db 1188 AGCGTGAGAAACCGGAGTGTGCTGTGCGGAACTGTCTTACCGCCCTTACAGAGATG 1129  
 Qy 493 AGCGTCTTGAAGAGATTCTCCGAGCGTCCGCGAGGAGGAGGAGGAGGAGATTCTG 552  
 Db 1128 CCGCGCTCGCGCTGCAAGCGGCTGAGGCTGCGGCGGAGGAGGAGGAGGAGGAGG 1069  
 Qy 553 ACG 555  
 Db 1068 CCG 1066

RESULT 19

US-09-488-725B-5012

; Sequence 5012, Application US/09488725B

; GENERAL INFORMATION:

; APPLICANT: Yuanhua T. Tang

; APPLICANT: John Tillinghaast

; APPLICANT: Ankura Sanku

; APPLICANT: Chenghua Liu

; APPLICANT: Radoje T. Dmanac

; TITLE OF INVENTION: Novel Contigs Obtained

; FILE REFERENCE: 784

; CURRENT APPLICATION NUMBER: US/09/488,725B

; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US 09/004,182

; PRIOR FILING DATE: 1998-01-07

; PRIOR APPLICATION NUMBER: US 09/034,341

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 09/045,400

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: US 09/321,214

; PRIOR FILING DATE: 1999-05-26

; PRIOR APPLICATION NUMBER: US 09/131,598

; PRIOR FILING DATE: 1998-08-10

; PRIOR APPLICATION NUMBER: US 09/170,294

; PRIOR FILING DATE: 1998-10-13

; PRIOR APPLICATION NUMBER: US 09/179,473

; PRIOR FILING DATE: 1998-10-27

; PRIOR APPLICATION NUMBER: US 09/181,430

; PRIOR FILING DATE: 1998-10-28

; PRIOR APPLICATION NUMBER: US 09/235,076

; PRIOR FILING DATE: 1999-01-20

; PRIOR APPLICATION NUMBER: US 09/234,611



```

PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 5012
; LENGTH: 5122
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)...(3744)
; OTHER INFORMATION: similar to g1189036 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-5012

Query Match      4.1%; Score 34.1999; DB 1; Length 5122;
Best Local Similarity 43.6%; Pred. No. 13;
Matches 196; Conservative 0; Mismatches 248; Indels 6; Gaps 1;

QY 121 GAGAGATCATGAGTTCCTGGGACAGACGAGGTGGAACGCGGACGCGGAAGGTGTC 180
DB 1505 GAGAGGCAAAACGACTCTGGAGAACGAGCGGGGAGCTGGCCAAAGAGTGAAGTG 1564
QY 181 ATCTGAGCCAGACAGAGTTCTTCAAGGTCTCTGACGCGCAGAGCAAGAGCCCTTG 240
DB 1565 CTGCTGAGGGCGGAGGAGACTCGAGACAAAGCGCAAGAAAGTGAAGCGCAGCTGCA 1624
QY 241 AAGAGACATGATCAATTTTGCATCCAGATGCTTTGATATATGTTTGAAGCAGAGACT 300
DB 1625 GAGCTGAGCTGCAAGTTCAACGAGGAGAGCGGTGGCCACAGCTGGCCGCAAGATGC 1684
QY 301 CTGAGAAACATCGAGGAGGGCAAAACGATGAGGTGCGACCTATGATTTTGTGACACAC 360
DB 1685 ACCAGCTGCAAGTGAAGCTGGAACAAGTACCGGGCTTCTACACGATCCGACACAG 1744
QY 361 TCAAGTTACAGACACAGCGTGTCTACCCCTGCGACGCTGTTCTGTTGAGGGCATC 420
DB 1745 TCCAG-----CAAGCTCACCAAGAGACTTCCGCGGTGAGGTGCCAGCTGACAGACT 1798
QY 421 TTGGTGTCTTACAGCCAGAGATCCGGACATGTTTCCACTGCGCTCTTCTGTGAGAC 480
DB 1799 CAGGAGCTGCTGCAAGGAGGAGAACCGGCAAGAGCTGAGCCCTGACCAACAGCTCA 1858
QY 481 GACTCCGACGTCAGCTGCTCGAAGATTCTCCGGGACGCGCCGAGGGAGGAGACTG 540
DB 1859 GTGAGGACGAGAAATTTCTTCCGAGCACTGAGAGAGAGAGAGAGAGGCAAG 1918
QY 541 GAGCAGATTCGACGACGATACACCACTTC 570
DB 1919 CACAACTGAGAGAGAGATGCACCCCTC 1948

RESULT 20
US-09-235-076-29236
; Sequence 29236, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; PRIORITY FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PatSeq for Windows Version 3.0
; SEQ ID NO 29236
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(471)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-29236

```

```

Query Match      4.1%; Score 34; DB 4; Length 471;
Best Local Similarity 48.5%; Pred. No. 16;
Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 21 AGACTCGAGAGAGCCCGCGGAGGCGGACCTCCGACACGAGCCCTCTCTATAGG 80
DB 151 AGACTCTGGAATAAACCGCTGACGAGAGCGGCCACTACAGCTCCAGCTGCCA 210
QY 81 GGTAGCCGGGAGCTGCCAGCGGAGATCGACCGGTGTGAGAAGATCATGAGTTGCT 140
DB 211 GTGACAGAGCTGATACCAACGTGAGTTCAGCTGGCAGAGATCCGCTGTACCTGGA 270
QY 141 GGACACAAACGAGGTGAACAGCGGACGCGAAGTGTATCTGATCCAGCAGAGAGTT 200
DB 271 GCGCAGAAACAGAGATGTCACAGGTGCTGTGACGTGCGGTGCCGCTGAGATGTGAGAT 330
QY 201 CTACAAAGTCTCTGA 214
DB 331 CAACAGTACCGGA 344

RESULT 21
US-09-488-725B-7758
; Sequence 7758, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuhua T. Tang
; APPLICANT: Anhua Slink
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIORITY FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIORITY FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 7758
; LENGTH: 1618
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (36)...(1222)
; OTHER INFORMATION: similar to g13724105 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-7758

Query Match      4.1%; Score 34; DB 1; Length 1618;
Best Local Similarity 48.5%; Pred. No. 15;
Matches 94; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

```



```

QY 21 AGACTCGAGAGCCCGCCGAGGCGGACCGTCCGACACGAGGCGCTTCTGATAGG 80
DB 914 AGACTCTGTGAGAAACGCTGACGAGACGAGGCCCATTAAGCTCCAGCTGCCA 973
QY 81 GGTGAGCGGGCGGACTGCGGAGGAGTGCACCGTGTGTGAGAAATCATGAGATTGCT 140
DB 974 GGTGACAGAGCTGATCAACCAAGTGAAGTCTCAGCTGGCAGAGATCCGCTGTGACCTGGA 1033
QY 141 GGGACAGAACGAGGTGGAACAGCGGACGCGGAAGTGTATCTTGAAGCAGACAGGTT 200
DB 1034 GCGGAGAAACGAGAGATCAAGGTGTCTGTGACGTGCGCGCTGAGATGTGAGAT 1093
QY 201 CTACAGGTCCTGA 214
DB 1094 CAACACTACCGGA 1107

```

```

RESULT 22
US-09-488-725B-3800/C
; Sequence 3800, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 3800
; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4309)...(2761)
; OTHER INFORMATION: similar to g11054874 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-3800

```

```

Query Match 4.1%; Score 34; DB 1; Length 4308;
Best Local Similarity 51.3%; Pred. No. 15;
Matches 79; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
QY 25 TCGAGAGCCCGCGCGGAGGCGGACCGTCCGACACGAGGCGCTTCTGATAGGAGTG 84
DB 3945 TTCGAGAGAGAGTGTGGGAGAGCGCGCGGCGGACGAGCGGCGCTGTGGAGAGTGAGC 3886

```

```

QY 85 AGCGGCGGACTGCGGAGGAGTGCACCGTGTGTGAGAAATCATGAGATTGCTGGA 144
DB 3885 AGCAGCGGCGGAGAGAGATCAAGCTTCAAGATGCGACAGGCGCTGAGAGAGCTGCGAGC 3826
QY 145 CAGAACGAGGTGGAACAGCGGCGGACCGGAAGGTGG 178
DB 3825 CAGCAGGAGAGAGAGTGGCGGCTCTACAAAGCTGG 3792

```

```

RESULT 23
US-09-488-725B-6591/C
; Sequence 6591, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 6591
; LENGTH: 4454
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4270)...(2550)
; OTHER INFORMATION: similar to g13882255 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-6591

```

```

Query Match 4.1%; Score 34; DB 1; Length 4454;
Best Local Similarity 52.1%; Pred. No. 15;
Matches 76; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
QY 121 GAGAAATCATGAGTGTGTGGAACAAGAGGTGGAACAGCGGCGGAGGAGTGTC 180
DB 3997 GAGGAGCTCCGGAACCTGGAAGAAACCAACGCGGAGATGCTCGGCGAGGCTGAGC 3938
QY 181 AATCGAGCGAGAGAGGTTCTACAAAGTCTGAGCGGACGAGCAGAGGCGCAAGGCTTG 240
DB 3937 CGGAGCGGCGGAGGAGTGAAGAGCAAGAGTGCAGAGAGTGTGAAGGCCAGC 3878
QY 241 AAAGACAGTACATTTGATACCATCC 266
DB 3877 ACCGAGAGCAGATGGCTCAGCAGCC 3852

```

```

RESULT 24
US-09-488-725B-5104
; Sequence 5104, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 5104
; LENGTH: 1746
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (693)...(1629)
; OTHER INFORMATION: similar to g13851703 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-5104

Query Match          4.0%; Score 33.6; DB 1; Length 1746;
Best Local Similarity 46.6%; Pred. No. 19;
Matches 108; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 40 CCGGAGCGCCACCGCTCCGACACGAGCGCCCTTCTGATGAGGGGTGAGCGGCGCACTGCC 99
DB 426 CTGGTGGGCGACTGGCGGCGCTGGGCTGTGCTGCTGCTGCTGGGCTATCGGCTGCC 485

QY 100 AGCGGAGTGCACCGCTGTGTGAGAAATCATGAGATTGTGGGACAGAAAGAGGTGGA 159
DB 486 GCGGTTGGCGCGCGGCGCGGCAAAAGCGGAGAGCCCGCCCGAAGCGGAGGCG 545

QY 160 CAGCGGCGAGCGGAGAGGTGTCTATCTGAGCCAGAGCAGGTTCTTACAGGTTCTTGA 219
DB 546 GCGGCGGTGGCGGCGCGCGCGCCCGACGACCTGGGCTTGTGAGAAATCTCCGAGCGAG 605

QY 220 GAGGAGAGGCGCAAGGCGCTTGAAAGAGAGTAAATTTTGAATCCAGATG 271
DB 606 GAAAGAAAGAAAGAACCGGAGAACTGTCCGAAAGCCCAACCAATG 657

RESULT 25
US-09-488-725B-8011

```

```

; Sequence 8011, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 8011
; LENGTH: 2586
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (156)...(2451)
; OTHER INFORMATION: similar to g1509241 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-8011

Query Match          4.0%; Score 33.6; DB 1; Length 2586;
Best Local Similarity 47.2%; Pred. No. 18;
Matches 102; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

QY 39 GCGGAGCGCCGACCGCTCCGACACGAGCGCCCTTCTGATGAGGGGTGAGCGGCGCACTGC 98
DB 1310 GCGGCGCCACGAGCCCGCTCCGAGAGCCAGGCCGAAAGGGGCGAAGGCGCTCCGA 1369

QY 99 CAGCGGAGTGCACCGCTGTGTGAGAAATCATGAGATTGTCTGGGACAGAAAGAGGTGA 158
DB 1370 GAAAGCCAGCGCGCGCTGTGCGGCATGTTCTTCTGAGAGAAAGAGGCGGCGACT 1429

QY 159 ACAGCGGACGAGAGAGGTGTCTATCTGAGCCAGAGCAGGTTCTTACAAAGTCTTGACGC 218
DB 1430 GCAAGAGAGCGGCGCTGAGCTTCCGAGAGCGAGCTGACCCGCTGCGCCGAATGTG 1489

QY 219 AGAGCAGAAAGCCAAAGGCTTGAAGAGCAGTACA 254
DB 1490 GAACGACCTGTGTGAGAAAGAAAGGCGCAAGTACA 1525

RESULT 26
US-09-488-725B-8980
; Sequence 8980, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast

```

```

; APPLICANT: Ankura Sinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dramac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 8980
; LENGTH: 1108
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (693)...(855)
; OTHER INFORMATION: similar to gi4809026 in the genepept database release 114,
; US-09-488-725B-8980

Query Match
Best Local Similarity 5.0%; Score 33; DB 1; Length 1108;
Matches 63; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 443 TCCGAGACATGTTCCACCTGCGCTCTTCGTGACACCGACTCCGACGTGAGCTGTCTC 502
DB 982 TCCTGCATATGTTTTCACAGGCTCTGAGGCTGACCTCGGCTGGAGCTCCAGGTGAAG 1041

QY 503 GAAGAATTCTCCGGACGTGCGCCGAGGAGGAGGACCTGAGCAGATTGTGACG 555
DB 1042 AAAAATCTGTCTCGAAGTGACACAGGAGACGTCAGCAGCTCTGTAGG 1094

RESULT 27
US-09-516-448-877/C
; Sequence 877, Application US/09516448
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/516,448
; CURRENT FILING DATE: 2000-02-29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 877
; LENGTH: 3285
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(3285)

```

```

; OTHER INFORMATION: n = A,T,C or G
US-09-516-448-877

Query Match
Best Local Similarity 4.0%; Score 33; DB 3; Length 3285;
Matches 132; Conservative 0; Mismatches 165; Indels 0; Gaps 0;

QY 27 CGAGAGCCCGCGGAGGCGGACCGTCCGACACAGCGGCGCTTCCTGATAGGGGTGA 86
DB 2149 CGACATGAGCGCCAGGAGCTCTGTGAGCAACAGTGTGACGCTGAGGAGTGGC 2090

QY 87 CGCGGCACTGCGGAGGAGTGCACCGTGTGAGAAAGATGAGTGTGAGGACA 146
DB 2089 CGACAAACAGCGCGGACAAACAGAGTTGTGAGAGCATGTACAAAGATTCTGATCCT 2030

QY 147 GAACGAGTGAACAGCGGACGGAAGTGTATCTTGAGCCAGACAGTTTCAAA 206
DB 2029 GGGGGCCAAACTGACCCGACGCTGAAGCTGAGAGCTTACCAACAAAGGAATGAC 1970

QY 207 GGTCTGACGCGGACGACAAAGGCCCTTGAAGACACTTAATTTGACCATTC 266
DB 1969 GCCGCTGCTGTGCGACAGAGACCGGGAAGATCGGGTCTTGGCTTAATTTCTCAGCG 1910

QY 267 AGATGCTTTGATTAATGATTGTGATGACAGACTTGAAGAACATGCTGAGGGCAA 323
DB 1909 GGAATCCAGAGACCCGAGTGCAGACCTGTCCAGAACTTACCGAGTGGGCTTA 1853

RESULT 28
US-09-235-076-2081
; Sequence 2081, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: HySeq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2081
; LENGTH: 478
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(478)
; OTHER INFORMATION: n = A,T,C or G
; US-09-235-076-2081

Query Match
Best Local Similarity 3.9%; Score 32.8; DB 4; Length 478;
Matches 94; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

QY 26 GCGAGAGCCCGCGGAGGCGGACCGTCCGACACAGGCGCTTCCTGATAGGGGTGA 85
DB 222 GCGTAGAGTGCCTTACAGACACCCCTGTGCTCACAGGGGCGACACCCCAAGCCCTGC 281

QY 86 GCGCGGACACTGCGGAGGAGTGCACCGTGTGAGAAAGATCATGAGATTGCTGGAC 145
DB 282 CAGCCCTGCGCCCACTGCGAGGACCAAGGAGGAGGCTGACTCATGACGGGCTGA 341

QY 146 AGAAGAGGTGAACAGCGGACGGAAGTGTGATCTTGAGCCAGACAGATTGTACA 205
DB 342 GGGAGGATTCAGAGAGCTGAGAGCCCAAGATGATGTATGCGGAGAGGCTGAGACAA 401

QY 206 AGGTCTGACGCA 221
DB 402 AGGACTGAGAGCGCA 417

RESULT 29
US-09-488-725B-9186

```

```

; Sequence 9186, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 9186
; LENGTH: 773
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (107)...(674)
; OTHER INFORMATION: similar to g11136404 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
; US-09-488-725B-9186

Query Match          3.9%; Score 32.8; DB 1; Length 773;
Best Local Similarity 52.1%; Pred. No. 28;
Matches 73; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 93 CACTGCCAGCGGGAAGTCGACCGGTGTGTGAGAGATCATGTGAGTTCGTGGACAGAAACA 152
DB 509 CAGTCCGGGACCTGTGTCACGTGCGGAGACAGATGCGGGTCCCTGCGGAAGCTGCG 568
QY 153 GATGGAACAGCGGAGCGAGAGTGTGATCTGTGAGCAGACAGAGTTCATCAAGTCTCT 212
DB 569 GCAGCTGGAGAGAGAGAGTGTGAGTGTGATCTGTGCTCTCAAGTGAAGCTCTCGAGCTTCA 628
QY 213 GACGCGACAGCAGAGAGGCCA 232
DB 629 GGAGGAAAAGCGGACGCTCA 648

RESULT 30
US-09-488-725B-10006
; Sequence 10006, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained

```

```

; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 10006
; LENGTH: 1573
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (229)...(713)
; OTHER INFORMATION: similar to g15926738 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
; US-09-488-725B-10006

Query Match          3.9%; Score 32.8; DB 1; Length 1573;
Best Local Similarity 54.0%; Pred. No. 27;
Matches 67; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

QY 148 AACGAGGTGAGACGCGGACCGGAAGTGTGATCTGTGAGCAGACAGAGTTCATCAAG 207
DB 1285 AAGGAGGAGGCCCTGAGGAGAGAAAGCTGAGAGCTGACGACGCAACGTCAGTGCAGAG 1344
QY 208 GTCTTGACGGCAAGACGAAAGGCCCTTGAAGAGACATCAATTGACCATCCA 267
DB 1345 ACCTCGTCCGAGAGGAGGAAAGCAAGCAAGAAAGGACGAGCCCAACGGGACCAATCA 1404
QY 268 GATG 271
DB 1405 GTTG 1408

RESULT 31
US-09-488-725B-3552/C
; Sequence 3552, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13

```

```

; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 3552
; LENGTH: 4367
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4368)...(707)
; OTHER INFORMATION: similar to gi4240217 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-3552

```

Query Match 3.9%; Score 32.8; DB 1; Length 4367;

Best Local Similarity 48.0%; Pred. No. 26; Matches 94; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

```

QY 26 GCGAGAGCCCGCGCGAGGCGGACCGTCCGACACGCGCCCTTCCTGATAGGGGTGA 85
DB 1909 GCCTGAGTGCTCTTCAGGACACCTCTGCTCCACGAGGGGCCACCCCAAGGCCCTGC 1850
QY 86 GCGCGCGCACTGCGACGCGGAGTCCACCGTGTGTGAGAAATCATGGAAGTTGCTGGAC 145
DB 1849 CACCCCTGCGCCCACTGCGACGCGGACCCAGGAGAGGCTGACTCCATACGCGGCTGA 1790
QY 146 AGAACGAGGTGGAACGCGGACGCGGAGGTGTCATCTGAGCCAGGAGTTTCTACA 205
DB 1789 GGGAGGCGATCCAGAGCTGAGAGCCCAATGATGTCTATCGGAGAGCTGGACACA 1730
QY 206 AGGTCTGACGGCAGA 221
DB 1729 AGGACCTGAGGGCGA 1714

```

```

RESULT 32
US-09-488-725B-3745/c
; Sequence 3745, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26

```

```

; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 3745
; LENGTH: 4372
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4373)...(713)
; OTHER INFORMATION: similar to gi4240217 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-3745

```

Query Match 3.9%; Score 32.8; DB 1; Length 4372;

Best Local Similarity 48.0%; Pred. No. 26; Matches 94; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

```

QY 26 GCGAGAGCCCGCGCGAGGCGGACCGTCCGACACGCGCCCTTCCTGATAGGGGTGA 85
DB 1914 GCCTGAGTGCTCTTCAGGACACCTCTGCTCCACGAGGGGCCACCCCAAGGCCCTGC 1855
QY 86 GCGCGCGCACTGCGACGCGGAGTCCACCGTGTGTGAGAAATCATGGAAGTTGCTGGAC 145
DB 1854 CACCCCTGCGCCCACTGCGACGCGGACCCAGGAGAGGCTGACTCCATGAGGGGCTGA 1795
QY 146 AGAACGAGGTGGAACGCGGACGCGGAGGTGTCATCTGAGCCAGGAGTTTCTACA 205
DB 1794 GGGAGGCGATCCAGAGCTGAGAGCCCAATGATGTCTATCGGAGAGCTGGACACA 1735
QY 206 AGGTCTGACGGCAGA 221
DB 1734 AGGACCTGAGGGCGA 1719

```

```

RESULT 33
US-09-488-725B-3680/c
; Sequence 3680, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13

```

PRIOR APPLICATION NUMBER: US 09/179,473  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: US 09/181,430  
 PRIOR FILING DATE: 1998-10-28  
 PRIOR APPLICATION NUMBER: US 09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 PRIOR APPLICATION NUMBER: US 09/234,611  
 PRIOR FILING DATE: 1999-01-22  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 10289  
 SOFTWARE: pc\_ct\_genes Version 1.01  
 SEQ ID NO 3680  
 LENGTH: 4410  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(441)  
 OTHER INFORMATION: n = a,t,c or g  
 NAME/KEY: misc feature  
 LOCATION: (441)...(749)  
 OTHER INFORMATION: similar to gi4240217 in the genepept database release 114,  
 OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
 US-09-488-725B-3680

Query Match 3.9%; Score 32.8; DB 1; Length 4410;  
 Best Local Similarity 48.0%; Pred. No. 26;  
 Matches 94; Conservative 0; Mismatches 102; Indels 0; Gaps 0;

Qy 26 GCGAGAGCCCGCGCGGAGCCGACCGTCCGACACAGCGGCCCTTCTGTATAGGGGTGA 85  
 Db 1952 GCTGAGGTGCTTTCAGACACCTCTCTCCACACAGGGGCCACACCCCAAGCCCTGC 1893  
 Qy 86 GCGGCGGCACTGCCAGCGGGAAGTCGACCGTGTGAGAGATGAGATTGCTGGGAC 145  
 Db 1892 CAGCCCTGCCCCCAACTGAGAGGCAACCGAGGAGAGGCTGATGCATGACGGGGCTGA 1833  
 Qy 146 AGAAGAGGTGAGAACAGCGGCAAGGAGGTGATCTTGAACCAAGACAGTTTCTCA 205  
 Db 1832 GCGAGCGCATCAGAGGCTGAGAGGCCAGATGATGATCATCGGAGAGCTGGGACACA 1773  
 Qy 206 AGTCTGACGAGCAGA 221  
 Db 1772 AGAAGCTGAGGGCCA 1757

RESULT 34  
 US-09-235-076-32  
 Sequence 32, Application US/09235076  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/235,076  
 CURRENT FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FASTSEQ for Windows Version 3.0  
 SEQ ID NO 32  
 LENGTH: 478  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1)...(478)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-235-076-32

Query Match 3.9%; Score 32.4; DB 4; Length 478;  
 Best Local Similarity 55.3%; Pred. No. 35;  
 Matches 63; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 121 GAGAGATCATGAGTTGCTGAGCAGAAAGAGGTGAAACAGCGGAGCGGAAGTGTTC 180  
 Db 103 GAGAAAGCAGAGAGCTGACAGGCGCTGCGGAGGGGCTATCCGGAGACAGAGGAG 162  
 Qy 181 ATCTGAGCCAGACAGAGTTCTTCAAGTCTTGAACGACAGAGCAAGGCCAAG 234  
 Db 163 GCGGCGGACACCCCAAGATCAAGAGAGGCGAGCTGACGCGCTGAGGCCACAG 216

RESULT 35  
 US-09-488-725B-8030/c  
 Sequence 8030, Application US/09488725B  
 GENERAL INFORMATION:  
 APPLICANT: Yuhua T. Tang  
 APPLICANT: Ankura Sunku  
 APPLICANT: Ankura Sunku  
 APPLICANT: Radoje T. Drmanac  
 TITLE OF INVENTION: Novel Contigs Obtained  
 FILE REFERENCE: 784  
 CURRENT APPLICATION NUMBER: US/09/488,725B  
 CURRENT FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US 09/004,182  
 PRIOR FILING DATE: 1998-01-07  
 PRIOR APPLICATION NUMBER: US 09/034,341  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 09/045,400  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: US 09/321,214  
 PRIOR FILING DATE: 1998-05-26  
 PRIOR APPLICATION NUMBER: US 09/131,598  
 PRIOR FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: US 09/170,294  
 PRIOR FILING DATE: 1998-10-13  
 PRIOR APPLICATION NUMBER: US 09/179,473  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: US 09/181,430  
 PRIOR FILING DATE: 1998-10-28  
 PRIOR APPLICATION NUMBER: US 09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 PRIOR APPLICATION NUMBER: US 09/234,611  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 10289  
 SOFTWARE: pc\_ct\_genes Version 1.01  
 SEQ ID NO 8030  
 LENGTH: 1749  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (1625)...(299)  
 OTHER INFORMATION: similar to g15734486 in the genepept database release 114,  
 OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
 US-09-488-725B-8030

Query Match 3.9%; Score 32.4; DB 1; Length 1749;  
 Best Local Similarity 58.2%; Pred. No. 33;  
 Matches 57; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 131 TGAAGTTGCTGAGCAGAGAGGTTGGAACAGCGGAGCGGAAGGTGATCTTGAGCC 190  
 Db 943 TGAAGTTGCAAGCGGAGAGAGGAGGAGAGAGCTGAGAGCGGAGCTGCGCTGCCGCCA 884  
 Qy 191 AGAAGAGTTCTTCAAGGTTCTTGAACGACAGAGCAGAG 228  
 Db 883 CGAGAGAGCGCCGACCAAGAGATCAATTCCAGAG 846

RESULT 36  
 US-09-488-725B-906  
 Sequence 906, Application US/09488725B

```

; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sinks
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/161,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 906
; LENGTH: 1955
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (17)...(1664)
; OTHER INFORMATION: similar to g13043634 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
; US-09-488-725B-906

Query Match      3.3%; Score 32.4; DB 1; Length 1955;
Best Local Similarity 55.3%; Pred. No. 33;
Matches 63; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 121 GAGAGATCATGAGTTGCTGGAGACAGAGGTGGAACGCGCGCGGAGAGTGTTC 180
DB 80 GAGAGAGACAGAGGAGCTGCGAGCGCTGCGGAGGCTCATCCGCGACGACGAGGAG 139

QY 181 ATCTGAGCGAGACAGTCTCTACAGGTCTGACGCGCAGAGCAAGAGCCAG 234
DB 140 GCGGCGCGACCGCCCAAGATCAAGAGCGGAGCTGACGCGCTGCGAGCGAG 193

RESULT 37
US-09-488-725B-1497
; Sequence 1497, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sinks
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182

```

```

; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/161,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 1497
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)...(550)
; OTHER INFORMATION: similar to g1380991 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
; US-09-488-725B-1497

Query Match      3.3%; Score 32.3; DB 1; Length 547;
Best Local Similarity 48.0%; Pred. No. 36;
Matches 120; Conservative 0; Mismatches 127; Indels 3; Gaps 1;

```

```

QY 398 ACCTGCTCTCTTGGAGGAGATCTTGTTCTACAGCCAGAGATCCGGAGATGTTCC 457
DB 52 ACATTCGTGTTGTTGTTGGGATGTCCTGTTCT---CCGTGATCGCGCTCGAGGCTC 108

QY 458 ACCTGCGCCTCTTCTGTCGACACCGACTCCGACGTGCTGTCGAAAGTTCCTCGGG 517
DB 109 GCTCCAGAGAGCTCTGCGCATGTGAGCGGACCGCGGCTGCGACGCCA 168

QY 518 ACCTGCGCGGAGGAGGACCTGAGCAGATTCTGACGACGATGATGATGATCCACGAG 577
DB 169 AGTTGGGACGCTGCGGAGACCTGAGGCCATCTGACAGGCGCTGAGACCATCTGAGAGG 228

QY 578 CGGCTTTCGAGAGTTCCTGCTGCGACCAAGAAAGTATGCGATGATATCCACGAG 637
DB 229 TGGTCTACACCAAGCTTCAACGCGCTTTCGCAAGCCATCGGCTGTTGAGAGGCGCAGAG 288

QY 638 GAGTGACAA 647
DB 289 GTCTGGGCCA 298

RESULT 38
US-09-488-725B-4795
; Sequence 4795, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sinks
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182

```





```

Db      1985 GCGTGAAGCGGAGCTGGAGCAGCGCGGAGCGCCGGGTGTGTGAGCAAGGGCTGCGAGG 2044
Qy      86 GCGCGCGCACTGCCAGCGGGAAGTTCACCGTGTGTGAAAGATCATGAGATTGCTGGAGC 145
Db      2045 CCGGCGCCCTCGCGCGCCAGTACTCGGCGCCAGATCGAAGACCTGCAGGTGAAGCTTGACGC 2104
Qy      146 AGAAGCAGGTGAAACAGCGGAGCGGAGGTGTCTATCTGAGCCAGAGCAAGGTTCTACA 205
Db      2105 ACCCGAGGCGGAGCGGAGAGCGCTGTGGGCGGACCTGTGCGGAGCGCGAGGCCCGAGG 2164
Qy      206 AGGTCTGACGCGGAG 220
Db      2165 AGCAGCTGGAGAAAG 2179

```

RESULT 41  
US-09-235-076-22668

; Sequence 22668, Application US/09235076  
; GENERAL INFORMATION:

```

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22668
; LENGTH: 493
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-235-076-22668

```

Query Match 3.8%; Score 31.4; DB 4; Length 493;  
Best Local Similarity 51.0%; Pred. No. 56;  
Matches 74; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

```

Qy      551 TGACGAGTACACCACTTGTGTAAGCGGCTTCGAGAGTTCTGCTCCGCAAAAGA 610
Db      237 TCAGAGAGAAAGTCAACGACAGAACCCACACGCTGTGTATGCGCTGAGGTCAATGG 236
Qy      611 AGTATGCCGATGTGATCATCCACGAGAGTGGACATATATGTCATCACTGATCG 670
Db      297 AATCTGTGTAAGAACTGTGGCCAGACATTTATGATGAGTGCCCAAGACAGCCA 356
Qy      671 TGCAGACATCCAGACATTTGAA 695
Db      357 TGAAGAGGCTGAAGACCTGCTGAA 381

```

RESULT 42

US-09-235-076-24688  
; Sequence 24688, Application US/09235076  
; GENERAL INFORMATION:

```

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24688
; LENGTH: 496
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(496)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-24688

```

```

Query Match 3.8%; Score 31.4; DB 4; Length 496;
Best Local Similarity 48.1%; Pred. No. 56;
Matches 89; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
Qy      394 GCGAGCGTGTGTTGTTGAGGCGCATCTGGTGTCTTACAGCCAGAGATCCGGGACATG 453
Db      112 GTGAGAGAGCTCTGTACGAAAGCCCTGAGCGGTACTCCGCTCAAGTCTTCATCACC 171
Qy      454 TTCCACTTGGGCTCTTCTTGAGACACGACTCCGAGTCAAGGCTGTCTCGAAGATTCTC 513
Db      172 CAGCAGCTTCAAGCTGTGTGAGCAGGCTGACCAATCTCTTCTTGAGAGAGCGGCTATC 231
Qy      514 CCGAGCGTGCAGCGGAGGAGGAGCTGAGCAGATTTGACGCGAGTACACACCTTGCTG 573
Db      232 CCGAGGCGGGAACCAACGACGAGCTCATGAGAAAAAGGGGTGCTACTGGGCGCATGTG 291
Qy      574 AAGCC 578
Db      292 CAGGC 296

```

RESULT 43

US-09-488-725B-6522/C  
; Sequence 6522, Application US/09488725B  
; GENERAL INFORMATION:

```

; APPLICANT: Yuhua T. Tang
; APPLICANT: Ankura Slinka
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dimaac
; TITLE OF INVENTION: Novel Configs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22

```

Remaining Prior Application data removed - See file wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 10289  
; SOFTWARE: pc\_ct\_genes Version 1.01  
; SEQ ID NO 6522  
; LENGTH: 910  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (878)...(263)  
; OTHER INFORMATION: similar to g1196436 in the genepet database release 114,  
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters  
US-09-488-725B-6522

Query Match 3.8%; Score 31.4; DB 1; Length 910;  
Best Local Similarity 56.2%; Pred. No. 55;  
Matches 59; Conservative 0; Mismatches 46; Indels 0; Gaps 0;



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

# OM nucleic - protein search, using frame\_plus\_n2p model

Run on: December 12, 2003, 10:39:44 ; Search time 3.5 Seconds  
(without alignments)  
1605.652 Million cell updates/sec

Title: us-09-896-522-1  
Perfect score: 3034.399410625  
Sequence: 1 ggcgggctgcctccgcctcc.....ccagcttgcggggccag 1624

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.1  
Ygapop 10.0 , Ygapext 0.1  
Fgapop 6.0 , Fgapext 0.1  
Delop 6.0 , Delext 0.1

Searched: 4515 segs, 1730228 residues  
Total number of hits satisfying chosen parameters: 9030

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODE=frame+ n2p.model -DEV=xlh -Q=us-09-896-522-1 -DB=\*pep -SUFFIX=pco  
-OUT=align1\_pep -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1  
-END=-1 -MATRIX=Bloum62 -TRANS=human40.cdi -LIST=45 -DOCALLIGN=700  
-THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pco  
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -ICPU=3 -NO\_XLPRX  
-THREDS=1 -DSBPOOL=100 -LONGLOG -DEV TIMEDOUT=120 -WARN TIMEDOUT=30  
-YGAPOP=0.1 -YGAPEXT=0.1 -YGAPOF=6 -YGAPEXT=0.1 -YGAPOP=10  
-YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database :  
\*pep:\*  
1: /home/sdavid/david-tmp/dectemp/swops522/US09488725A.pep:\*  
2: /home/sdavid/david-tmp/dectemp/swops522/6579708.pep:\*  
3: /home/sdavid/david-tmp/dectemp/swops522/PCUUS0005988.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1551	51.1	296	US-09-488-725A-6219	Sequence 6219, Ap
2	1450	47.8	277	US-09-488-725A-2647	Sequence 2647, Ap
3	1363	44.9	260	US-09-536-647-2	Sequence 2, Appl1
4	1325	43.7	277	US-09-536-647-3	Sequence 3, Appl1
5	969.8	32.0	337	PCT-US00-05988-1160	Sequence 1160, Ap
6	961.6	31.7	335	US-09-488-725A-5411	Sequence 5411, Ap
7	960.2	31.6	261	US-09-488-725A-1839	Sequence 1839, Ap
8	501.7	16.8	4618	US-09-488-725A-2188	Sequence 2188, Ap
9	494	16.5	1454	US-09-488-725A-3367	Sequence 3367, Ap
10	492.6	16.5	2044	US-09-488-725A-2369	Sequence 2369, Ap
11	492.6	16.5	2044	US-09-488-725A-5941	Sequence 5941, Ap
12	487.8	16.3	2626	US-09-488-725A-5708	Sequence 5708, Ap
13	469.2	15.7	1409	US-09-488-725A-3457	Sequence 3457, Ap
14	462.7	15.2	1078	US-09-488-725A-3157	Sequence 3157, Ap
15	462.6	15.4	954	US-09-488-725A-2519	Sequence 2519, Ap
16	460.6	15.4	954	US-09-488-725A-6091	Sequence 6091, Ap
17	458.9	15.3	722	US-09-488-725A-2174	Sequence 2174, Ap

C 18	458.5	15.3	2063	1	US-09-488-725A-3209	Sequence 3209, Ap
C 19	456.4	15.2	1565	1	US-09-488-725A-5990	Sequence 5990, Ap
C 20	455	15.2	1502	1	US-09-488-725A-2418	Sequence 2418, Ap
C 21	451.3	14.9	4618	1	US-09-488-725A-2188	Sequence 2188, Ap
C 22	450.7	14.9	1409	1	US-09-488-725A-3457	Sequence 3457, Ap
C 23	448.8	14.8	1588	1	US-09-488-725A-2440	Sequence 2440, Ap
C 24	447.5	15.0	839	1	US-09-488-725A-5469	Sequence 5469, Ap
C 25	447.3	14.9	1233	1	US-09-488-725A-6059	Sequence 6059, Ap
C 26	446.4	14.9	1121	1	US-09-488-725A-2638	Sequence 2638, Ap
C 27	446.4	14.9	1124	1	US-09-488-725A-6210	Sequence 6210, Ap
C 28	446.4	14.9	1124	1	US-09-488-725A-6211	Sequence 6211, Ap
C 29	446.4	14.7	1672	1	US-09-488-725A-2222	Sequence 2222, Ap
C 30	446.2	14.9	1224	1	US-09-488-725A-2487	Sequence 2487, Ap
C 31	445	14.7	2044	1	US-09-488-725A-2369	Sequence 2369, Ap
C 32	444.5	14.6	1659	1	US-09-488-725A-5794	Sequence 5794, Ap
C 33	443.4	14.8	1551	1	US-09-488-725A-6012	Sequence 6012, Ap
C 34	442.2	14.6	751	1	US-09-488-725A-2653	Sequence 2653, Ap
C 35	442.2	14.6	773	1	US-09-488-725A-6225	Sequence 6225, Ap
C 36	442	14.8	1588	1	US-09-488-725A-2440	Sequence 2440, Ap
C 37	441.9	14.6	1551	1	US-09-488-725A-6012	Sequence 6012, Ap
C 38	441.9	14.6	2044	1	US-09-488-725A-5941	Sequence 5941, Ap
C 39	439	14.7	825	1	US-09-488-725A-1897	Sequence 1897, Ap
C 40	438.9	14.5	1454	1	US-09-488-725A-3367	Sequence 3367, Ap
C 41	438.6	14.7	1154	1	US-09-488-725A-2639	Sequence 2639, Ap
C 42	435.6	14.6	1078	1	US-09-488-725A-3157	Sequence 3157, Ap
C 43	435.3	14.5	987	1	US-09-488-725A-2372	Sequence 2372, Ap
C 44	435.3	14.5	1086	1	US-09-488-725A-5944	Sequence 5944, Ap
C 45	435.3	14.5	1672	1	US-09-488-725A-2222	Sequence 2222, Ap

## ALIGNMENTS

RESULT 1  
US-09-488-725A-6219  
; Sequence 6219, Application US/09488725A  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq Inc  
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
; FILE REFERENCE: 784FLPCT  
; CURRENT APPLICATION NUMBER: US/09/488, 725A  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US/09/488, 725  
; PRIOR FILING DATE: 2000-01-21  
; PRIOR APPLICATION NUMBER: US09/552, 317  
; PRIOR FILING DATE: 2000-04-25  
; PRIOR APPLICATION NUMBER: US09/598, 042  
; PRIOR FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: US09/620, 312  
; PRIOR FILING DATE: 2000-07-19  
; PRIOR APPLICATION NUMBER: US09/653, 450  
; PRIOR FILING DATE: 2000-08-31  
; PRIOR APPLICATION NUMBER: US09/662, 191  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: US09/693, 036  
; PRIOR FILING DATE: 2000-10-19  
; PRIOR APPLICATION NUMBER: US09/727, 344  
; PRIOR FILING DATE: 2000-11-29  
; NUMBER OF SEQ ID NOS: 7144  
; SOFTWARE: pc\_fl\_genes\_b Versions 1.0  
; SEQ ID NO 6219  
; LENGTH: 296  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; US-09-488-725A-6219

Alignment Scores:  
Pred. No.: 1 64e-22 Length: 296  
Score: 1551.00 Matches: 296  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 51.11% Indels: 0  
DB: 1 Gaps: 0

us-09-896-522-1 (1-1624) x US-09-488-725A-6219 (1-296)

```

QY      37 GCCGGGCCCCGGGAGAGGGGGCGGGGACCCGATGCCGGAGCGGAGCCGAGATG 96
Db      1 AlaGlyProGlyGlyGlyAlaGlyAlaGlyThrArgCysAlaGlyAlaGlyAlaGlyMet 20
QY      97 GCTTCGGCGGGAGCGGAGAGCTGGAGAGCCCGCGCGCGGAGCGGAGCCGTCGCGACAG 156
Db      21 AlaserAlaGlyGlyGlyAlaSerCysGlySerProAlaProGlyAlaAlaSerProHisGln 40
QY      157 CGGCGCTTCCTGATAGGGGTGAGCGCGCGCATCTCCAGCGGAGAAAGTCAGCCGTGTGAG 216
Db      41 ArgProPheLeuIleGlyAlaSerGlyGlyThrAlaSerGlyLysSerThrValCysGlu 60
QY      217 AAGATCATGAGTTGCTGGGACAGAACGAGGTGGAAACGCGGACCGGAGAGTGTGATC 276
Db      61 LysIleMetGlyLeuLeuGlyGlyAlaSerGlyAlaGlyGlyAlaGlyValAlaIle 80
QY      277 CTGACGACGAGCAGAGTTCTACAGAGTCTGACGCGGACGAGAGCGGACCGCTTGAAA 336
Db      81 LeuSerGlnAspArgPheThrLysValLeuThrAlaGlyGlyAlaLysAlaLeuLys 100
QY      337 GACAGATACAAATTTGACCATCCAGATGCCCTTGATTAATGATTTGATGCACAGACTCTG 396
Db      101 GlyGlnIleThrAsnPheAspHisProAspAlaPheAspAsnAlaLeuMetHisArgThrLeu 120
QY      397 AAGAACATCGTGGAGGGGCGGAAACGGTGGAGGTGCCGACCTTATGATTTTGTACACACTCA 456
Db      121 LysAsnIleValGlyGlyLysThrValGlyAlaProThrLysAspPheValThrHisSer 140
QY      457 AGGTACACAGAGACACAGGTGTCTACCTCGGACGCGGTCTGTGTTGAGGGATCTTG 516
Db      141 ArgLeuProGlyIleThrValValIleProAlaAspValValLeuPheGlyGlyIleLeu 160
QY      517 GTGTTCTACACGACGAGATCCGGGACATGTTCCACTGCGCTTTCGTGGACACCGAC 576
Db      161 ValPheThrSerGlnGlyIleArgAspMetPheHisLeuArgLeuPheValAspThrAsp 180
QY      577 TCCGACGTCAGGCTGTCTCGAAGAGTTTCCGGGACGTCGCCCGGAGGAGGAGCACTGGAG 636
Db      181 SerAspValArgLeuSerArgArgValLeuArgAspValArgArgGlyArgAspLeuGlu 200
QY      637 CAGATTCGACGACGATACACACCTTCGTGAAGCGGCTTCGAGAGTCTTCGCTGCGCG 696
Db      201 GlnIleLeuThrGlnIleThrThrPheValLysProAlaPheGlyGlyLysLeuPro 220
QY      697 ACAAGAAGTATGCCGATGATCATCCACGAGAGTGAACAATATGTTGCCATCAAC 756
Db      221 ThrLysLysThrAlaAspValIleIleProArgGlyValAspAsnMetValAlaIleAsn 240
QY      757 CTGATCGTGCAGCATTCAGACATTTGATGTGACATCTGCAATGGCACCAGGA 816
Db      241 LeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysValYstPheHisArgGly 260
QY      817 GGGTCACATGGGCGGAGCTACAGCGGACCTTTCTGAGCCGAGGAGACACCTGGAGATG 876
Db      261 GlySerAsnGlyArgSerThrLysArgThrPheSerGlyProGlyAspHisProGlyMet 280
QY      877 CTGACCTTGCGCAACGCTCATTTGGAGTCCAGACGAGACCCGAC 924
Db      281 LeuThrSerGlyLysArgSerHisLeuLysSerSerArgProHis 296

```

RESULT 2  
 US-09-488-725A-2647  
 ; Sequence 2647, Application US/09488725A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq Inc  
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 ; FILE REFERENCE: 784FLEPCT  
 ; CURRENT APPLICATION NUMBER: US/09/488, 725A  
 ; PRIOR FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: US/09/488, 725  
 ; PRIOR FILING DATE: 2000-01-21

; PRIOR APPLICATION NUMBER: US09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: US09/598,042  
 ; PRIOR FILING DATE: 2000-06-20  
 ; PRIOR APPLICATION NUMBER: US09/620,312  
 ; PRIOR FILING DATE: 2000-07-19  
 ; PRIOR APPLICATION NUMBER: US09/653,450  
 ; PRIOR FILING DATE: 2000-08-31  
 ; PRIOR APPLICATION NUMBER: US09/662,191  
 ; PRIOR FILING DATE: 2000-09-14  
 ; PRIOR APPLICATION NUMBER: US09/693,036  
 ; PRIOR FILING DATE: 2000-10-19  
 ; PRIOR APPLICATION NUMBER: US09/727,344  
 ; PRIOR FILING DATE: 2000-11-29  
 ; NUMBER OF SEQ ID NOS: 7144  
 ; SOFTWARE: pc\_files\_versions 1.0  
 ; SEQ ID NO 2647  
 ; LENGTH: 278  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-488-725A-2647

Alignment Scores:  
 Pred. No.: 1,2e-20 Length: 277  
 Score: 1450.00 Matches: 277  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 47.79% Indels: 0  
 DB: 1 Gaps: 0

us-09-896-522-1 (1-1624) x US-09-488-725A-2647 (1-277)

```

QY      94 ATGCTTCGGCGGGAGCGGAGAGCTGGAGAGCCCGCGGAGCGGACCGTCGCGAC 153
Db      1 MetAlaSerAlaGlyGlyGlyAlaSerCysGlySerProAlaProGlyAlaAspArgProHis 20
QY      154 CAGCGGCTTCCTGATAGGGGTGAGCGCGGCACTGCCAGCGGAAAGTGCAGCCGTGTGT 213
Db      21 GlnArgProPheLeuIleGlyAlaSerGlyGlyThrAlaSerGlyLysSerThrValCys 40
QY      214 GAGAAATCATGAGATTGCTGGGACAGAACGAGTGGAAACGCGGACCGGAGAGTGTCTC 273
Db      41 GlyLysIleMetGlyLeuLeuGlyGlyAlaSerGlyGlyAlaGlyGlyAlaGlyValAla 60
QY      274 ATCTGAGCCAGACGAGTTCTACAGTCTTACCGGCAAGAGAGGCGGACCTTG 333
Db      61 IleLeuSerGlnAspArgPheThrLysValLeuThrAlaGlyGlyAlaLysAlaLeu 80
QY      334 AAAGACAGTACAAATTTGACCATCCAGATGCCCTTGATGATGATTTGATGCACAGACT 393
Db      81 LysGlyGlnIleThrAsnPheAspHisProAspAlaPheAspAsnAlaLeuArgThr 100
QY      394 CTGAAGAACATCGTGAAGGCGGAAACGGTGGAGGTGCCGACTATGATTTTGTGACACAC 453
Db      101 LeuLysAsnIleValGlyGlyLysThrValGlyAlaProThrLysAspPheValThrHis 120
QY      454 TCAGGTTACAGACGACGAGTGTCTACCTCCGACGAGTGTCTGTTGAGGGGATC 513
Db      121 SerArgLeuProGlyIleThrValValIleProAlaAspValAlaLeuPheGlyGlyIle 140
QY      514 TTGGTGTCTACAGCAGGAGATCCGGGACATGTTCACTGCGGCTTCCTGAGGACAC 573
Db      141 LeuValPheThrSerGlnGlyIleArgAspMetPheHisLeuArgLeuPheValAspThr 160
QY      574 GACTCCAGAGTCAGGCTGTCTCGAAGATTCTCCGGGACGTGCGCGAGGAGGAGACTTG 633
Db      161 AspSerAspValArgLeuSerArgArgValLeuArgAspValArgGlyArgAspLeu 180
QY      634 GAGCAGATTCTGACGACGATACACCACTTGTGAAAGCGGCTTCGAGAGTTCGCTG 693
Db      181 GlnGlnIleLeuThrGlnIleThrThrPheValLysProAlaPheGlyGlyLysLeu 200
QY      694 CCGACAAAGAAGTATGCCGATGATCATCCACGAGAGTGAACAATATGTTGCCATC 753

```

Dp	141	LeuValPheTyrSerGlnGlnIleArgAspMetPheHisLeuArgLeuPheValAspThr	160
Qy	574	GACTCCGACGTCAGAGCTGTCTCGAAGAATTCTCCGGAACGTGCGCCGAGGAGGACTTG	633
Dp	161	AspSerAspValArgLeuSerArgArgValLeuArgAspValArgArgGlyArgAspLeu	180
Qy	634	GAGCAGATTCTGACGCGAGTACACCACTTCTGTGAAGCCGCGCTTGGAGAGATTTCGCTTC	693
Dp	181	GlnGlnIleLeuThrGlnTyrThrThrPheValLysProAlaPheGlnGluPheCysLeu	200
Qy	694	CCGACAAAGAAGTATGCCGATGTGATCATCCACGAGAGAGTGGACAAATATGGTGGCATC	753
Dp	201	ProThrLysLysTyrAlaAspValIleLeuProArgGlyValAspAspMetValAlaIle	220
Qy	754	AACCTGATCTGACAGCAGCATCCAGGACATCTTGAAATGGTGAATCTGCAATGGACCGA	813
Dp	221	AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysLysTrpHisArg	240
Qy	814	GGAGGGTTCATATGGCGGAGCTACAGCGGACCTTTTCTGACCCAGGGGACCACTCTGGG	873
Dp	241	GlyGlySerAsnGlyArgSerTyrLysArgThrPheSerGlnProGlyAspHisProGly	260

RESULT 4  
 US-09-536-647-3  
 ; Sequence 3, Application US/09536647  
 ; Patent No. 6579708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ho, Yen Sen  
 ; APPLICANT: Johnson, Randall  
 ; TITLE OF INVENTION: No. 6579708el Human Uridine Kinase  
 ; FILE REFERENCE: GP50020  
 ; CURRENT APPLICATION NUMBER: US/09/536,647  
 ; CURRENT FILING DATE: 2000-03-27  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 277  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 US-09-536-647-3

Alignment Scores:  
 Pred. No.: 3,03e-18 Length: 277  
 Score: 1325.00 Matches: 254  
 Percent Similarity: 95.67% Conservative: 11  
 Best Local Similarity: 91.70% Mismatches: 12  
 Query Match: 43.67% Indels: 0  
 DB: Gaps: 0

us-09-896-522-1 (1-1624) x US-09-536-647-3 (1-277)

Qy	94	ATGGCTTGCGCGGAGGAGGAAGTCTGCGAGAGCCCGCGCGCGAGGCGGACCGTCCGAC	153
Dp	1	MetAlaSerAlaGlyGlyGlyGlySerGlnSerAlaAlaProGlnAlaAspArgProGln	20
Qy	154	CAGCGGCGCTTCTGTATAGGGGTGAGCGCGGCACTGCCAGCGGGAAGTGCAGCTGTGT	213
Dp	21	ProArgProPheLeuIleGlyValSerGlyThrAlaSerGlyLysSerThrValCys	40
Qy	214	GAGAAAGATCATGAGTGTGCTGGGAGACAGAACGAGGTGGAAACACCGGACGGGAAGGTGTC	273
Dp	41	GlnLysIleMetGlnLeuLeuGlyGlnAsnGlnValAspArgArgGlnArgLysLeuVal	60
Qy	274	ATCCTGAGCCAGGACAGGTTCTACAAAGTCTTGACGCGGACAGACAGAAAGCGCTTG	333
Dp	61	IleLeuSerGlnAspCysPheTyrLysValLeuThrAlaGlnGlnLysAlaLysAlaLeu	80
Qy	334	AAAGGACAGTACAATTTTGACCATCCAGATGCGCTTGTATATGATTGTGATGACAGAGCT	393
Dp	81	LysGlyGlnTyrZnAsnPheAspHisProAspAlaPheAspAsnAspLeuMetHisLysThr	100
Qy	394	CTGAAGAACAATCGTGAGAGGCAAAACGATGGAGGTGCGGACCTATGATTTTGGACACAC	453

Db 101 LeuYshaniLevalGluglYlysThrValGluValProThrTyrAspPheValIthrHis 120

QY 454 TCAAGGTTACCAAGAGACCAACGGTGGTCTAACCTGGCGAGCGTGGTTCTGTGTTAGAGGCATC 513

Db 121 SerArgLeuProGluThrThrValValTyrProAlaAspValValLeuPheGluGlyIle 140

QY 514 TTGGTGTCTTCACGCCAGAGAGATCCGGGACATGTTCCACCTGGCCTCTTCTGTGACACAC 573

Db 141 LeuValPheTyrThrGlnGlnIleArgAspMetPheHisLeuArgLeuPheValAspThr 160

QY 574 GACTCCGACGTCACAGGCTGTCTCGAAGAGTTCTCCCGGACGTGCGCGAGAGGAGCACTG 633

Db 161 AsperAspValArgLeuSerArgValValLeuAlaGAspValGlnArgGlyArgAspLeu 180

QY 634 GAGCAGATTCTGACCGCAGTACACACCTTCGTGAACCGCGCTTCGAGGAGTTGTGCTG 693

Db 181 GluGlnIleLeuThrGlnTyrThrAlaPheValTyrProAlaPheGluGluIlePheCysLeu 200

QY 694 CCGACAAAGAAAGTATGCCGATGTGATCATCCACGAGAGAGTGAACATATGTTGGCATC 753

Db 201 ProThrIysLysTyrAlaAspValIleIleProArgGlyValAlaAspAsnMetValAlaIle 220

QY 754 AACCGATCGTCGACACATCCAGACATTTCTGAATGGAGCATCGCAATGGACACCGA 813

Db 221 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspLeuCysLysArgHisArg 240

QY 814 GGAGGGTCCAAATGGCGCGAGCTTACCAAGCGGACCTTTCTGAGCCAGGGGACCACTGTGG 873

Db 241 GlyGlyProAsnGlyArgAsnHisLysArgThrPheProGluProGlyLysHisProGly 260

QY 874 ATGCTGACCTCTGGCAACGGTCACATTTGGAGTCCAGACGACACCCCAAC 924

Db 261 ValLeuAlaThrGlyLysArgSerHisLeuGlnSerSerArgProHis 277

RESULT 5

PCT-US00-05988-1160

Sequence 1160, Application PC/TUS0005988

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Rubin

TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides

FILE REFERENCE: PA101PCT

CURRENT APPLICATION NUMBER: PCT/US00/05988

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1160

LENGTH: 337

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (38)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (46)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (155)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (169)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

PCT-US00-05988-1160

Alignment Scores:

3.51e-11 Length: 337

Prod. No.:

Score:	969.80	Matches:	206
Percent Similarity:	63.96%	Conservative:	30
Best Local Similarity:	55.83%	Mismatches:	51
Query Match:	31.96%	Indels:	82
DB:	3	Gaps:	4

us-09-896-522-1 (1-1624) x PCT-US00-05988-1160 (1-337)

QY	7	TCGGCTCCGACCTCGCGCTGGCGGCGC-----GGCGCGGG	42
DB	26	SerProGlySerGluArgLeu-AlaGlyAspAspThr**SerAlaProAlaAlaProSe	45
QY	43	CCCGGGGAAAGGGGCGGCGCGGGGACCCGATCCGCGGGACCGAGGCGGAGATGGCTTCG	102
DB	45	r***GlyCysGlyAspArgGluSerAspAla-GlyAlaGlyGly-GluArgHisSer	64
QY	103	GCG-----GAGGCG-----GAA	114
DB	65	ValArgThrGlySerGlyArgArgGlyGlyGlyAlaAsnHisGlyArgGlyGlnArgAlaAsp	84
QY	115	GACGCCGAGAGCCCGCGCGCGAGGCCACGCTCCGACACAGCGGCCCTTCTGTATAGGG	174
DB	85	ProAlaGluProProAlaAlaGlnArgArgAsp-----AlaLeuProTyrArga	101
QY	175	GTGAGCGGCGGACGCTCGGCGGAGAGCGACCGCGTGGTGAGAAATCATGAGATGGCTGCG	234
DB	101	rgHis-GlyGlyThrAlaSerGlyIlySerSerValCysAlaGlyAlaValGlnLeuLeu	120
QY	235	GACACGAACAAGGTGGAAACAGCGGACGCGAAGGTGGTATCTGTAGCCAGACAGATTC	294
DB	121	GlyGlnAsnGluValAspTyrArgGlnGlyGlnValValIleLeuSerGlnAspSerPhe	140
QY	295	TACAAAGTCTCGACGGCGACGACAAAGGCCCAAGGCCCTTGAAGAGACATGACATTTTGA	354
DB	141	TyrArgValIleuThrSerGlnGlnIlyAspAlaIleuLys**GlnPheAsnPheAsp	160
QY	355	CATCCAGATGCCCTTGATATGATGTTATGACACAGACTCTGAAGAACATCGGAGGGC	414
DB	161	HisProAspAlaPheAspAsnGlu**IleLeuLysThrIleuLysGluIleThrGlnGly	180
QY	415	AAACCGGTGAGGTGCCACCATATGATTTTGTGACACACTCAAGGTTTACAGAGCCAG	474
DB	181	LysThrValGlnIleProValTyrAspPheValSerHisSerArgGlyGlnIleThrVal	200
QY	475	GTGGTTCACCTCGGACGCTGTTCTGTTTGAAGGCGATCTTGCTGTCTACAGCCAGAG	534
DB	201	ThrValTyrProAlaAspValIleLeuPheGlnGlyIleLeuAlaPheTyrSerGlnGln	220
QY	535	ATCCGGGACATGTTCCACCTCGGCTCTCGGACACCGACCTCGGACGCTCGGCTGCT	594
DB	221	ValAlaGAspLeuPheGlnMetLysLeuPheValAspThrAspAlaAspThrArgLeuSer	240
QY	595	CGAAGAGTTCCTCGGACGCTG---CGCCGAGGAGAGGACCTTGAGCAGATTTGACGAC	651
DB	241	ArgArgValIleuArgAspIleSerGlnArgGlyArgAspLeuGlnIleLeuSerGln	260
QY	652	TACACCACCTTGTGTAAGCGGCGCTTCAGAGATTCTGCTCCGACAAAGAGATGTC	711
DB	261	TyrIleThrPheValIysProAlaPheGlnGluPheCysLeuProThrIlySlyTyrAla	280
QY	712	GATGATGATCTCCACGAGAGGTGACAAATATGCTTGCATGAACTTATTCGCGACAC	772
DB	281	AspValIleIleProArgGlyAlaAspAsnLeuValAlaIleAsnLeuIleValGlnHis	300
QY	772	ATCCGAGCATTTCTGAATGGTGAACATCTGCAATGGCACCGAGAGAGTCTCAATGGGCGG	831
DB	301	IleGlnAspIleLeuAsnGly-----GlyProSerIlySer	312
QY	832	AGCTCAAGACCGGACCTTTTCTGAGCCAGGAGGACCAACCTGGAGTGTGACCTTGGCAAA	891
DB	312	GlnIleThrAsnGly---CysLeuAsn-----GlyTyrThrProSerArgLys	326
QY	892	CGGTCACTTTGGAGTCCAGACGACAGACCCAC	924

```

Db          327 ArgGlnAlaSerGlnUSeRSeRSeRAlaProHis 337
|||||
RESULT 6
US-09-488-725A-5411
; Sequence 5411, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 5411
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5411

Alignment Scores:
Pred. No.: 4,97e-11 Length: 335
Score: 961.60 Matches: 206
Percent Similarity: 64.54% Conservative: 27
Best Local Similarity: 57.06% Mismatches: 54
Query Match: 31.69% Indels: 74
DB: 1 Gaps: 4

US-09-896-522-1 (1-1624) x US-09-488-725A-5411 (1-335)
QY      8 CGCGCTCGAAGCTCGGCGCTGGGCGGCGCGCGCGCGCGGGAAGGGGCGGCGCGGGA 67
Db      31 AATThATrPrProSerAlaProAla--AlaProSerValGlyCYbGlyLVyAATrGlu 49
QY      68 CCCGATGCGCGGAGCGCGAGCGCGGAGTGGCTTCGCGCGGAGCGAGAGACTGCCAGAGCC 127
Db      50 SerAspAla-GlyAlaGlyGly-GluATrAlaSerVal-----ArgThrGlySerGI 66
QY      128 CGCGCGCGGAGCGCGA----- 143
Db      66 yATgATrGlyGlyArgThrMetAlaGlyAePserGIuGlnThrLeuGlnAenHISGlnGI 86
QY      144 -CGGTCCGACACAGCGCGCCCTTCGATATAGGGGTGTAGCGGCGGCGACCTCCAGCGGAACT 202
Db      86 nProAenGly-GlyGlnProPheLeuIleGlyValSerGIyGlyThraLaserGIyLys 106
QY      203 CGACCTGTGTGTGAGAAGATCATGATGAGTTGCTGTGGACAGAAAGAGGTGGACAGCGGAGC 262
Db      106 eATSerValCYbAlaLysIleValGlnLeuLeuGlyGlnAenGIuValAePTrArgGlnL 126
QY      263 GGAATGTGTCTATCTGACCCAGAGCAAGGTTTCAACAAGTCTTGAACGACAGAGCAAGG 322
Db      126 ySeGIuValValIleLeuSerGlnAePserPheTrArgValLeuThrSerGIuGlnLysA 146
QY      323 CCAAGGCTTTGAAAGGACGATCATTTTGTACATCCACAGAGCCCTTGATTAATGATTTGA 382
Db      146 TAlaLysAlaLeuLysGIyGlnPheAenPheAePHisPtoAsPAlaPheAePAsnGIuLeuT 166

```

```

QY      389  TGCACAGGACTCTGGAAGAACATCTGCGAGAGGCGGAAAACGGTGAAGCGGACCGCACTATGATT 442
Db      166  TLeuunYrThrLeuunYsgluIleThmRgluGlyLysThrValGlnIleProValIYrAsp 186
QY      443  TTGTGACACACTCAAGGTTTACCAAGAGACCAAGCGGTGCTTACCTCTGGCGAGCTGTGTTCTGT 502
Db      166  heValSerHisSerThrYsgluIuThrValThrValIYrProIlaAspValValLeuP 206
QY      503  TTGAGGGGCACTTGTGTTCTTACAGCCAGAGAG---ATCCGGGACATGTTCCACCTGGCC 559
Db      206  hegluGlyIleLeuunIaPheYrSerGlnIuArgIleArgAspLeuPheGlnMetLysL 226
QY      560  TTTTGTGGACACACGAGCTCCGACGTCAGGCTGTCTCGAAGAGTTCTCCGGGACGTG---C 616
Db      226  euPheValaAspThrAspAlaAspThrArgLeuSerSerArgValLeuLysAspIleSerG 246
QY      617  GCCGAGGAGGAGCACTTGAGACAGATTTCTGACCGACAGTACAC---ACCTTCGTGTAACCCGG 673
Db      246  luArgGlyArgAspPheuGlnIuGlnIleLeuSerSerSerThrLeuArgPheValIYrPro 266
QY      674  CTTTGGAGGAGTTCCTGCTGCTGCCGCAAAAGATGATGCCATGTGATCATCCACGAGAG 733
Db      266  laPheGlnIuGlnPheCysLeuProProLysIYrLysIYrAlaAspValIleIleProArgGlyA 286
QY      734  TGGACAATATGTTGTCGCATCAACCTGATGTGCGACAGATCCAGACATTTGGAATGCTG 793
Db      286  laAspAsnArgAlaIProIleAsnLeuIleValGlnHisIleGlnAspIleLeuAsnGly- 305
QY      794  ACATCTGCAAATGTGACACCGAGAGGGGTCCAAATGGGCGAGACTACAAAGCGAGACCTTTTCTG 853
Db      306  -----GlyProSerAsnArgGlnThrAsnIY---CysLeu 316
QY      854  AGCCAGAGGAGACCACTTGATGCTGACCTCTGCGAAACGCTACATTTGGAAGTCCAGCA 913
Db      317  Asn-----GlyYrThrProSerArgLysArgGlnIaSerGlnIuSerSers 332
QY      914  GCAGACCCCCAC 924
Db      332  eArgProHis 335

RESULT 7
US-09-488-725A-1839
; Sequence 1839, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pf FL_genes_b Versions 1.0
; SEQ ID NO 1839
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-1839

```



Alignment Scores:  
Pred. No.:

Pred. No.:	2.64e-11	length:	261
Score:	960.20	Matches:	196
Percent Similarity:	64.55%	Conservative:	30
Best Local Similarity:	55.91%	Mismatches:	35
Query Match:	31.64%	Indels:	8
DB:	1	Gaps:	1

US-09-896-522-1 (1-1624) x US-09-488-725A-1839 (1-261)

OY	61	GGCGGAGACCCCATGGCGGGAGGCGGAGGACGAGATGGCTTCGGCGGGAGGCGGAACGTCG	120
Db	2	AlaGly---AspSerGluGlnThr-----LeuGlnAsnHis-----G	13
OY	121	GAGAGCCCCCGCGCGGAGGCCGACCGCTCCGACACGAGCGGCCCTTCGTATAGGGGTGAC	180
Db	13	GlnGlnProAsn---GlyGly-----GluProPheLeuIleGlyValSer	26
OY	181	GGCGGCACCTGGACGGGGAGGTCGACCGTGTGTGGAAGAATCATGTGAGTGTCTGGACAG	240
Db	27	GlyGlyThrAlaSerGluLysSerSerValCysAlaLysIleValGlnLeuLeuGlyGln	46
OY	241	AAACGAGTGGAAACAGCGCGACGCGAGAGGTGGTCTATCTTGACCGAGACAGGTTCTCAAC	300
Db	47	AsnGluValAspTyrArgGlnLysGlnValIleIleLeuSerGlnAspSerPheTyrArg	66
OY	301	GTCCTGACGGCAGAGACGAGAAAGCCGACGGCTTGAAGACAGTAAATTTTGACCAATCC	360
Db	67	ValLeuThrSerGluGlnLysAlaLysAlaLeuLysGlyGlnPheAsnPheAspHisPro	86
OY	361	GATGCGCTTGAATATGATTTTGATGCACAGAGACTCTGAGAAACATCTGTGAGGGCAAAACG	420
Db	87	AspAlaPheAspAsnIleuLeuIleLeuLysThrLeuLysGluIleThrGlnGlyLysThr	106
OY	421	GTTGAGGTCCCGACCTATGATTTTGTGACACACTCAAGGTTTACCAGAGACCGGTGCTC	480
Db	107	ValGlnIleProValTyrAspPheValSerHisSerThrGlySerGluGlnThrVal	126
OY	481	TACCCGCGGACGCTGGTCTGTTTGAAGGGGATCTGGGTGTTTCAACGCCAGAGATCCGG	540
Db	127	TyrProAlaAspValValLeuPheGluGlyIleLeuAlaPheTyrSerGlnGluValArg	146
OY	541	GACATGTTCCACCTCGCGCCTCTTGATGACACCGGACTCCGACGTCAGGCTGTCTCGAAGA	600
Db	147	AspLeuPheGlnMetLysLeuPheValAspThrAspAlaAspThrArgLeuSerArg	166
OY	601	GTTCTCCGGGACGTG---CGCCGAGGAGGAGCCTGGAGAGATTTGAGCGAGTAAACC	655
Db	167	ValLeuArgAspIleSerGluArgGlyArgAspLeuGlnIleLeuSerGlnTyrIle	186
OY	658	ACCTGTGTGAGAGCGGCGCTTCGAGAGATTCTGCTGCGACAAAGAAATGTCGGATGTG	717
Db	187	ThrPheValLysProAlaPheGluGlnLysPheCysLeuProThrLysLysTyrAlaAspVal	206
OY	718	ATCATCCACGAGAGATGACATATGTGTTGCCATCACTGATCTGGCAGACAAATCCAG	777
Db	207	IleIleProArgGlyAlaAspAsnLeuValAlaIleAsnLeuIleValGlnHisIleGln	222
OY	778	GACATCTGAAATGATGTGACATCTGCAAATGTGCACCGAGAGGGTCCCAATGGCGGAGCTAC	837
Db	227	AspIleLeuAsnLys-----GlyProSerLysArgGln	233
OY	838	AAACCGACCTTTTCTGAGCCAGGGGACCAACCTGGAGATCTGACCTCTGGCAAAACGTTCA	897
Db	238	rsAngly---CysLeuAsn-----GlyTyrThrProSerArgLysArgGln	255
OY	898	CATTGGAGTCCAGACAGACAGCCAC	924
Db	253	AlaSerLysSerSerArgProHis	261

RESULT 8  
US-09-488-725A-2188

```

Sequence 2188, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488, 725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pc FL_genes_b Versions 1.0
SEQ ID NO 2188
LENGTH: 4619
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-2188

Alignment Scores:
Pred. No.:      48.2          Length:    4618
Score:         501.70        Matches:   203
Percent Similarity: 17.10%     Conservative: 36
Best Local Similarity: 14.52%   Mismatches: 126
Query Match:    16.76%       Indels:   1033
DB:             1           Gaps:      22

US-09-896-522-1 (1-1624) x US-09-488-725A-2188 (1-4618)
QY      1612 AAGCGTGGGTGATGTCGGTGCTCCAGAGGCATCCGCCCTTCCTCCTGACTTTAAAG 1553
Db      117  LysGIugInCySthngIyGIcys-CysProAlaserIAglnala----- 132
QY      1552 CACAGCAAGGGGGGAACA-----TCC 1528
Db      132 yThr-----GlyGlnThrAspValALrgThrlEuCsSerleuHISglyAlphear 149
QY      1528 CTCAGTGGCTCCCATATCCGTGTAGGCCAGCTGG----- 1493
Db      150 LeuSerIarCySthnCysSerCySeSlubProGIyTrpGIyGLyIProThrCyseSarpro 169
QY      1492 -----ACTGCMAACSACTGGGTGATAAAATT 1466
Db      170 ThrAspAlagluileProProSerSerProProSerAla-----Gls 185
QY      1465 GGTTGTAGGCCAACAGAGCCTTGTTATGAAGAAGAAAACAGAAAAATGAGACAT 1400
Db      186 ---Cys-----ProArPaRcyaAhnsRp---GlngIyAg----- 195
QY      1405 GTTAACATGTAAGAAAGAAAGTAATTCTTTCCACAAACTTTGATGTTATGTGTGAGTGT 1344
Db      196 -----CysValArgIyAg-----CysValCyS 203
QY      1345 GTAAGAACCAAGTCAGACTGGAAAAAATCTCTCCCACTGTGGGTCACTGTCAACAATA 128
Db      204 Phe----ProGIyTyTrnGlyProSer-----CysGIyTrp----- 214
QY      1285 CATCAGGCCAGCACAGNGCTTAGGC----- 126

```



```

QY 1261 -----TGTCCTCAATTTCCCAATATATGTCCTCAATTTCTTCAAGAGCCTCCCA 1208
Db      |||
QY 232 CysValCysArgAlaGlyPheSerGly-----ProAspCysSerGlnArgSerCysPro 249
Db      |||
QY 1207 GGCTCTCTGACA----- 1195
Db      |||
QY 250 -ArgGlyCysSerGlnArgGlyArgCysGlnGlyArgCysValCysAspProGlyTyr 269
Db      |||
QY 1194 -----TTCTGTGCAATTTCTCAGTACCTAGAGGGATCTTTAAACCGACAGC 1145
Db      |||
QY 269 rThrGlyAspAspCysGlyMetArgSerCysProArgGlyCys-----SerGlnArgGly 287
Db      |||
QY 1144 CTAAGTGCGTAAACCTCAGAGAACGCTGTCAAGTGTCCAGCAAGTTGAGTGAAGTGA 1085
Db      |||
QY 287 y---ArgCysGlnAsnGlnArg-----CysValCysAsnProGlyTyrThrGlyGlnAs 304
Db      |||
QY 1084 CACATCTGAAGTTTCCACTCTGAGTGAAGAGGCTGCTGAACATCCCTGGGGTGG 1025
Db      |||
QY 304 pCysGly-----ValArgSer-----Cys-----ProArgGlyCys 314
Db      |||
QY 1024 CGCCGAGGAGAGACAGTGG-----TGNGGGTGGGGCTCC 989
Db      |||
QY 314 sSerGlnArg-----GlyArgCysLysAspGlyArgCysValCys-----Asp 329
Db      |||
QY 988 CAGGCTCAAGTCCCTGAACACACATGCGGAGGAGACTGCTGAGGCTCGGACAGCC 929
Db      |||
QY 329 rGlyTyrThrGlyGln-----AspCys-GlyThrArgSerCysPro----- 342
Db      |||
QY 928 CTCAGTGG-----GGTGTGCTGTGACCTCAATATGATGACGTTTGGCAG 884
Db      |||
QY 343 -----TrpAspCysGlyGlnGlyGlyArgCysValAspGlyArgCys-----ValCysTrp 359
Db      |||
QY 883 AGGTCAAGCATCCAGGGTGGTCCCTGCTCAGAAAAGTCCGTTTACTCCGCCAT 824
Db      |||
QY 360 -----ProGlyTyrThr-----GlyGlnAsp-----CysSerTrpArg----- 370
Db      |||
QY 823 TGGACCTCTCTCG-----TGCCATTGG 800
Db      |||
QY 371 --ThrCysProAspArgAspCysArgGlyArgGlyArgCysGlnAspGlyGlnCys-IleCys 389
Db      |||
QY 800 ----- 800
Db      |||
QY 390 AspThrGlyTyrSerGlyAspAspCysGlyValArgSerCysProGlyAspCysAsnGln 409
Db      |||
QY 799 -----AGATGTACCATTCAGAAATG-----CTTGA-----TGT 770
Db      |||
QY 410 ArgGlyArgCysGlnAspGlyArgCysValCysTrpProGlyTyrThrGlyThrAspCys 429
Db      |||
QY 769 GGTGACGATCAAGTTGATGCAACCATATTTGCACTCTCGTGGAGATGATCAATCGG 710
Db      |||
QY 430 GlySerArgAla-----Cys-----ProArg-----Asp----- 437
Db      |||
QY 709 CATATCTTTTGTGGCAGGAGCAACTCTCGAAGCCGGCTTCAGAAAGTGTACT 650
Db      |||
QY 438 -----CysArg--GlyArg-----GlyArgCys--GlnAsnGlyVal-C 449
Db      |||
QY 649 GC-----GTCAAAATCTGCTCAAGTCCC 626
Db      |||
QY 449 yValCysAsnAlaGlyTyrSerGlyGlnAspCysGlyValArgSerCys-ProGlyAsp 468
Db      |||
QY 625 TCCCTCGGCGCAGTCCCGAGAACTTTGAGACAGCTGAGTGAAGTGGTGGTCCA 566
Db      |||
QY 469 CysArgGly-----ArgGlyArgCys----- 475
Db      |||
QY 565 CGAAGAGCGCGAGTGAACATGT-----TGTAGA 521
Db      |||
QY 476 -----GlySer-----GlyArgCysMetCysTrpProGlyTyrThrGlyThrAspCysGly 492
Db      |||
QY 520 ACACCAAGATGCCCTTAAACAGAACACAGTCCGAGGTAGACCAACCGTGTCTGTGTA 461
Db      |||
QY 493 ThrArgAlaCysPro-----Gly-AspCysArgGly-ArgGly- 504
Db      |||
QY 460 ACCTTGAGTGTGTCAAAATATCATAGTGGCAGCTTCAACCGTTTGGCTTCAGCATGT 401

```

```

Db      |||
QY 505 -----ArgCysValAsp-----GlyArgCysVal-----CysAsnProGlyPhe 517
Db      |||
QY 400 TCTTCAGAGTCTGTGATCATTAATCATTAATCAAGAGCATGTGATGTCAAATTTGACT 341
Db      |||
QY 518 ThrGlyGlnAspCysGlySer-----ArgArgCysProGly-----AspCys--- 531
Db      |||
QY 340 GTCTTTCAAGGCTTGGGCTTGTGCTGCTGCGTCAAGCACTTGT 296
Db      |||
QY 532 -----ArgGlyHisGlyLeu--CysGln-----AspGlyValCysValCysAspAlaGly 547
Db      |||
QY 295 -----AGAACCTGTCTGTGCTCAGAGTGAACACCTTCGGCT 260
Db      |||
QY 548 TyrSerGlyGlnAspCysSerThrArgSerCysProGly--Gly-----C 562
Db      |||
QY 259 GCCGC----- 255
Db      |||
QY 562 yAspGlyArgGlyGlnCysLeuAspGlyArgCysValCysGlnAspGlyTyrSerGlyG 582
Db      |||
QY 255 ----- 255
Db      |||
QY 582 LysAspCysGlyValArgGlnCysProAsnAspCysSerGlnHisGlyValCysGlnAspG 602
Db      |||
QY 254 -----TGTTCACCTCGTTCTGTGCCA 233
Db      |||
QY 602 LysAlaCysIleCysTrpGlnGlyTyrValSerGlnAspCysSerIleArgThrCysProS 622
Db      |||
QY 232 GCAATCCATGATCTTCTCACAACAGCTGCA----- 202
Db      |||
QY 622 eArgn-----CysHisGlyArgGlyArgCysGlnGlnGlyArgCysLeucy 637
Db      |||
QY 201 -----CTTCCGGCTGGAGTCCGC 182
Db      |||
QY 637 AspProGlyTyrThrGlyProThrCysAlaThrArgMetCysProAla--AspCysArg 656
Db      |||
QY 181 CGCTCAACCTTATCAGAAAGCGCGTGTGCGAGCGTCCG----- 140
Db      |||
QY 657 -----GlyArg-----GlyArgCysValGlnGlyValCys 666
Db      |||
QY 139 -----CTTCGGCG----- 131
Db      |||
QY 667 LeuCysHisValAlaGlyTyrGlyGlnGlnAspCysGlyGlnGlnProProAlaSerAla 686
Db      |||
QY 131 ----- 131
Db      |||
QY 687 CysProGlyGlyCysGlyProArgGlnLeuCysArgAlaGlyGlnCysValCysValGln 706
Db      |||
QY 130 -----CGGGCG 125
Db      |||
QY 707 GlyPheArgGlyProAspCysAlaIleGlnThrCysProGlyAspCysArgGlyArgGly 726
Db      |||
QY 124 TCT----- 122
Db      |||
QY 727 GlnCysHisAspGlySerCysValCysLysAspGlyTyrAlaGlyGlnAspCysGlyGln 746
Db      |||
QY 122 ----- 122
Db      |||
QY 747 GlnValProThrIleGlnGlyMetArgMetHisLeuLeuGlnGlnThrThrValArgThr 766
Db      |||
QY 122 ----- 122
Db      |||
QY 767 GluTrpThrProAlaProGlyProValAspAlaTyrGlnIleGlnPheIleProThrThr 786
Db      |||
QY 122 ----- 122
Db      |||
QY 787 GlnGlyAlaSerProProPheThrAlaArgValProSerSerAlaSerAlaTyrAspGln 806
Db      |||
QY 121 -----CGCAGTCTTGG----- 110
Db      |||
QY 807 ArgGlyLeuAlaProGlyGlnGlnTyrGlnValThrValArgAlaLeuArgGlyThrSer 826
Db      |||
QY 110 ----- 110

```

```

Db      827 TrpGlyLeuProAlaSerLysThrIleThrThrMetIleAspGlyProGlnAspLeuArg 846
QY      110 -----
Db      847 ValValAlaValAlaThrProThrThrLeuGluLeuGlyTyrLeuArgProGlnAlaGluVal 866
QY      109 -----
Db      867 AspArgPheValValSerTyrValSerAlaGlyAsnGlnArgValArgLeuGluValPro 886
QY      103 CCG-----
Db      887 ProGlnAlaAspGlyThrLeuLeuThrAspLeuMetProGlyValGluTyrValValThr 906
QY      101 -----
Db      907 ValThrAlaGluArgGlyArgAlaValSerTyrProAlaSerValArgAlaAsnThrGly 926
QY      101 -----
Db      927 HisGlnGlnTrpTrpAlaTyrArgGlyMetGlyGlyLeuArgAspThrAspArgPhePro 946
QY      100 -----
Db      947 SerValLeuPheProAlaProGlyHisTyrSerTyrProGluValArgProProAlaPro 966
QY      85 CCGGTCCCGCGCATCGGGTCCCGCGCCCTTCCCGCGCGCGCGCGCGCGCGCGCA 26
Db      967 Pro---ProLys-SerArgProArg-ProAlaProAlaProArgProProArgPro-Pro 984
QY      25 GCCCG-----
Db      985 TrpProSerArgProAlaGluGluArgGluGluGluGluSerPro 998

```

```

RESULT 9
US-09-488-725A-3367
; Sequence 3367, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784PLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PL FL_genes_b Versions 1.0
; SEQ ID NO 3367
; LENGTH: 1455
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3367

```

```

Alignment Scores:
Pred. No.:      2.84      Length:      1454
Score:          494.00    Matches:      227
Percent Similarity: 16.99%  Conservative: 61
Best Local Similarity: 13.39%  Mismatches: 119
Query Match:    16.51%    Indels:      1289

```

```

DB:      1      Gaps:      34
us-09-896-522-1 (1-1624) x US-09-488-725A-3367 (1-1454)
QY      1606 GGGTGTGATGCTGGGTGC-----TTCCAGGGGATCCGCTGCTCTGCTTAA 1556
Db      32 GlyAlaAsp---GlyCysIlePheSerPhe---GlyHis-----MetSerLeuGlyLys 47
QY      1555 AGGCACACAGCAAGGGGGGAAAACATCCCTCAGTGGCTCCCA-----TAT 1511
Db      48 SerTyrThrMetIleGlyLysAspSer-----SerProGlnSerLeuGlyIleVal 64
QY      1510 CCGTGTAGGCCACGCTGGACCTGCACAAACACTGGGTCAATGAATTAG----- 1465
Db      65 ProCys-----AlaIleSerTrpLeuPheArgLeuIleGluGluArgArg 79
QY      1464 -----GTTTGT----- 1459
Db      80 GluArgThrGlyThrArgPheSerValArgValSerAlaValGluValCysGlyArgAsp 99
QY      1459 ----- 1459
Db      100 GlnSerLeuArgAspLeuLeuAlaGluValAlaProGlySerLeuGlnAspThrGlnSer 119
QY      1458 -----AGGCCACACACAGCCCTGGTTATGAAACAGAAAAACAGAAAAACAT 1414
Db      120 ProGlyValTyrLeuArgGluAspProValCysGlyAlaGlnLeuGlnAsnGlnSerGlu 139
QY      1414 ----- 1414
Db      140 LeuArgAlaProThrAlaGluLysAlaAlaPheTyrLeuAspAlaAlaLeuAlaValArg 159
QY      1413 -----GAGACATGTAACATGTAATAAAGAAAGTAATTGT 1378
Db      160 SerThrSerArgAlaGlyCysGlyGluAsp-----AlaArgArgSerSer----- 174
QY      1377 TCACAAAACTTTGAGTTATGTGTGTGAGTGTGTAAGAACACAGATCAGCTGAAAAAAC 1318
Db      175 HisMetLeuPheThrLeuHisVal-----TyrGlnTyrArgMetGlnLys-- 189
QY      1317 TCTCTCCCACTGTGGC----- 1302
Db      190 -----CysGlyArgGlyGlyMetSerGlyGlyArgSerArgLeuHisValLeuIleAs 206
QY      1301 -----TTCACTGTCAAAACATCAGGCCAGCCAGTGTCT 1267
Db      206 PheGlySerCysGluAlaAlaAlaAlaGlyArgAlaGlyGluAlaAlaGlyLysProLeu-- 225
QY      1266 TAGGCTGTCTC-----CTCAATTCCCAATGATGTGC 1234
Db      226 -----CysLeuSerLeuSerAlaLeuGlySerValIleLeuAlaLeuValAsnGlyAlaL 244
QY      1233 CTCACATTCTCTCACAGA----- 1217
Db      244 YshIshValProTyrArgAspHisArgLeuThrMetLeuLeuArgGluSerLeuAlaThrA 264
QY      1217 ----- 1217
Db      264 IeGlyCysArgThrThrMetIleAlaHisValSerAspAlaProAlaGlnHisAlaGluT 284
QY      1217 ----- 1217
Db      284 HisLeuSerThrValGlnLeuAlaAlaArgTleHisArgLeuArgGlyLysValaLysT 304
QY      1217 ----- 1217
Db      304 YrAlaSerSerSerSerGlyGlyGluSerSerCysGluGluGlyArgAlaArgArgProp 324
QY      1217 ----- 1217
Db      324 RohIshLeuArgProPheHisProArgThrYrAlaAlaLeuAspProAspArgThrProProc 344
QY      1216 -----AGCCTCCAGGCTTCCTGACAACTTCTGTGGC 1186

```



```

QY 251 ----- 251
Db 992 ysaAlaArgAlaSerIysValGluAlaAlaHisArgLeuAlaGlyHisAlaSerLeuGluA 1012
QY 250 ----- CCACCTC 244
Db 1012 rgtTyrGluGlyLeuAlaHisSerSerSerIysGlyArgGluAlaProGlyArgProProA 1032
QY 243 GTTCTGTC-----CCAGCAACTCCATGATCTTCTCACACACGGTCGA 202
Db 1032 rgaIaValProIysLeuGlyValProProSerSerPro-----ThrHisGlyPro 1048
QY 201 CTTCCCGCGCTGGACGTGCGC----- 182
Db 1049 AlaProAla-----CysArgSerGlyAlaAlaIysAlaValGlyAlaProIysProProV 1067
QY 182 ----- 182
Db 1067 aIGlyGlyGlyGlyArgGlyLeuValAlaGlyGlySerArgAlaLeuGlyProServ 1087
QY 181 -----CGCTCACCC----- 173
Db 1087 aIlysLeuSerThrAlaSerValThrGlyArgSerProGlyGlyProValAlaGlyProA 1107
QY 173 ----- 173
Db 1107 rgaIaAlaProArgAlaGlyProServAlaGlyAlaIysAlaGlyArgGlyThrValMetG 1127
QY 172 -----CTATCAGAGAGCGCG 157
Db 1127 lyThrIysGlnAlaLeuArgAlaAlaHisSerArgValHisGluLeuSer-----AlaS 1145
QY 156 CTGGTGGCAGCGCTCG----- 140
Db 1145 erGlyAlaProGlyArgGlyGlySerSerTrpGlySerAlaAspSerAspSerGlyHisA 1165
QY 140 ----- 140
Db 1165 spSerGlyValAsnValGlyGluGluArgProProThrGlyProAlaLeuProSerProT 1185
QY 140 ----- 140
Db 1185 yIserIysValThrAlaProArgArgProGlnArgTyrSerSerGlyHisGlySerAspA 1205
QY 139 -----CCTCCGCGCGCGCGC----- 125
Db 1205 snSerSerValLeuSerGlyGluLeuProProAlaMetGlyArgThrAlaLeuPheHis 1225
QY 125 ----- 125
Db 1225 tsSerGlyGlySerSerGlyTyrGluSerLeuArgArgAspSerGluAlaThrGlySerA 1245
QY 124 -----TCTC 121
Db 1245 laSerSerAlaProAspSerMetSerGluSerGlyAlaAlaSerProGlyAlaArgThrA 1265
QY 120 GCACTCTTCGCCCTCCCGCG----- 101
Db 1265 rGSerLeuIysSerProIysIysArgAlaThrGlyLeuGlnArgArgArgLeuIleProA 1285
QY 100 -----AAGCCATCTCGGCT----- 86
Db 1285 laProLeuProAspThrThrAlaLeuGlyArgIysIysProSerLeuProGlyGlnTrpValA 1305
QY 85 -----CCGCTCCCGCGCATCGGTCGCCCGCGCGCGCC----- 53
Db 1305 spleuProProProLeuAlaGlySerLeuIysGluProPheGluIleIysValTyrGluI 1325
QY 52 -----CTTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGGTCGAGGCGAGCC 4
Db 1325 laeAspAspValGluArgLeuGlnArgProArgProThrProArg-----GluAla-Pro 1342

```

```

RESULT 10
US-09-488-725A-2369
; Sequence 2369, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/538,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2369
; LENGTH: 2044
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2369

Alignment Scores:
Pred. No.: 7.77 Length: 2044
Score: 492.60 Matches: 222
Percent Similarity: 17.96% Conservative: 75
Best Local Similarity: 13.42% Mismatches: 157
Query Match: 16.46% Indels: 1202
DB: 1 Gaps: 44

us-09-896-522-1 (1-1624) x US-09-488-725A-2369 (1-2044)
QY 1621 GCCCGCAGACGCTGGGTGTGATGCTGGGTCTTCAGGCGATCCGCTGCT----- 1568
Db 21 AlaProGlyLeuProPheCys--Cys--Gly-----GlySerLeuAlaValVal 36
QY 1567 -----TCTTGCTTTTAAGGACACAGCAGGCGGAA--AACATCCCTCAGTGGC 1520
Db 37 ValLeuAlaLeuProVal-----AlaTrpGlyGlnCysAsnAlaProGluTrpL 54
QY 1519 TCCCCA----- 1514
Db 54 eu-ProPheAlaArgProThrAsnLeuThrAspGluPheGluPheProIleGlyThrTyr 73
QY 1513 -----TATCCGTGTAGCCACGC----- 1496
Db 74 LeuAsnTyrGluCysArgProGlyTyrSerGlyArgProPheSerIleIleCysLeuIys 93
QY 1495 -----TGCACTGCA----- 1487
Db 94 AsnSerValTrpThrGlyAlaIysAspArgCysArgArgIysSerCysArgAsnProPro 113
QY 1487 ----- 1487
Db 114 AspProValAsnGlyMetValHisValIleIysGlyIleGlnPheGlySerGlnIleIys 133
QY 1487 ----- 1487
Db 134 TyrSerCysThrIysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleSer 153
QY 1487 ----- 1487

```

```

Db      154 GlyAspThrValIleTrpAsnGluThrProIleCysAspArgIleProCysGlyLeu 173
QY      1487 -----
Db      174 ProProThrIleThrAsnGlyAspPheIleSerThrAsnArgGluAsnPheHisTyrGly 193
QY      1487 -----
Db      194 SerValValThrTyrArgCysAsnProGlySerGlyIleArgIleValIlePheGluLeuVal 213
QY      1487 -----
Db      214 GlyGluProSerIleTyrCysThrSerAsnAspGlnValGlyIleTrpSerGlyPro 233
QY      1487 -----
Db      234 AlaProGlnCysIleIleProAsnLysCysThrProProAsnValGluAsnGlyIleLeu 253
QY      1487 -----
Db      254 ValSerAspAsnArgSerLeuPheSerLeuAsnGluValValGluPheArgCysGlnPro 273
QY      1486 -----
Db      274 GlyPheValMetLysGlyProArgArgValLysCysGlnAlaLeuAsnLysTrpGluPro 293
QY      1471 AATTAG-----GTTTGAGGCCAACACCCCTTGCTTGTGAAACAGAA 1426
Db      294 GluLeuProSerCysSerArgValCysGlnProProProAspValLeuHisAlaGluArg 313
QY      1425 AACAGAAAATGAGCATGTAAACATGTAAAGAAAGTACTGTTGCACAAACTTT 1366
Db      314 ThrGlnArgAspLysAsp-----AsnPhe-SerProGlyGlnGluValPhe----- 328
QY      1365 TGAATTATGTGTGAG-----TGTTAA 1342
Db      329 -----TyrSerCysGluProGlyTyrAspLeuArgGlyAlaAlaSerMetArgCysThr- 346
QY      1341 GAACGATTCAGCTCGAATAAACTCTCTCCCACTGGGGTTCAGTCTCAACAAACATC 1282
Db      347 --ProGlnGlyAspTrpSerProAlaAlaProThr-----Cys-----G 359
QY      1281 AGGCCAGCCAGTGT-----CTAGGCTGTCTCCTCAAT-----TTCCCA 1243
Db      359 LuvAllySerCysAspAspPheMetGlyGlnLeuAsnGlyArgValLeuPheProV 379
QY      1242 ATAATGTGCTCA-----TTCTCTACA 1219
Db      379 AlaAsn-----LeuGlnLeuGlyAlaLysValAspPheValCysAspArgGluGlyPheGlnLeu 397
QY      1218 GAAGCTCCAGGCTTCTGCAATTTCTGTGGCAATTTCTGAGTACCTTGAAGGAACTTT 1159
Db      398 LysGlySerSerLaser-----TyrCys-----ValLeuAlaGlyMetCysLeuLeuTr 414
QY      1158 AAACCCAGCAGAGCTTAAGTGGTAAACCTCAGAGAACCCCTGAGTGTCCACAG 1099
Db      414 PheAsnSerValPro--ValCysGlnGlnIle-----PheCysPheProSerPro 429
QY      1098 TTGAGTCTAGTGAACATCTGAGTTTCACTCTGAGTGAAGAGAGCCCTGCTGAAC 1039
Db      430 ProValIleProAsn-----GlyArgHisThr-----GlyLysPro--LeuGluVal 444
QY      1038 ACTCCCTGGGGTGGC----- 1023
Db      444 LheProPheGlyLysThrValAsnTyrThrCysAspProHisProAspArgGlyThrIse 464
QY      1022 -----CCGAGGAGAGAGAGTGG 1006
Db      464 rPheAspLeuIleGlyGluSerThrIleArgCysThrSerAspProGlnGlyAsn---G 483
QY      1005 GTGTGGTGGGCGTCCCAAGC-----TCAGTCCCTGA 973
Db      483 LysVal--TrpSerSerProAlaProArgCysGlyIleLeuGlyHisCysGlnAlaProAs 502

```

```

QY      972 ACAC----- 969
Db      502 PhePheLeuPheAlaLysLeuLysThrGlnThrAsnAlaSerAspPheProIleGlyTh 522
QY      968 -----ACATGCCGCGGCGGAGACTGCTCCCTGAG-----GCTCGGAGAGCCC 928
Db      522 rSerLeuLysTyrGluCysArg-----ProGluTyrTyrGlyArg---ProP 537
QY      927 TCAGTGGGGTCTGCTGC-----TGAACTCCAATGTGACCGCTTTGCCAGA 883
Db      537 heSer---IleThrCysLeuAspAsnLeuValTrpSerSerProLysAspValCysLysA 556
QY      882 GGTCAACATCCAGGGGTGATCC----- 860
Db      556 rGlySerCysLysThrProProAspProValAsnGlyMetValHisValIleThrAspI 576
QY      859 -----CTGCTCAGA 850
Db      576 IeGlnValGlySerArgIleAsnTyrSerCysThrThrGlyHisAlaGlyLeuIleGlyHis 596
QY      849 AAAGTCCGCTGT-----AGCTCGCCCATTTGACCTCTCGTGCCATTT 802
Db      596 rSerAlaGluCysIleLeuSerGlyAsnAlaAlaHisTrpSerThrLysProProIleC 616
QY      801 GC----- 800
Db      616 YedIleArgIleProCysGlyLeuProProThrIleAlaAsnGlyAspPheIleSerThra 636
QY      799 -----AGATGTCAACATTCAAGATGTC 778
Db      636 snArgGluAsnPheHisTyrGlySerValValThrTyrArgCysAsn-----P 652
QY      777 CTGATGTGCTGACGATCA-----GTTGAGGCAACCA-----TATT 739
Db      652 rGlySerGlyArgValPheGluLeuValGly-----GluProSerIleTyrC 670
QY      738 GTCCACTCCTCGGGAGATGATCAGATCGGACATCTTCTTTCGGAGGC----- 689
Db      670 ys-----ThrSerAsnAspGlnValGlyIleTrp-----SerGlyProAlaProG 686
QY      689 ----- 689
Db      686 IncysIleIleProAsnLysCysThrProProAsnValGluAsnGlyIleLeuValSerA 706
QY      689 ----- 689
Db      706 sPAsnArgSerLeuPheSerLeuAsnGluValValGluPheArgCysGlnProGlyPheV 726
QY      688 -----AGAACTCTCGAAG-----CCGGCTTACGAAGGTGG----- 656
Db      726 AlMetLysGlyProArgArgValLysCysGlnAlaLeuAsnLysTrpGluProGluLeuP 746
QY      655 -----TGTACTGGTCAAGATCTGCTCAGAGTCCCTCCGAGCG--CAGGTCGGAG 604
Db      746 rSerCysSer-----ArgValCys--GlnProProAspValLeuHis--AlaGluLys 763
QY      603 AACTTTTCAAGC----- 591
Db      763 gThrGlnArgAspLysAspAsnPheSerProGlyGlnGluValPheTyrSerCysGluP 783
QY      590 -----AGCTGACGTCGAGTGGGTGTCCACGAAGAGGG 556
Db      783 oGlyTyrAspLeuArgGlyAlaAlaSerMet-----ArgCysThrProGlnGly- 799
QY      555 CAGGTGAACATGTCCCGGATCTCTGCTGTAGA----- 521
Db      800 -AspTrpSer-----ProAlaAlaProThrCysGluValLysSerCysAspAspPheMetG 818
QY      521 ----- 521
Db      818 LysIleLeuLeuAsnGlyArgValLeuPheProValAsnLeuGlnLeuGlyAlaLysValA 838

```

```

QY 521 ----- 521
Db 838 sPheValCysAspGluGlyPheGlnLeuYsGlySerSerAlaSerTyrCysValLeu 858
QY 521 ----- 521
Db 858 IaGlyMetGluSerLeuTPrAsnSerSerValProValCysGluGlnIlePheCysPro 878
QY 521 ----- 521
Db 878 ePrProValIleProAsnGlyAArgHieThrGlyLysProLeuGluValPheProPheG 898
QY 521 ----- 521
Db 898 LyLysAlaValAsnTyrThrCysAspProHisProAspArgGlyThrSerPheAsnLeu 918
QY 521 ----- 521
Db 918 LeGlyGluSerThrIleArgCysThrSerAspProGlnGlyAsnGlyValTPrSerSer 938
QY 520 --ACACCAAGATGC----- 509
Db 938 roAlaProArgCysGlyIleLeuGlyHisCysGlnAlaProAspHisPheLeuPheAla 958
QY 508 -----CCTCAACA-----GAAC 496
Db 958 YsLeuYsThrGlnThrAsnAlaSerAspPheProIleGlyThrSerLeuYsTyrGluC 978
QY 495 CACGTCCGACG-----GGTAGACA----- 476
Db 978 YsArgProGluTyrGlyArgProPheSerIleThrCysLeuAspAsnLeuValTPrs 998
QY 475 -----CCGGGCTC 466
Db 998 ePrSerProLysAspValCysLysArgLysSerCysLysThrProAspPro--ValAs 1017
QY 465 TGGT-----AACCTTGAGTGT 448
Db 1017 nGlyMetValHisValIleThrAspIleGlnValGlySerArgIleAsnTyrSerCysTh 1037
QY 447 CACAAATCATAGG----- 434
Db 1037 rThr-GlyHisArgLeuIleGlyHisSerSerAlaGluCysIleLeuSerGlyAsnTha 1057
QY 433 -----TCGGACCTCCACCGTTTGC-----CCTCA----- 407
Db 1057 IaHisTPrSerThrLysProProIleCysGlnArgIleProCysGlyLeuProThrI 1077
QY 407 ----- 407
Db 1077 LeAlaAsnGlyAspPheIleSerThrAsnArgGluAsnPheHisTyrGlySerValT 1097
QY 406 -----CGATGTTCTTCAGAGTCC----- 389
Db 1097 hTyrArgCysAsnLeuGlySerArgGlyArgLysValPheGluLeuValGlyLupros 1117
QY 388 -----TGCGATCAAAATCATATCAAA--GGATCTGC----- 358
Db 1117 eTlleTyrCysThrSerAsnAspArgValGlyIleTPrSerGlyProAlaProGlnC 1137
QY 358 ----- 358
Db 1137 YsIleIleProAsnLysCysThrProProAsnValGluAsnGlyIleLeuValSerAspA 1157
QY 358 ----- 358
Db 1157 sNArgSerLeuPheSerLeuAsnGluValValGluPheArgCysGlnProGlyPheValM 1177
QY 357 -----ATGCTCAAAATTTGACTGTCTTTCAAGCGCTTGGCCTTCTGCT 312
Db 1177 eTlyGlyProArgArgValLys--CysGlnAlaLeuAsnLys--TPrGluProGluLe 1195
QY 311 GCCGTGACGACCTTGT--AGAACCTGT----- 287

```

```

Db 1195 uProSer-----CysSerArgValCysGlnProProGlnIleLeuHisGlyGlnI 1213
QY 286 -----CCTGGCTCAGATGACCACTTCCGCTGC-- 258
Db 1213 eThrProSerHisGlnAspAsnPheSerProGly-GlnGlu-ValPheTyrSerCysGlu 1232
QY 258 ----- 258
Db 1233 ProGlyTyrAspLeuArgGlyAlaIleSerLeuHisCysThrProGlnGluAspTPrSer 1252
QY 257 -----CGTGTTCACCTGTGTGTGTCCAGCACTCCATGATCTTCTACAC 210
Db 1253 ProGluAlaProArgCysAlaValLysSerCys-----AspAspPheLeu----- 1267
QY 209 ACGTGCAGCTTCC----- 196
Db 1268 --GlyGlnLeuProHisGlyArgValLeuPheProLeuAsnLeuGlnLeuGlyAlaLysV 1287
QY 195 -----GCTGACAGTGCCTCCGCTCACCCTATC 168
Db 1287 aIserPheValCysAspGluGlyPheArgLeuLysGlySerSerValSerHis----- 1304
QY 167 AGAAGGCGCGTGGTCCGACGCTGCGCTCCGAGCGAGGCTTCCAGTCTTGCGCT 108
Db 1305 -----CysVal--LeuValGlyMetArg--SerLeuTPrAsnAsnSer-Va 1318
QY 107 CCGG-----CCGAAGCATCTCGGCTCCGCTCCGCGCATC-- 71
Db 1318 lProValCysGlnHisIlePheCysProAspPro-----ProAlaIleLe 1333
QY 70 -----GGTCCCGCGCGCGCGCTCCCGCGCGCGCGC----- 35
Db 1333 uAsnGlyAArgHisThrGlyThrProSerGlyAspIleProTyrGlyLysGluIleSerTy 1353
QY 35 ----- 35
Db 1353 rThrCysAspProHisProAspArgGlyMetThrPheAsnLeuIleGlyGluSerThrI 1373
QY 34 -----GCCCGCGCAAGCGCGAGTCCGA 12
Db 1373 eArgCysThrSerAspProHisGlyAsnGlyValTPrSerSerProAlaIleArgCysGl 1393
QY 11 G-----CGAAGCCCA 2
Db 1393 uLeuSerValArgAlaGlyHisCysLysThrProGlnGlnPheProPheAlaSerPro 1412

RESULT 11
US-09-488-725A-5941
; Sequence 5941, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144

```

SOFTWARE: pc\_fl\_genes\_b Versions 1.0  
 ; SEQ ID NO 5941  
 ; LENGTH: 2045  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-488-725A-5941

## Alignment Scores:

Pred. No.:	7 77	Length:	2044
Score:	492.60	Matches:	222
Percent Similarity:	17.96%	Conservative:	75
Best Local Similarity:	13.42%	Mismatches:	157
Query Match:	16.46%	Indels:	1202
DB:	1	Gaps:	44

us-09-896-5522-1 (1-1624) x US-09-488-725A-5941 (1-2044)

```

QY 1621 GCCCGCACAGCCTGGGTGTGATGCTGGGTCTCCAGGACATCCGCTCGCT----- 1568
DB 21 AlaProGlyLeuProPheCys--Cys--Gly-----GlySerLeuLeuAlaVal 36
QY 1567 -----TCTTGCTTTAAGCACACAGAGGGGAA---AACATCCCTCAGTGGC 1520
DB 37 ValLeuLeuAlaLeuProVal-----AlaTrpGlyGlnCysAsnAlaProGluTrpL 54
QY 1519 TCCCA----- 1514
DB 54 eu-ProPheAlaArgProThrAsnLeuThrAspGluPheGluPheProIleGlyThrTyr 73
QY 1513 -----TATCCGTGTAGGCCACGC----- 1496
DB 74 LeuAsnTyrGlnCysValArgProGlyTyrSerGlyArgProPheSerIleIleCysLeuLys 93
QY 1495 -----TGACTGCA----- 1487
DB 94 AsnSerValTrpThrGlyAlaLysAspArgCysArgArgLysSerCysArgAsnProPro 113
QY 1487 ----- 1487
DB 114 AspProValAsnGlyMetValHisValIleLysGlyIleGlnPheGlySerGlnIleLys 133
QY 1487 ----- 1487
DB 134 TyrSerCysThrLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleSer 153
QY 1487 ----- 1487
DB 154 GlyAspThrValIleTrpAspAsnGluThrProIleCysAspArgIleProCysGlyLeu 173
QY 1487 ----- 1487
DB 174 ProProThrIleThrAsnGlyAspPheIleSerThrAsnArgGluAsnPheHisTyrGly 193
QY 1487 ----- 1487
DB 194 SerValValThrTyrArgCysAsnProGlySerGlyArgLysValPheGluLeuVal 213
QY 1487 ----- 1487
DB 214 GlyGluProSerIleTyrCysThrSerAsnAspAspGlnValGlyIleTrpSerGlyPro 233
QY 1487 ----- 1487
DB 234 AlaProGlnCysIleIleProAsnLysCysThrProProAsnValGluAsnGlyIleLeu 253
QY 1487 ----- 1487
DB 254 ValSerAspAsnArgSerLeuPheSerLeuAsnGluValValGluPheArgCysGlnPro 273
QY 1486 -----AACCACTGGGTCAAG 1472
DB 274 GlyPheValMetLysGlyProArgArgValLysCysGlnAlaLeuAsnLysTrpGluPro 293

```

```

QY 1471 AAATAG-----GTTTGAGGCCAACACGACCTTGTTATGAAACAGAA 1426
DB 294 GluLeuProSerCysSerArgValCysGlnProProProAspValLeuHisAlaGluArg 313
QY 1425 AACGAAACATGAGACATGTACATGTAAAAAGAAAGTACTTTTCACAAACCTTT 1366
DB 314 ThrGlnArgAspLysAsp-----AsnPhe-SerProGlyGlnGluValPhe----- 328
QY 1365 TGAGTTATGTGTGTAG-----TGTTAA 1342
DB 329 -----TyrSerCysGluProGlyTyrAspLeuArgGlyAlaAlaSerMetArgCysThr- 346
QY 1341 GAACGATCAGCTGGAATAAACTCTCTCCCACTGGGTTCACGTCAACAAACATC 1282
DB 347 --ProGlnGlyAspTrpSerProAlaAlaProThr-----Cys-----G 359
QY 1281 AGCCAGCAGCTGT-----CTAGGCTGTCTCTCAAT-----TTCCCA 1243
DB 359 IValLysSerCysAspAspPheMetGlyGlnLeuLeuAsnGlyArgValLeuPheProV 379
QY 1242 ATATATGCTCTACA-----TTCCTCACA 1219
DB 379 AlaAsn-----LeuGlnLeuGlyAlaLysValAspPheValCysAspGluGlyPheGlnLeu 397
QY 1218 GAAGCTCCAGGCTCTGCACATCTGGGCACTTCTCAGAGACCTAGAGGATCTTT 1159
DB 398 LysGlySerSerAlaSer-----TyrCys--ValMetAlaGlyMetGlnSerLeuTr 414
QY 1158 AACCGCAACGAGCCTTAAGTGTGTAATAAATCAGAGACGCTGTGATGCTCCACAG 1099
DB 414 PAsnSerSerValPro-ValCysGlnGlnIle-----PheCysProSerPro 429
QY 1098 TGAAGTCTAGTGACACATCTGAGTTTCCATCTCTAGTGAAGAGCCTCGCTGTAAC 1039
DB 430 ProValIleProAsn-----GlyArgHisThr-----GlyLysPro-LeuGluVal 444
QY 1038 ACTCCCTCGGCTGCG----- 1023
DB 444 IheProPheGlyLysValAlaValAsnTyrThrCysAspProHisProAspArgGlyThrSe 464
QY 1022 -----CCGAGAGAGACAGTGA 1006
DB 464 rPheAspLeuIleGlyGluSerThrIleArgCysThrSerAspProGlnGlyAsn-----G 483
QY 1005 GTGTGGGTGGCGCTCCACAGC-----TCACTCCCTGA 973
DB 483 IYVal--TrpSerSerProAlaProArgCysGlyIleLeuGlnHisCysGlnAlaProAs 502
QY 972 ACAC----- 969
DB 502 PHisPheLeuPheAlaLysLeuLysThrGlnThrAsnAlaSerAspPheProIleGlyThr 522
QY 968 -----ACATGCCGGCGGAGACCTGCGCTGAG-----GCTCGGAGAGCC 928
DB 522 rSerLeuLysTyrGlnCysArg-----ProIuLysTyrGlnArg--ProP 537
QY 927 TCAGTGGGTCTGTGCTC-----TGAACTCCAAATGACCGTGTGACAA 883
DB 537 hEser-----IleThrCysLeuAspAsnLeuValTrpSerSerProLysAspValCysLys 556
QY 882 GGTCAGCATCCACGAGGTGTGCC----- 860
DB 556 rGlySerCysValSerThrProProAspProValAsnGlyMetValHisValIleThrAspI 576
QY 859 -----CTGAGCTCAGA 850
DB 576 IeGlnValGlySerArgIleAsnTyrSerCysThrThrGlyHisArgLeuIleGlyHis 596
QY 849 AAAGTCCGCTTGT-----AGTCCGCGCCATTTGACACCTCTCGGTGCATTT 802
DB 596 rSerValGlnCysIleLeuSerGlyAsnAlaAlaHisIleTrpSerThrLysProProIleC 616
QY 801 GC----- 800

```

```

Db      616 ysglnarglleprocygslyleuoprothrllealaenglyasppheileserthra 636
      ||
Qy      799 -----AGATTCACCAATTCAGATGTC 778
Db      636 snargluapnenhietrglysevalvalthrtgkgsyasn-----P 652
Qy      777 CTGAGTGTGTCGACGATCA-----GGTTGATGGCAACA-----TATT 739
Db      652 rogliserglyalarglyvalphegluleuvalgly-----gluprosertletryc 670
Qy      738 GTCCACCTCGTCGAGATGATCATCGCATCTTCCTTGTCCGACGC----- 689
      |||
Db      670 ys-----Thrsenapraparglnvalglylertp-----serglyproalapro 686
      |||
Qy      689 ----- 689
Db      686 lncysllelleproasnlyscythrproprodenvalgluasnglylleuvalsera 706
Qy      689 ----- 689
Db      706 spasnargserleupheserleuasngluvalglupheargcyegluproglyphev 726
Qy      688 -----AGACTCTCTGAGAG-----CCGACTTCACGAGGTGC----- 656
      |||
Db      726 almetrysglyproarglvalarglyscysglnalaleuasnlystprgluproglyleup 746
Qy      655 -----TGTACTGCTCGAATCTGCTCCAGAGCTCCCTCCGCGC---CACCTCCGCGAG 604
      |||
Db      746 rosercyser-----argvalcys---glnproproasprvalleuuhis-alaqluar 763
Qy      603 AACCTTCGAGAC----- 591
      |||
Db      763 gthnclargasrlyasapnpheserproglnglnluvalpheytryscysglupr 783
Qy      590 -----AGCTGACCTCGAGTCCGCTGTCCACGAGAGCG 556
      |||
Db      783 oglytryasprleuarglyalalasermet-----ArgCysythrproglngly- 799
Qy      555 CAGGTGACATGTCGCGATCTCTGCTGATCA----- 521
      |||
Db      800 asptpser-----proalalaprrothrcysgluvallysercysasprapnemetc 818
Qy      521 ----- 521
Db      818 lylglnleuasnlyalargvalleupheprovalasnleuglvalalysvala 838
Qy      521 ----- 521
Db      838 sphphevalcyasprgluglypheglnleuylsglysersealasertrycysvalleua 858
Qy      521 ----- 521
Db      858 laqlmetgluserleutprasnsersevalprovalcyasgluglnleuphecysapros 878
Qy      521 ----- 521
Db      878 erproprovalleerproasnlyalarghietnrglylvsproleugluvalpheproheg 898
Qy      521 ----- 521
Db      898 lylusalaalaasntyrthrasyasprprohisproasprargglythrserspheasprleu 918
Qy      521 ----- 521
Db      918 leglyluserthrilleargcysrhrserasprproglnglyasnlyvaltrpsersepr 938
Qy      520 -----ACACCAAGATGC----- 509
      |||
Db      938 roalaproargcyasglylleuenglyhis-cysglnalalaproasprhiepheuleuvalal 958
Qy      508 -----CTCAACA-----GAAAC 496
      |||

```

```

Db      958 yleuylsthrnglnthrasnalaserasprapheprolleuglythrsertleuyltrycgluc 978
Qy      495 CAGTCCGAG-----GGTAGACA----- 476
      |||
Db      978 ysargprogluyltrygllyargpophesertlethrcysleuapnleuvaltrps 998
Qy      475 ----- 466
      |||
Db      998 erserprolyasprvalcysylsarglysercyslysthrproproasprpro--valaa 1017
Qy      465 TGGT-----AACCTTAGCTGT 448
      |||
Db      1017 nglymetvalhnsvalillethrasprleuglnvalglyserarglylaasnlysercysrth 1037
Qy      447 CACAAATCATAG----- 434
      |||
Db      1037 rthn-gllyhsargyleulleglyhissersealaglucyslleleuaserglyasnthra 1057
Qy      433 -----TCGACACTCCACCGTTTGC-----CCTCCA----- 407
      |||
Db      1057 lahtsrpserthnlyspoprololecyasgluarglleprocygslyleuoprothrt 1077
Qy      407 ----- 407
Db      1077 lealaasnlyasppheilesertthrasnargluasnphenietrglysevalvalt 1097
Qy      406 -----CGATGCTCTCAGAGTCC----- 389
      |||
Db      1097 hrtyrargcyasbnleuglyserargglyalarglyvalphegluleuvalglyglupros 1117
Qy      388 -----TGTGCATCAATCATTTACAA--GGCATCTGG----- 358
      |||
Db      1117 erllytrycsthrserasnaprasprlnvalglylertpserglyproalaproglnc 1137
Qy      358 ----- 358
      |||
Db      1137 ysillelleproasnlyscythrproproasnvalgluasnglylleuvalseraspa 1157
Qy      358 ----- 358
      |||
Db      1157 snargserleupheserleuasngluvalglupheargcyegluproglyphevalm 1177
Qy      357 -----ATGTCMAAATGTACTGCTCTTCAAGGCTTGCGCTTCTGCTCT 312
      |||
Db      1177 etlysglyproarglvallyse--cysglnalaleuasnlys--trpdluproglyle 1195
Qy      311 GCGGTCAAGACTTGT--AGAACTGT----- 287
      |||
Db      1195 uproser-----cysserargvalcysglnproproprogluileuuhisgllygluuh 1213
      |||
Qy      286 -----CCTGGCTCAGATGACACACTTCGCGTGC----- 258
      |||
Db      1213 sthrproserhieglnapnpheserprogly-glnghu-valpheytryscysglu 1232
Qy      258 ----- 258
      |||
Db      1233 progllytryasprleuarglyalalaserleuuhiscysrthrproglnglyasptpser 1252
Qy      257 -----CGCTTTCACCTGCTTGTGTCACGACATCCATGATCTTCTACAC 210
      |||
Db      1253 progluialproargcysalalalysercys-----AspAsppheleu----- 1267
Qy      209 ACGGTGACTTCC----- 196
      |||
Db      1268 --glylnleuprohieglyalargvalleupheproleuasnleuglvalalysv 1287
Qy      195 -----GCTGGCAGTCCGCGCTCACCCTATC 168
      |||
Db      1287 alserphevalcyasprgluglypheargleuylsglysersevalserhis----- 1304
Qy      167 AGAAGGCGCGTGTGCGAGCGGTCCGCGCGGCGGCTCTCGCATCTTCCGCT 108
      |||
Db      1305 -----cysval-----leuvalglymetarg--serleutprasnasnser-Va 1318
      |||

```



```

QY 107 CCGG-----CCGAAGCATCTGGCTCGCTCCGCGCATC-- 71
Db 1318 lProValCysGluHisIleIlePheCysProAlaPro-----ProAlaIleLe 1333
QY 70 -----GGGTCGCCGCGCGCCGCTTCCCGCGCGCGCGC----- 35
Db 1333 uAengIyArgHisThrGlyThrProSerGlyAspIleProTyrGlyIysGluIleSerTy 1353
QY 35 ----- 35
Db 1353 rThrCysAspProHisProAspArgGlyMetThrPheAsnLeuIleGlyGluSerThrI1 1373
QY 34 -----GCCCGCCGACGCGCGAGTCCGA 12
Db 1373 eArgCysThrSerAspProHisIleGlyAsnGlyValTTrpSerSerProAlaProArgCysG1 1393
QY 11 G-----GCCGCCCA 2
Db 1393 uLeuSerValArgAlaGlyHisCysIysThrProGluInPheProPheAlaSerPro 1412

```

## RESULT 12

```

US-09-488-725A-5708
; Sequence 5708, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784P/PT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pf_fl_genes_b Versions 1.0
; SEQ ID NO 5708
; LENGTH: 631
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(626)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-5708

```

## Alignment Scores:

```

Pred. No.: 0.361 Length: 626
Score: 487.80 Matches: 198
Percent Similarity: 23.80% Conservative: 40
Best Local Similarity: 19.80% Mismatches: 171
Query Match: 16.30% Indels: 592
DB: 1 Gaps: 15

```

US-09-488-522-1 (1-1624) x US-09-488-725A-5708 (1-626)

```

QY 1624 CTGGCCCGCAGCAGCTGGGTGTATGCTGGTCTTCAGGAGCATCCGCTCGCTTCT 1565
Db 22 LeuSerPro-ValSerLeuGlyAla--AlaGly--TrpProGlyInProArgProTyrTL 40
QY 1564 CTGCTTTAAAGCAGCAGGAGGAGGAGAAACATCCCTCAGTGGCTCCCATATCCGTGT 1505

```

```

Db 40 eLeuLeuProAlaIleAla-----SerValSer-ArgProHisAspArgAl 55
QY 1504 A-----GCCACGCTGACT 1490
Db 55 a**GlyGluAlaValSerLeuSerLeuSerSerGlyAspValCysGlyHisThr-AspG 75
QY 1489 GCAAACTGAGTGTGATGAAATTAGGTTGTAGCCCAACGACGCTGTGTTATGAAAC 1430
Db 75 IyGlyGlyAlaGlySerAspProGln--AlaIysProIysProProArgCysProPheTh 94
QY 1429 AGAAAAACAGAAACATGAGACATGTAACTGTAAAAAGAAAGTACTTTTCACAAAA 1370
Db 94 r-AlaMetProSerProArgThr-----LysGluIysVal-----ArgAs 107
QY 1369 CTTTGAAGTTATGTGTGTAGTGTGTAAACACGA-----TACAGTGG 1325
Db 107 n-----LysValCysLeuLeuIleAlaIleArgTyrSerAspIleProSerAspVal 124
QY 1324 AAAAACTGCTCCGACGCTGCTGCTGCTCAACAAAACATGACGCGCAG----- 1271
Db 125 SerIys--AlaPro-----GlyProAlaGlyAsnProHisAspArgSerSerThrAla 141
QY 1270 -----TGCTAGGCTGTCTCTC----- 1253
Db 142 Ala**LeuHisArgArgAlaGlyAlaGlySerLeuCysLeuSerAlaSerLeuLeuPro 161
QY 1252 --AATTTCCCAATATATGTGCTTCACTTCT----- 1223
Db 162 ProSerPheSerLeuGlyAlaProGlyAlaProSerProLeuArgValSerProAlaSer 181
QY 1223 ----- 1223
Db 182 GlyGlyProArgIysGlyGlyAlaArgGlnIysGlyGly**AlaGlyGlyGlyGlyPro 201
QY 1222 -----CAGAAAGCTCCGAGGCTTCTGACATCTGTGAGCATTTCTCAGTGACC 1172
Db 202 AlaArgThrHisAlaAspLeuPro-----Cys-----ValGlyPheValCys----- 215
QY 1171 TTAGAGGATCTTTAAACGCAACGACCTTAAGTGTGTAACAACTGAGAACGCTGTGCA 1112
Db 216 -----SerProProLeuLeuIys**SerAspSerProVal- 227
QY 1111 GTGTCCACAGATTTAGTGTAGTGACATCTGATGTTCCACTCTCCTGAGCAGAAAG 1052
Db 228 -----LysGlnLeuPro--AlaSerGlyGlnG1 236
QY 1051 CCTCGCTGTAACACTCCCTGGGTCGCGCGAGGAGGAGGAGTGGGTGGGCGCT 992
Db 236 IysGlnLeuPro-----ProValGlySerSerAsp-----IleLeuArg 251
QY 991 CCCAAGGCTCACTCCCTGTAACACATGCGCGGAGGAGACCTGCTGAGCTCGGCGAG 932
Db 251 gProArg-----Pro--ThrSerValSerGly-----Thr-----GlyArgAla 264
QY 931 CCCCTCAGTGGGTCGTGCTGCTGACTGCAATGTGACCGTGTGCCAGAGTCAAGCATTC 872
Db 264 Ia-----Gly**CysSerTrpGlnPro--AlaAlaCysCysThr-----Pr 277
QY 871 CAGGTCGTCCTCGCTGCTC----- 853
Db 277 oArgSerGln**TrpAlaValAlaArgSerProSerArgCysSerArgTrp**ArgG1 297
QY 852 -----AGAAAGGTCCGCTGTGATCTCCGC 827
Db 297 nSerGlyArg**ArgGly**SerSerArgArgArgArgGlyPro**AlaAlaGlyArg 317
QY 826 CATTGACCTCTCTCTGTCGTCGTCATTTGACATGTCAACATTC-----A 785
Db 317 gSerThrPro--AlaValPro-----ProCysSer**GlyGlyAlaGlyA 333
QY 784 GAATGTCTGATGTGTCGACGATCAGTGTGATGAGCAACATATGTCCTCCTC----- 730
Db 333 rArgAlaIyAlaCys--ArgThrGly--Trp--GlyTyrAlaPro-SerArg** 349

```

```

QY 729 -----TCGTGGATGATCAC----- 715
Db 349 *LeuGluProSerGlyProThrSerGlySerAlaLeu**ThrtipAlaSerHisSerTh 369
QY 714 -----ATCGCATCTTCTTGTGGGCA 692
Db 369 rglYAla*****SerArgLeuGlySerGlyThrAlaGlyThrdly---ProLeuGlySerGly 388
QY 691 GGCAGAACTCTCGAAGGCGGCTTCAGAAAGGTGTTACGCTCAGAA----- 641
Db 388 nser-SerArgSer***AlaGly***ArgCysCysCysThrAlaAlaSerProCysGly 407
QY 640 -----TCTGCTCAGGTCCTCCCTGGCGCAGTCCCGAGAACTCTTCG-- 595
Db 408 GlySerGlyProSerHisProGly-SerProSerAlaHisCysLeuSerTrpSerGlyG1 427
QY 594 -----AGACAGCTCGAGCTCGAGTGGTTCACGAAAGGCGCAGGTGA-- 548
Db 427 YATGThrdlnPro-----ArgAlaPro-----SerAlaHisGlyArgGlyArg 441
QY 547 -----ACATGTCGCGATCTCTGGCTGTAGAACACCAAGA 512
Db 442 AlameGlySerArgCysValCysThrCysThrGlyLeuPro----- 455
QY 511 TGCCT----- 506
Db 456 CysProGlyIleProLeuSerGlyAlaSerProGlyGlySerGlyGlyThrdlyAlaGly 475
QY 505 -----CAACAGAACCAAGTCCGCGAGGT----- 482
Db 476 ArgSerHisThrLeuYsAlaAlaArgSerArgLeuSerProAlaPro---GlySerGly 494
QY 481 -----AGACCAAGCTGG 470
Db 495 SerArgGlySerTyr***SerHisAsnAspAsnTrpGlyThrdTrpAlaProPro-S 514
QY 469 TCTCTGTAACTTGAAGTGTGTCAAAATATAGTGTGGAGCTCCACCGTTTGGCCT 410
Db 514 exAlaGly-----HisLeuLeuValGly-Gly*** 523
QY 409 CCAGAGTGTCTTCAAGATCTGTGACATCATATATCAAGACATCTGATGTCAA 350
Db 524 -----AenSerGlnArgThrsSerAspHis**Tyr----- 534
QY 349 AATGTACTGTCTTCAAGGCTTGGCTTCTGTCTGCGTCAAGACCTTGTAGAACC 290
Db 535 -----ThrdGlyThrdArgArgProTrp-----AlaGlyProGlyThrdArgCysSerThr 550
QY 289 TGTCTGTGGCTCAGATGACCACTTC---CGTGGCGCTTTCACCTGTTCTGTCC 234
Db 551 AlaProSerArgAlaAlaProAlaSerArgCysArg-ProProProProProProPr 570
QY 233 AGCAACTCCATGATCTTCAACACAGGTCGATCCCGCTGGAGTGGCCGCTCAACC 174
Db 570 oProArgPro-----ProArgLeuProAla-----AlaAlaSer----- 581
QY 173 CCAATCAGAAAGGCGCTGTGGCGAGTGGCTCCGCGGCGGCTCTCGCACTT 114
Db 582 -----SerGly-----GlyAlaSerGlySerProAlaAlaSerCysSerCys 597
QY 113 TCGCTCCCGCGAAGCATCTCGGCTCCGCTCCCGGACATCGGATCCCGCGCCGCC 54
Db 597 sArgAlaProAlaYsPro--AlaSerSerGlyGlyAla-----ProAlaProPro 613
QY 53 CTTTCCCGGCGCGCGCGCGCGCGCGCGCGCGAGTCCGAGGCGCAACC 4
Db 614 ProArgProGluProProProProProAla-----ArgArgPro 626

```

RESULT 13  
 US-09-488-725A-3457  
 ; Sequence 3457, Application US/09488725A  
 ; GENERAL INFORMATION:

```

; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 3457
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-3457

```

## Alignment Scores:

```

Pred. No.: 7.8 Length: 1409
Score: 469.20 Matches: 222
Percent Similarity: 17.30% Conservative: 51
Best Local Similarity: 14.07% Mismatches: 119
Query Match: 15.68% Indels: 1167
DB: 1 Gaps: 31

```

us-09-896-522-1 (1-1624) x US-09-488-725A-3457 (1-1409)

```

QY 1624 CTGGCCCGGACAAAGCTGGGTGTGATGCT-----GGTGGCTTCCAGGCGATC 1577
Db 65 ValAlaThrHisArgYs---CysGluAlaYsValThrsAlaCys--GlnAlaLeuP 83
QY 1576 CGCTCGCTTCTCTGCTTTAAGGCACAAAGGCGGAAACATCCCTCAGTGGCTCC 1517
Db 83 roPro-----ValGluLeuArgArg-----AsnThrAlaPr 93
QY 1516 CCAATCCGTGTAGGCCACGCTGA----- 1492
Db 93 oValArgArgIleGlnHisLeuGlySerThrYsSerLeuAsnHisSerYsGlnArgSe 113
QY 1491 -----CTGCAAAACACTG----- 1479
Db 113 rThrdLeuProArgSerPheSerLeuAsp-ProLeuMetGluArgArgTrpAspLeuAspL 133
QY 1479 ----- 1479
Db 133 euthrTyrValThrdGluArgIleLeuAlaAlaPheProAlaArgProAspGluGlnA 153
QY 1478 -----GCTCATGAATAGTTGTTGAGCCCAACAGCCTTGTGTATGAACAGA 1427
Db 153 rghIsArgGlyHis--LeuArgGluLeuAlaHis-----ValLeu-- 165
QY 1426 AAACAGAAACATGAGACATGTAACTGTAAAAAGAAAGTACTTGTTCACAAACTT 1367
Db 166 -GlnSerYsHisArgAsp-----LysTrpYsLeuLeu-----P 176
QY 1366 TT----- 1365
Db 176 heAsnLeuSerGluYsArgHisAspLeuThrdArgLeuAsnProYsValGlnAspPheG 196
QY 1364 -----GAGTTATGTGTGTGAGTGTGAAG----- 1341

```

```

Db      196  lYTrpProGluLeuH1a1aPProLeuAspLysLeuCySer---lleCyLeuValam 215
Qy      1341  -----
Db      215  eGluThrTrpLeuSerAlaAspProGlnH1eValValLeuTyrCyLeuGlyAsnL 235
Qy      1341  -----
Db      235  ySgGlyLysLeuGlyVal11leValSerAlaTyrMetHisTyrSerLys11leSerAlaGlyA 255
Qy      1341  -----
Db      1341  -----
Db      255  lAaSpGlnAlaLeuAlaThrLeuThrMetArgLysPheCysGluAspLysValAlaThrG 275
Qy      1340  -----
Db      275  luleGlnPProSerglnArgArgTyr11eSerTyrPheSergLysLeuLeuSergLysEri 295
Qy      1333  TCAGACTGAAAAAACTCTCCCACTGTGGGTTCA-----
Db      295  lchrgMet---AsnSerSerProLeuPheLeuH1eTyrValLeu11eProMetLeuPr 313
Qy      1297  -----
Db      313  oAlaPheGluProGlyThrGlyPheGlnProPheLeuLys11eTyrGlnSerMetGlnLe 333
Qy      1297  -----
Db      333  uVal1TyrThrSergLysValTyrH1e1a1aGlyProGlyProGlnGlnLeuCy11eSe 353
Qy      1297  -----
Db      353  rLeuGlnProAlaLeuLeuLeuLysGlyAspValMetValThrCySerTyrH1eLysGlyG 373
Qy      1296  -----
Db      373  yArgGlyThrAspArgThrLeuVal1PheArgVal1GlnPheH1eThrCys---Thr11eHis 392
Qy      1282  CAGGCCAGCCAGTGTCTAGGCTGTCTCTCAATTTCCCAATAATGGCTCCTCAATTCTCT 1223
Db      393  -----
Qy      1222  CACAGAGACC-----
Db      403  uAspGlnAlaTrpThrAspGlnLysArgPheProPheGlnAlaSerVal1GlnPhe---ValP 422
Qy      1183  TTCTCAGTGAAC-----
Db      422  heSerSerSerProGlnLys11eLysGlySerThrProArgAsnAspProSerVal1Sery 442
Qy      1142  -----
Db      442  a1aAspTyrAsnThrThrGlnProAlaValArgTrp---AspSerTyrGlyAsnDheAsnG 461
Qy      1111  G-----
Db      461  nh1eH1eGluAspSerVal1aSpGlySerLeuThrH1eThrArgGlyProLeuAspGlySe 481
Qy      1111  -----
Db      481  rProTyrAlaGlnVal1aGlnArgProArgProArgGlnThrProProAlaProSerProGlnPr 501
Qy      1110  ----TCTCCAGCAAGTTGAGTGTGATGACACATCT-----
Db      501  oProProProProMetLeuSerVal1eSerSerAspSergLysH1eSerSerThrLeuThrTh 521
Qy      1077  -----
Db      521  rGluProAla1a1aGlnSerPro-----
Qy      1030  GGGGTGCGCCGAGAGAGACAGT-----
Db      533  oThr1a1a1aGlnArgGlnGlnLeuAspArgLeuGlnGlyGlyCyGlyVal1a1a1aSerG 553

```

```

Qy      987  AGGCTCAGTCCCTGGAACACATGCGGCGGAGACTGC-----
Db      553  yGly-----
Qy      947  -----
Db      569  lnrProThrVal1GlyGlyProH1eLeuGlyVal1TyrProGlnH1eArgProGlyLeus 589
Qy      947  -----
Db      589  eArgH1eCySerSerCyAspGlnGlyTyrArgGlnProCySgLyVal1ProAsnGlyGlyT 609
Qy      947  -----
Db      609  yTrTyrArgProGlnGlyThrLeuGlnLysArgArgLeuAlaTyrGlyGlyTyrGlnGlys 629
Qy      947  -----
Db      629  erProGlnGlyTyrAlaGlnAlaSerMetGlnLysArgArgLeuCyAspSerLeuSerg 649
Qy      946  -----
Db      649  lueGlyLeuTyrProTyrProProGln-MetGlyLysProAlaThrGlyAspPheGlyTyr 668
Qy      919  -----
Db      669  ArgAlaProGlyTyrArgGlnVal11leLeuGluAspProGlyLeuProAlaLeuTyr 688
Qy      918  -----
Db      689  ProCyProAlaCySgGlnGlyLysLeuAlaLeuProThrAla1a1aLeuTyrGlnLysMa 708
Qy      900  ARGTCACGTTGGCCAGAGTCAGCATCCAGGAGTGTCCTCCCTGCAAAAAGGTCCG 841
Db      709  leu-GluArg-GluAlaGlyGln-----
Qy      840  CTGTAGCTCCGCGCCATTGGACCT-----
Db      725  leu---LeuH1eProVal1ArgProGlyH1eSProLeuProLeuLeuProAlaCySg 743
Qy      806  -CATTTGAGATGTGCATTCAGAAATGTCCT-----
Db      743  yH1e-----
Qy      775  -----
Db      760  lAgLyGlnGlnGlnH1eSgGlnGlyCySerTyrThrMetCySProGlnGlnArgTyrGly 779
Qy      753  GATGGCAACA-----
Db      780  ----HisProGlyTyrProAlaLeuVal1ThrTyrSerTyrGlyAlaVal1ProSery 798
Qy      741  ATTGTCCACTCCTCGTGGGATGATCATCGGCAATCTTTGTTCGGAGAGAGACAC 682
Db      798  yTrCySerPro-----
Qy      681  CTCGAAGCGCGCTTCACGAGAGTGATGTCGTCAGAAATCTGTCTCCAGGT-----
Db      806  ro-----
Qy      628  -----
Db      816  rGlyTyrProSer-----
Qy      576  GTCGGTGTCACAGAGAGCGAGGTGGAACATGTCGGAGATCTCT-----
Db      823  lHisSerProArg-----
Qy      529  -----
Db      841  eArgLysLeuSerTyrGln11eProThrGlnGlnGlyGlyAspArgTyrPro--LeuTr 860

```

```

QY 507 CTGAACAGAACCACTCCGAGGCTAGACCA----- 476
Db 860 OGlyHis---LeuAlaSerAlaGly---ProLeuAlaSerAlaGlySerLeuGluPro 878
QY 475 -----CCGTGCTCTGCTGTAACCTGAGTGTCAAAATCATGAGT 433
Db 878 AlaSerTPArgGluGlyPro-----SerGlyHis-SerThrLeuProArgSerProArg 896
QY 432 CGGCACTTCCACCGCTTTGCCCTCCACGAGTGTCTTCAAGACTCTGTCATCAATCAT 373
Db 896 spAlaPro-----CysSer-----AlaSer----- 902
QY 372 ATCAAGACCATCTGAGTGTCAAAATGTAATGTAATGTAATGTAATGTAATGTAATGTA 320
Db 903 -SerGluLeuSerGlyProSer-----ThrProLeuHisThrSerSerProValGlu 920
QY 320 ----- 320
Db 920 LyLysGluSerThrArgArgGlnAspThrArgSerProThrSerAlaProThrGlnArg 940
QY 319 -----TCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 308
Db 940 euSerProGlyGlyAlaLeuProProValSerGlnAlaGlyThrGlyLysAlaProGlu 960
QY 307 -----TCAGACCTTGTGAACCTGTCCGTGCTGAGATGACCACTTCCGCTG 259
Db 960 euProSerGlySerGlyPro-----GluPro-----LeuAla-----ProSer 972
QY 258 CCGCTGTTCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 199
Db 973 ProVal-SerProThrPheProProSer-----SerProS 984
QY 198 CCGCTGCTGCACTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 140
Db 984 euAspTrpProGlnGluArgSerPro---GlyGlyHisSerAspGlyAlaSerProArgS 1003
QY 140 ----- 140
Db 1003 euProValProThrThrLeuProGlyLeuAlaArgHisAlaProTrpGlnGlyProArgGlyP 1023
QY 140 ----- 140
Db 1023 roProAspSerProAspGlySerProLeuThrProValProSerGlnMetProTrpLeuV 1043
QY 139 -----CCTCCGCGCGCGCGCGCTGCTGCGAGCTTCCGCTCCCGCGCAAGCA- 95
Db 1043 AlaAlaSerProGluProPro-----GlnSerSer-----ProThrProA 1056
QY 94 -----TCTCGGCTCCGCTCCGCG- 77
Db 1056 laPheProLeuAlaAlaSerTyraSerThrAsnGlyLeuSerGlnProProLeuProGlu 1076
QY 76 ---CGCATCGAGTCCCGCGCGCGCGCTTCCCGCGGC----- 42
Db 1076 ysArg- HisLeuProGlyProGlyGlnGlnProGlyProTrpGlyProGluGlnAla 1095
QY 41 ---CCGCGCGGC----- 33
Db 1095 rSerProAlaArgGlyLeuSerHisHisValThrPheAlaProLeuLeuSerAspAsnVa 1115
QY 33 ----- 33
Db 1115 lProGlnThrProGluProProThrGlnGluSerGlnSerAsnValLysPheValGlnAs 1135
QY 33 ----- 33
Db 1135 pTherSerLysPheTrpTyLysProHisLeuSerArgAspGlnAlaAlaLeuLeuTy 1155
QY 33 ----- 33
Db 1155 sAspLysAspProGlyAlaPheLeuLeuArgAspSerHisSerPheGlnGlyAlaTyrgl 1175
QY 32 -----CCGCGCAAGCGCGCGAGTGC---GGAGGCGAAGCCCG 3

```

```

Db 1175 yLeuAlaLeuLysValAlaAlaThrProProProSerAlaGlnProTrpLysGlyAspPro 1194
RESULT 14
US-09-488-725A-3157
; Sequence 3157, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyeeg Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784PLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc fl_genes_b Versions 1.0
; SEQ ID NO 3157
; LENGTH: 1079
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3157
Alignment Scores:
Pred. No.: 4.95 Length: 1078
Score: 462.70 Matches: 204
Percent Similarity: 18.60% Conservative: 40
Best Local Similarity: 15.55% Mismatches: 137
Query Match: 15.25% Indels: 932
DB: 1 Gaps: 20
us-09-896-522-1 (1-1624) x US-09-488-725A-3157 (1-1078)
QY 1 GTGGGGTCCGCTCCGACCTCGGCGCTGCGCG----- 31
Db 8 ValAlaGlyProAlaLeu-ArgArgTrpLeuLeuGlyThrValThrValGlyPheLe 27
QY 31 ----- 31
Db 27 uAlaGlnSerValLeuAlaGlyValLysPheAspValProCysGlyGlyArgAspCy 47
QY 31 ----- 31
Db 47 sSerGlyGlyCysGlnCysTyTrProGluLysGlyGlyArgGlyGlnProGlyProValGl 67
QY 31 ----- 31
Db 31 ----- 31
QY 67 yProGlnGlyTyraSnglyProProGlyLeuGlnGlyPheProGlyLeuGlnGlyArgGly 87
QY 32 -----GGCGCGCGCGCG----- 43
Db 87 sGlyAspLysGlyGlyLysArgGlyAlaProGlyValThrGlyProLysGlyAspValGlyAl 107
QY 44 -----CCGCGCAAGCGCG----- 57
Db 107 aArgGlyValSerGlyPheProGlyAlaAspGlyLleProGlyHisProGlyGlnGly-- 126
QY 58 GCGCGCGGAGCCGATCGCGCGCGAGCGGAGCGCGAGTGTGCGCGCG----- 107
Db 127 ---GlyPro---ArgGlyArgProGlyTyraSerGlyCysAsnGlyThrGlnGlyA 143

```

```

QY 107 ----- 107
Db 143 spseretgLyProGlnGlyProProGlySeretGlnGlyPheThrGlyProProGlyProGlnG 163
QY 108 ----- AGCGAAGACTGC 120
Db 163 lYProLyseGlyGlnGlyGlyProGlyAlaLeuProLyseGlnGlyAlaGAspArgIyAla 183
QY 121 GAGAGCCCGCGCGCGAGCGGACCGTCCGACCAAGCGCCCTTCTGATGAGGGGTGAGC 180
Db 183 rg-----GlyGluProGlyGluPro-Gly-----LeuValGlyPheGln 195
QY 181 GCGGCACTGCGACGCGGAGATGACCGGTGTGAGAAAGATCATGAGAGTTCGGGACAG 240
Db 196 Gly-----ProProGly--ArgPro-----GlyHis-----ValGlyGln 206
QY 241 AAGAGGTGAGAACGCGGACGCGAAGGT-----GTCATCTCGAGCCAGACAGGTTTC 294
Db 207 Met-----GlyProValGlyAlaProGlyArgProGlyProProGlyPro----- 221
QY 295 TACAAAGTCTTGAACGCGACGACGAAAGCCAGAGCTTGAAGGACATAC----- 345
Db 222 --ProGlyProLyseGlyGlnGlnGlyAsnArgGlyLeu--GlyPheTyrGlyValIys 239
QY 345 ----- 345
Db 240 GlyGlnLysGlyAspValGlyGlnProGlyProAsnGlyTyrLeuSerAspThrLeuHis 259
QY 346 -----AATTTGACCATTCAGATGCCTTTGATTAATGATTTG 381
Db 260 ProIleIleAlaProThrGlyValThrPhe--HisProAspGlnTyrIysGlyGlu-- 277
QY 382 ATGCACAGACTGTGAAGAACATCTGGA----- 410
Db 278 ----LysGlySerGlnGlyGluProGlyTyrLeaArgGlyIleSerLeuLysGlyGlnG 296
QY 410 ----- 410
Db 296 lYtlMetGlyPheProGlyLeuArgGlyTyrProGlyLeuSerGlyGlnLysArgIySerp 316
QY 411 -GGGCAAAACGCTGGA--GGTCCGACCTATGATTTGTGACACATCAAGATTACCA 465
Db 316 roGlyGlnLysArgIySerArgGlyLeuAsp-----GlyTyrGln 328
QY 466 GAGACCAAGGTGTCTACCTCGCGAGCGTGTCTGTGAGGACATCTTGATTTCTAC 525
Db 328 nGlyPro-AspGly--Pro--ArgGlyPro--LysGly-----G 339
QY 526 AGCGAAGATATCCGGACATGTTCCACTGCG--CCTCTTCTGAGACACCACTCCGAC 582
Db 339 lualaGlyAspProGly-----ProProGlyLeuPro--AlaTyrSerProHisProse 356
QY 583 G-----TCAGGCTGTCTGAGAGATTTCCCGGACGTCGCGGAGAGAGGA-- 629
Db 356 rIeuAlaLysGly--AlaArgGlyAspProGlyPheProGlyAlaGlnGlyGluProG 375
QY 629 ----- 629
Db 375 lYSerGlnGlyGluProGlyAspProGlyLeuProGlyProProGlyLeuSerIleGlyA 395
QY 629 ----- 629
Db 395 spGlyAspGlnArgArgGlyLeuProGlyGlnMetGlyProLyseGlyPheIleGlyAsp 415
QY 630 -----CCTGAGACAGATTCTGACGAGCATCAACACC 660
Db 415 roGlyTyrLeuProAlaLeuTyrGlyGlyProProGlyProAspGly--LysArgGlyProPr 434
QY 661 TTCTGTAAGCCGAGCTTTCGAGAGTTCTGCT----- 692
Db 434 oGly--ProProGlyLeuProGly-----ProProGlyProAspGlyPheLeuPheGlyL 452

```

```

QY 692 ----- 692
Db 452 euLysGlyAlaLysGlyArgAlaGlyPheProGlyLeuProGlySerProGlyAlaProG 472
QY 693 -----GCCGCAAAAGATATCCGATGT----- 716
Db 472 lYProLyseGlyTyrPlyseGlyAspAlaGlyGlnLysArgIySerThrGlnGlyAspGlnAla 492
QY 717 -----GATCATCCCA 726
Db 492 lYLeGlyLeuProGlyLeuProGlyProLyseGlyPheAlaGlyIleAsnGlyGluProG 512
QY 727 CGAGAGTGGACAAATGTTGTTCATCAACCTGATGTGAGACAT----- 773
Db 512 lYArgLysGlyAspLysGly-----AspProGlyGlnHisGlyLeuProGlyP 528
QY 774 -----CCAGACATTCGTAATGTGACATCTGACATTCGCAATGCAACCGA 813
Db 528 heProGlyLeuLysGlyValProGlyAsn-----IleGlyAlaProGly--ProL 544
QY 814 GAGAGTCCAAATGGCGGAGCTACAAAGCGACCTTTCTGAGCCAGGAGCAC----- 867
Db 544 ys-GlyAlaLysGlyAspSer-----ArgThrIleThrLysGlyGlnArgGlyGln 561
QY 868 -----CCTGGAGTGTGACCTCTGCGAAACGTCATTTGAGTCC 909
Db 562 ProGlyValProGlyValProGlyMet-----LysGlyAspAspGlySerPr 577
QY 910 AGCAGACAGACCCCACTGAGGCGCTCGGAGCTCAGAGGAGGTCTCCGCGCGCATGTG 969
Db 577 oGlyArgAspGlyLeuAspGlyPheProGlyLeu--ProGly--ProProGlyAspGln 595
QY 970 TGTTCAGGACCTGAGCTGTGGAGCGCCACCAACCCACTGCTGCT----- 1017
Db 595 yIleLysGly--ProProGlyAsp--Pro-GlyTyrProGlyTyrLeuProGlyThrLysGly 613
QY 1018 -----CTCGCGCACCC-----CAGGAGAGTGTAGC 1044
Db 614 ThrProGlyGlnMetGlyProProGlyLeuGlyLeuProGlyLeuLysGly-----G 631
QY 1045 AGCAGAGCTCTCTCACTCAGAGTGAAGAAACAGATGTGTCACTCAGACTCAACTAATGCT 1104
Db 631 lArgGlyPhePro-----GlyAsp-----Ala 638
QY 1105 GCGACACTGACAGGCGCTTCTGAGGTTTCAACCACTTAGGCTGTGCGGTTTAAAGAT 1164
Db 639 Gly--LeuProGlyProPro--GlyPhe-----LeuGly----- 648
QY 1165 CCTCTAGGTCACTGAGAAATGCCACAGAAATGTGACAGAAAGCTGTGGAGGCTTCTGTAG 1224
Db 649 -ProProGly-----ProAlaGlyThr-----ProGlyGlnIle----- 659
QY 1225 GAATGTAG--GCACATTATTGGGGAATATTGAGAGACAGCCCTAGAC 1269
Db 660 AspCyAspThrAspValLysArgAla--ValGly-----GlyAspArgGlnGln 675
QY 1270 ACT----- 1272
Db 676 AlaIleGlnProGlyCysIleGlyGlyProLyseGlyLeuProGlyLeuProGlyProPro 695
QY 1272 ----- 1272
Db 696 GlyProThrGlyAlaLysGlyLeuArgGlyIleProGlyPheAlaGlyAlaAspGlyGly 715
QY 1273 -----GGCTGCGCTGATGTGTTGTTGACAGTGAACCAACGAGGAGAGATT 1320
Db 716 ProGlySerArgGlyLeuProGly-----Asp-----AlaGlyArgGlnGln 729
QY 1321 TTTCGAGTGTGATGTGTTCTTACACTCAGACATTAACCTAAAGTTTGTGACAA 1380
Db 729 yPhePro-----GlyPro-----ProGlyPheIleGly-- 738
QY 1381 AGTACTTTCCTTTTAACTGATGCTCAATGCTTCTGTTTCTGTTTCAATPACA 1440

```

```

Db      739  -----Pro-----ArglySer-----742
Qy      1441 CAAGCGTGTGGCTGCTACAACTTAATTTCATGACCAGTGTGGCTTCAG-----1496
Db      743  -lySGlyAlaValGlyLeu-----ProGly-----SerProGlyPr757
Qy      1497 -----CGTGCTTACACGA-----1511
Db      757  oileGlyLeuProGlyProAspGlyProProGlyGluArgGlyLeuProGlyGluValLe777
Qy      1511 -----1511
Db      777  uGlyAlaGlnProGlyProArgGlyAspAlaGlyValProGlyGlnProGlyLeuLysG1797
Qy      1512 -----TATGGAGGAGCCACTGAGGGA1531
Db      797  yLeuProGlyAspArgGlyProProGlyPheArgGlySerGlnGlyMetPro-----GlyM816
Qy      1532 TGTTCCTCCCTCTGCTTGCTGCTTAAGCGACGAAAGCAGGCGGATGCCCTGGAGCA1591
Db      816  et-----ProGly-----LeuLysGlyGlnPro-----GlyLeuProGly-----827
Qy      1592 CCCAGCATCACACCAGGCTTGCGGGGCGCA1623
Db      828  -ProSerGlyGlnProGlyLeu-TyrGlyPro837

```

## RESULT 15

```

US-09-488-725A-2519
: Sequence 2519, Application US/09488725A
: GENERAL INFORMATION:
: APPLICANT: Hyseq Inc
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
: FILE REFERENCE: 784FLEPT
: CURRENT APPLICATION NUMBER: US/09/488, 725A
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US/09/488, 725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: US09/620,312
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: US09/653,450
: PRIOR FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: US09/662,191
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: US09/693,036
: PRIOR FILING DATE: 2000-10-19
: PRIOR APPLICATION NUMBER: US09/727,344
: PRIOR FILING DATE: 2000-11-29
: NUMBER OF SEQ ID NOS: 7144
: SOFTWARE: Pf_FL_genes_b Versions 1.0
: SEQ ID NO 2519
: LENGTH: 948
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-488-725A-2519

```

## Alignment Scores:

```

Pred. No.: 3.48 Length: 948
Score: 462.60 Matches: 204
Percent Similarity: 20.22% Conservative: 55
Best Local Similarity: 15.93% Mismatches: 138
Query Match: 15.46% Indels: 884
Db: 1 Gaps: 24

```

```
us-09-896-522-1 (1-1624) x US-09-488-725A-2519 (1-948)
```

```

Qy      1622 GAGCCCGACAGCCTGGGTGTGAT-----GCTGGGTG1590
Db      82  GlyProSerAsp-ProProAlaAspHisAlaValArgProLeuHisGlyAlaArgGly--100

```

```

Qy      1589 CTTCCAGGAGATCCGCTGCTTCTGCTTTAAGGCAC-----1550
Db      101  -----GlyGlnProPro-----ValProGlnGlnHisValLeuGluArgGlnValG116
Qy      1549 -----AACCAAGGGGGGAAAC1533
Db      116  nLeuSerGlnGlyGlnAsnValValIleLysValLysProProSerLysSerGlySerAl136
Qy      1532 ATCCCTCAGTGGCTCC-----CCATAT-----1511
Db      136  aSerAlaSerGlyAlaGlnArgGlySerLeuGlnGlnPheGluAspThrProTyrSerAs156
Qy      1510 -----CCGTGTAGGCC1500
Db      156  pGlnArgProArgGlnGlyGlnGlyGlnProProArgGlyGlnLeuGlnProSerArgPr176
Qy      1499 A-----1499
Db      176  oThrArgAlaArgGlyThrCysSerValGluAspProLeuLeuValCysGlnLysGluPr196
Qy      1499 -----1499
Db      196  oGlyLysProArgMetValLysSerValGlySerValGlyAspSerProArgGluProAr216
Qy      1499 -----1499
Db      216  gArgThrValSerGlnSerValIleAlaValLysAlaSerPheProSerSerAlaLeuPr236
Qy      1498 -----CGCTGAGCTGCMAACCACTGGGTCACTGAATTTAGG1464
Db      236  oProArgThrGlyValAlaLeuGlnLysGlyLysSerHisSerValAlaSer-----254
Qy      1463 TTTGTAGGCCACAAACGACCTTGTATTATGAACAGAAACAGAAACATGAGACAT--1406
Db      255  -CysAlaProGln-----LeuLeuGlyAspArgValAspAla--GlyHisThr270
Qy      1406 -----1406
Db      270  rAspGlnProValProSerGlySerValGlyGlyProAlaArgProAlaSerGlyProAr290
Qy      1405 -----GTACATGTAAAGAAAGAAAGTACTGTTTCACAA1371
Db      290  gGlnAlaArgGluAlaSerLeuValValThrCysArgThrAsnLysPheArg-----307
Qy      1370 ACTTTGAGTTATGTGTGAGTGTGAAGCTGTAAGACCAAGTCAAGCTGG-----1325
Db      308  -----LysAsnAsnTyrLys-TripAlaAlaAlaSerSe318
Qy      1324 -----AAAAAAGCTCTCCCACTGTGGGTTCACCTGTCACAA1287
Db      318  rLysSerProArgValAlaArgArgAlaLeuSerProArgValAlaAla-----GluA336
Qy      1286 ACATCAGCGACGACCGCTGTAGGCTGTCTCTCAATTTCCCAATATATGTGCTCACAT1227
Db      336  snValCysLysAlaSerAla-----GlyMetAlaAsnLysVal-----348
Qy      1226 TCCTCAGCAAGACCT-----CCAGGCTTCCGTCACAT1194
Db      349  -----GluLysPProGlnLeuIleAlaAspProGluProLysProArgLysProAlaThr366
Qy      1193 TCTGTGGCATTTCTCAGTACCTAGAGGATCTTTAAACGCAACGACCTTAAGTGGCTG1134
Db      367  Ser-----SerLys-----Pro-----GlySer--AlaProSerLysTyr-LysTyr---379
Qy      1133 AAAAAGCTCAGAGACGCTGTCTAGTGTCCAGCAAGTTGAGTCTGAGTGACATCTGAGT1074
Db      380  LysAlaSer--SerPro-----SerAlaSerSerSerSerSerP392
Qy      1073 TTCACCTCTCAGTGTAGAGAGGC-----1051
Db      392  nArgTyrGlnSerGlnAlaGlySerLysAspHisAlaSerGlnLeuSerProValLeuS412

```

```

QY 1050 -----CTGCTG 1044
Db 412 eArGerSerProSerGlyAspArgProAlaValGlyHisSerGlyLeuLeuProLeuSerG 432
QY 1043 CTAAACCTCCCTGGGGTGGCCGAG-----AGGAAGCACT 1008
Db 432 lYgluThrProLeuSerAlaTyrLeuValLysSerArgThrLysIleIleArgArgArg- 451
QY 1007 GGGTGGGGGGGGCTCCCAAGGCTCAGTCCCTGAAACACACATGCCGGGGGAGA----- 952
Db 452 -----GlySer-----ThrSerLeuProGlyAspLysLys 462
QY 952 ----- 952
Db 462 eRcGlyThrSerProAlaAlaThrAlaLysSerHisLeuSerLeuAlaArgGlnAla 482
QY 951 -----CCTGCCCTGAGGCTCGGCAAGCCCTCAGTGGGGTCTGCTGCTG 909
Db 482 euArgGlyLysSerSerProValLeuLys-----LysThrProAsnLysGlyLeuValGln 500
QY 908 GACTCCAA-----TGTGACGTTTCCGAGAGGTACGATCCC----- 871
Db 501 ValThrLysHisArgLeuCys---ArgLeuPro-----ProSerArgAlaHisL 516
QY 871 ----- 871
Db 516 euProThrLysGlnAlaSerSerLeuHisAlaValArgThrAlaProThrSerLysValI 536
QY 870 -----AGGGTGGTCCCTGGCTCAGAAAAGGTCCGCTTGTAGTCCGCCA 825
Db 536 lElyThrArgTyrArgIleValLysLysThrProAlaSerProLeuSerAlaProProp 556
QY 824 TTGGACCTCCTCGGTGCCATTGTCAGATGTCAACATTGCAAGATGTCGATGCTGC 765
Db 556 he---ProLeuSerLeuPro-----SerTrp---ArgAl 565
QY 764 AGCA----- 761
Db 565 ArgArgGluSerLeuSerArgSerLeuValLeuAsnArgLeuArgProValAlaSerG 585
QY 760 -TCAGATTGATGGCAACATATTGCTCACTCTCGTGGATGATCATCGCATCTTC 702
Db 585 yEgLyGlyLysAlaGlnProGlySerPro-----Trp-TPArgSerLysGlyTyrArg 602
QY 701 TTTGTGGCAGGC----- 689
Db 603 CysIleGly-GlyValLeuTyrLysValSerAlaAsnLysLeuSerLysThrSerGly 622
QY 688 -----AGAATCTCCGAAAGCGCGCTTCACGAG 660
Db 622 nProSerAspAlaGlySerArgProLeuLeuArgThr-----GlyArgLeuAspPro 640
QY 659 GTGGTGTACTGCTCAGAACTCTGCTCAGGCTCCCTCGGCGGCAAGTCCGAGAACT 600
Db 640 lEgLy-----SerCysSerArgSerLeuAlaSerArgAlaValGlnArgSer 655
QY 599 CTT----- 597
Db 656 LeuAlaIleIleArgGlnAlaArgGlnArgArgGlyLysArgLysGlyLysCysMetLys 675
QY 596 -----CGAGACAGCCCTGAGTCCGAGTCCGCTGCTCCACGAAGAGCCGAG 552
Db 676 TyrAsnArgPheGlyLysArgCysAsn---ArgGlyGlnArgCysPro-----T 690
QY 551 TGGAACTGTCCCGATCTCTGCTGTAGAACACCAAGATGCTCAAAAGAACACAG 492
Db 690 yLleHisAspProGlyLysValAlaVal-----Cys----- 700
QY 491 TCCGACGGGTAGACCACTGGTCTCTGTAACCTTGAGTGTCAAAAATCATAGTTC 432
Db 701 -----ThrArgPheValArgGly-----ThrCysLysLysThrAspGly- 713
QY 431 GGCACCTCAACGTTTGGCCT-----CCAGAGT 402

```

```

Db 714 -----Thr-----CysProHisSerHisValSerLysGlyLysMetProValCys 729
QY 401 TTCT----- 398
Db 729 sSerTyrPheLeuLysGlyIleCysSerAsnSerAsnCysProTyrSerHisValTyrVa 749
QY 397 -----TCAGACTCCGTGCATCAATATCTTCAAGGCACTGTGATGTCAAA 348
Db 749 lSerArgLysAlaGlnValCysSerAsp-----PheLeuLysGly----- 762
QY 347 TTGACTGTCTTTCAAGGCTTGGC-----CTTCTGCTGCTGC- 310
Db 763 ---TyrCysPro-----LeuGlyAlaLysCysLysLysLysHisThrLeuLeuCysP 779
QY 309 -----CGTCAGACCTTGT----- 296
Db 779 roAspPheAlaArgArg-GlyAlaCysProArgGlyAlaGlnCysGlnLeuLeuHisAr 798
QY 295 -----AGAACCTGTCTGCTCAGATGACCA----- 269
Db 798 gThrGlnLysArgHisSerArgArgAlaAlaThrSerProAlaProGly---ProSerAs 817
QY 269 ----- 269
Db 817 palThrAlaArgSerArgValSerAlaSerHisGlyProArgLysProSerAlaSerG 837
QY 268 -----CCTTCGCTGCGCTGTTCCACCTGCTTGTGTCGACCAAC 228
Db 837 nArgProThrArgGlnThrProSerSerAlaAlaLeuThrAlaAlaValAlaAlaPr 857
QY 227 TCGATATCTTTCACACACAGGTGCACTTCGCTGGCAGTGGCGGCTCACCCTATC 168
Db 857 oPro-----His-----CysProGlyLysSerAla-----SerProSerSe 869
QY 167 AGAAGAGCGCGTGGTGGCGGAGCGTCCGCGGCGGGGCTCTCGCATGTTGAGCT 108
Db 869 lSerLysAla-----SerSerSerSerSer-----SerSerSerSerPro 882
QY 107 CCGCGC-----GAAGCATCTCGGCTTCGCTCC 78
Db 883 ProAlaSerLeuAspHisGlnAlaProSerLeuGlnAlaAlaLeuAlaAlaLys 902
QY 77 GCGCATCGGCTC-----CCGCGCGCGCC 54
Db 903 SerAsnArgLeuCysLysLeuProSerPheIleSerLeuGlnSerSerProSerProGly 922
QY 53 CTTCCCGGGCGCGCGCGCGCGCGCGCGCGCGCGAGTCCGAGGCGAGC 5
Db 923 AlaGlnPro-----ArgValArg---AlaProArgAlaProLeuThr 935

RESULT 16
US-09-488-725A-6091
; Sequence 6091, Appl:ication US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036

```

```

; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b versions 1.0
; SEQ ID NO 6091
; LENGTH: 955
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-6091

Alignment Scores:
Pred. No.:      3.87      Length:      954
Score:          460.60    Matches:      209
Percent Similarity: 20.70%  Conservative: 53
Best Local Similarity: 16.51% Mismatches: 140
Query Match:      15.39%  Indels:      864
DB:                1      Gaps:      26

us-09-896-522-1 (1-1624) x US-09-488-725A-6091 (1-954)

QY      1622 GGGCCGCGCAGAACGCTGGGTGTGAT-----GCTGGCTG 1590
DB      88  GlyProSerAsp-ProProAlaAspHisAlaValArgProLeuHisGlyAlaArgGly-- 106
QY      1589 CTTCAGAGGCAATCCGCTCGCTTCTCTGCTTAAAGCAC----- 1550
DB      107  -----GlyGlnProPro-----ValProGlnGlnHisValLeuGlnArgGlnValG1 122
QY      1549 -----AAGCAAGGCGGGAAC 1533
DB      122 nLeuSerGlnGlyGlnSerValValLeuValValLysProProSerLysSerGlySerAl 142
QY      1532 ATCCCTGAGTGGCTCC-----CCATAT----- 1511
DB      142 aSerAlaSerGlyAlaGlnArgGlySerLeuGlnPheGlnAspThrProTrpSerAs 162
QY      1510 -----CCGTGTAGGCC 1500
DB      162 pGlnArgProArgGlnGlyGlnGluProProArgGlyGlnLeuGlnProSerArgPr 182
QY      1499 A----- 1499
DB      182 oThrArgAlaArgGlyThrCysSerValGluAspProLeuLeuValCysGlnLysGluPr 202
QY      1499 ----- 1499
DB      202 oGlyLysProArgMetValLysSerValGlyLysSerProArgGluProAr 222
QY      1499 ----- 1499
DB      222 gaArgThrValSerGlnSerValIleAlaValLysAlaSerPheProSerSerAlaLeuPr 242
QY      1498 -----CGCTGAGCTGCAACCACTGGGTGATGAAATTAGG 1464
DB      242 oProArgThrGlyValAlaLeuGlyArgLysLeuGlnSerHisSerValAlaSer----- 260
QY      1463 TTGTGAGCCCAACAACAGCTTGTGTATGAAACAGAAACAGAAACATAGACAT- 1406
DB      261 --CysAlaProGln-----LeuLeuGlyAspArgArgValAspAla---GlyHisThr 276
QY      1406 ----- 1406
DB      276 rAspGlnProValProSerGlySerValGlyGlyProAlaArgProAlaSerGlyProAr 296
QY      1405 -----GTAACATGTAAAGAAAGTAAGTCTGTTTCACAA 1371
DB      296 gGlnAlaArgGlnAlaSerLeuValValThrCysArgThrAsnLysPheArg----- 313
QY      1370 ACTTTAGATTATGTGTGAGTGTGTAAGAACAGATCAAGCTGG----- 1325
DB      314 -----LysAsnAsnLysLys-TripAlaAlaAlaSerSe 324

```

```

QY      1324 -----AAAAACTCTCTCCCACTGGGTTCACGTCAACAA 1287
DB      324 LysSerProArgValAlaArgArgAlaLeuSerProArgValAlaAla-----GluA 342
QY      1286 ACATCAGGCCAGCCAGTGTCTAGGCTGTCTCTCAATTTCCCATTAATGTGGCTCAAT 1227
DB      342 snValCysLysAlaSerAla-----GlyMetAlaAsnLysVal----- 354
QY      1226 TCCTCAGAGAGCT-----CCAGGCTTCCTGCACAT 1194
DB      355 -----GluLysProGlnLeuIleAlaAspProGlnProLysProArgLysProAlaThr 372
QY      1193 TCTGTGCATTTCTCAGTACCTAGAGGATCTTTAAACCGCAACGCTTAATGGCTG 1134
DB      373 Ser-----SerLys---Pro---GlySer--AlaProSerLysLysr-LysTrp--- 385
QY      1133 AAAAAGCTCAGAAAGCCTGTCAAGTGTCCAGCAAGTGAAGTCTGATGACATCTGAGT 1074
DB      386 LysAlaSer---SerPro-----SerAlaSerSerSerSer 398
QY      1073 TTCACCTCCTGAGTGAAGAGC----- 1051
DB      398 heArgTrpGlnSerGlnAlaGlySerLysAspHisAlaSerGlnLeuSerProValLeuS 418
QY      1050 -----CTGCTG 1044
DB      418 eArgSerProSerGlyAspArgProAlaValGlyHisSerGlyLeuLysProLeuSerG 438
QY      1043 CTACACTCCCTCGGGGTGCGCGAG-----AGAACCACT 1008
DB      438 LysGlnThrProLeuSerAlaLysLysValLysSerArgThrLysIleLeuArgArg- 457
QY      1007 GGGTGGCGGAGGCGTCCCGCAGCTCAGTCCGCAACATACCGCGGC----- 958
DB      458 -----GlySer-----ThrSerLeuProGlyAspLysLys 468
QY      957 --GGAGACCTGCTGAGAGCT-----CGGACGCC 930
DB      468 erGly--ThrSerProAlaThrAlaThrAlaLysSerHisLeuSerLeuArgArgGlnAl 487
QY      929 CTTCAGTGGG-----GTCTGCTGCTGAGCTGCAAAATGACCGTTTGGCAG-- 884
DB      487 aLeuArgGlyLysSerSerProValLeuLysLysThrProAlaLysGlyLeuValGlnVa 507
QY      884 ----- 884
DB      507 lThrThrHisArgLeuCysArgLeuProProSerArgAlaHisLeuProThrLysGluAl 527
QY      883 -----AGTCAAGCATCC-----A 870
DB      527 aSerSerLeuHisAlaValAlaArgThrAla-ProThrSerLysValIleLysThrArgTyrA 547
QY      869 GGGTGTGCTCCCTGAGTGAAGAAAGTCCGTTGAGTCCGCCCATTTGACCTCCCTCGG 810
DB      547 rGlyLeuValLysLysThrProAlaSerProLeuSerAlaProProPhe--ProLeuSerL 566
QY      809 TGCATTTGAGATGTCAACATTCAGAAATGCTCGATGTGTCAGCA----- 761
DB      566 euPro-----SerTrp---ArgAlaArgArgLeuSerLe 576
QY      760 -----TCAGGTGATGCA 747
DB      576 uSerArgSerLeuValLeuAsnArgLeuArgProValAlaSerGlyGlyLysAlaG1 596
QY      746 ACCATATTGCTCACTCTCTGAGATATCATCGGCATACCTTTGTCGCGAGCC-- 689
DB      596 nProGlySerPro-----Trp-TrpArgSerLysGlyLysArgCysIleGly-GlyVa 613
QY      689 ----- 689
DB      613 lLeuTyrLysValSerAlaAsnLysLeuSerLysThrSerGlyGlnProSerAspAlaG1 633
QY      688 -----AGAACCTCCTCGAAGCGCGCTTCAAGAAAGTGTGTTACTGCGTCC 645

```



[illegible]

```

Db          932 -Argvalaag---AlaProhArgAlaProLeuThr 941

RESULT 17
US-09-488-725A-2174
; Sequence 2174, Application US/09488725A
; GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptidea
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US/09/488, 725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US09/552,317
PRIORITY FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: US09/598, 042
PRIORITY FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: US09/620,312
PRIORITY FILING DATE: 2000-07-19
PRIORITY APPLICATION NUMBER: US09/653,450
PRIORITY FILING DATE: 2000-08-31
PRIORITY APPLICATION NUMBER: US09/662,191
PRIORITY FILING DATE: 2000-09-14
PRIORITY APPLICATION NUMBER: US09/693,036
PRIORITY FILING DATE: 2000-10-19
PRIORITY APPLICATION NUMBER: US09/727,344
PRIORITY FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc FL_genes_b Versions 1.0
; SEQ ID NO 2174
; LENGTH: 723
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2174

```

Alignment Scores:			
Pred. No.:	1.93	Length:	722
Score:	458.90	Matches:	204
Percent Similarity:	23.39%	Conservative:	46
Best Local Similarity:	19.08%	Mismatches:	168
Query Match:	15.33%	Indels:	651
DB:	1	Gaps:	19
us-09-896-522-1 (1-1624) x us-09-488-725A-2174 (1-722)			
QY 1624 CTGGCCCCGCACAGACCTGGGTGTGAT-----	1598		
DB 13 LeuAlaIserProProAlaIaPheAspGlyGluLeuAspLeuGlnAlaGlyrSerLeuGly 32			
QY 1597 -----GCT 1595			
DB 33 ProAlaValSerAlaGlySerLeuGlyMetGlyAlaValSerTrpSerGluSerArgAla 52			
QY 1594 GGG-----TGCTCCAGGGCATCGCCTTCCTCTGCT 1559			
DB 53 GlyAlaIaGArgRheProCysProValCysGlyLysArgPheArgPheAsnSerLeu 72			
QY 1558 TTAAAGCAGACAGAGGGGGAAACCTCCCTAGTG-----GCTCCCATAT 1511			
DB 73 AlaLeuHisLeuAlaGla-----HisProGlyAlaGlnAlaPheGlnCysProHis 89			
QY 1510 CCGGTAGGCCAC----- 1498			
DB 90 ---Cys-GlyHisArgAlaAlaGlnAlaLeuLeuAspSerHisLeuArgThrHisGly 108			
QY 1498 ----- 1498			
DB 108 nProGluArgProArgSerProAlaAlaArgLeuLeuGlnLeuGlnAlaGlaLe 128			
QY 1497 -----GCTGACCTGCACAACTGGGTC 1475			
DB 128 uLeuArgGlnAlaArgLeuGlyArgAlaArgSerGlyGlyMetGlnAlaThrProAl 148			





```

Db      829 ValProHistiValGlnAlaMetGlnGlyAsnSerAlaSerGlyAsnHisPheSerGly 848
Qy      737 -----
Db      849 HisGlyMetSerPheAsnAlaProPheSerGlyAlaProAsnGlyAsnGlnMetSerCys 868
Qy      736 -----
Db      869 GlyGlnAsnProGlyPheProValAsnLysAspValThrLeuThrSerProLeuLeuVal 888
Qy      724 -----
Db      889 AsnLeuLeuGlnSerAspHisSerAlaGly-----HisPheGlyVal-----AsnAsn 905
Qy      691 GGCAGAACTCCTCGAAGGCC-----
Db      905 ysgGlnAsnAsnThrAsnHisAsnLysProLysLysLysProProArgLysLysLys 925
Qy      672 -----
Db      925 snSerGlnGlnAspLeuAsnThrProAspThrArgProAlaGlyLeuGlnGlnAlaAspG 945
Qy      671 -----
Db      945 LnPProLeuProGly-----GlnGlnGlyLysSerLeuAspAsn-----SerGlyPro 961
Qy      625 TCCTCGCGCGACGCTCCGGAACCTCTTCAGACAGCCTGACGCTGAGTGGGTGCCA 566
Db      962 LysLeu-----ProGlnPheSerAsnArgProPro-----GlyTyr-----Pro 974
Qy      565 CGAAGAGCGGACG-----
Db      975 -----SerLnPProValGlnGlnArgProLeuGlnGlnMetProProGlnLeuMetG 992
Qy      547 ACATGTCCTGGATGCTGGGTGAGAACACCAAGATCCCTGAAACAGAACCAAGTCGCG 488
Db      992 nHisVal-----AlaPro-----ProProGlnProProGlnGlnGlnProGlnPro 1007
Qy      487 CAGGGTAGACCA-----
Db      1008 Gln-----LeuProGlnGlnGlnGlnProProProProSerGlnProGlnSerGlnGln 1026
Qy      475 -----
Db      1027 GlnGlnGlnGlnGlnGlnMetMetMetMetMetGlnGlnAspProLysSer--- 1045
Qy      463 GTAACCTTGAGTGTGCAAAAT---CATAGGTGGGACCTGCCA-----CCGTTTGC 413
Db      1046 ValArgLeuProValSerGlnAsnValHis-----ProProArgGlyProLeuAsn 1062
Qy      412 CCTCCACGATGTTCTTCAGAGTCTGTGCATCAATCATTAATCAAGGATCTGGATGAT 353
Db      1063 Pro-----AspSerGlnArgMetProMetGlnGln-----SerGly-----SerVa 1076
Qy      352 CAATAATTACTGTCCTTCAAGGCTTGCGCTTGTCTGCGCTGACGACCTTGATGA 293
Db      1076 LProValMetValSerLeuGlnGly-----ProAlaSerValProProSerProAspLys 1094
Qy      292 ACCTGTCTGTGGTCCGATGACCACTTCGCTGCGCGCTG-----
Db      1095 Gln-----ArgMet-----ProMetProValAsnThrProLeuGlySerAs 1108
Qy      253 -----
Db      1108 nSerArgLysMetValTyrGlnGlnSerProGlnAsnProSerSerSerProLeuAlaG 1128
Qy      253 -----
Db      1128 uMetAlaSerLeuProGlnAlaSerGlySerGlnAlaProSerValProGlyGlyProAs 1148
Qy      252 -----TTCCACCTGCTGCTGCTCCAGCAATCCATGATGTTCTTCACACAGCTGC 203

```

```

Db      1148 nAsnMetProSerHisValValLeu-ProGlnAsnGlnLeu-MetMetThr---GlyP 1166
Qy      202 ACTTCCCGCTGGAGTGGCCGCTGACCCCTTATCAGAAAGGCCCTGTTGGAGCGT 143
Db      1166 oLysPro---Gly-----Pro-SerProLeuSerAlaThrGlnGlyAlaThrProGln 1182
Qy      142 CGGCTCCGCGCGGGGCTCTCGCAGT-----
Db      1183 GlnProProValAsnSerLeuProSerSerHisGlyHisHisPheProAsnValAlaAla 1202
Qy      106 CGCCCGAAGCCATCTGCGCTCGCTCCGCGGATCGGATCGCCGCGCCGCTTCCC 47
Db      1203 ProThrGlnThrSerArgProLysThrProAsnArgAlaSerProArgProLysTyrPro 1222
Qy      46 CGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAGTCCGAGCGCACCC 4
Db      1223 GlnThrProAsnAsnArgPro---ProSerThrGln---Pro 1234

RESULT 19
US-09-488-725A-5990
; Sequence 5990, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784PLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_ft_genes_b Versions 1.0
; SEQ ID NO 5990
; LENGTH: 1567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5990

Alignment Scores:
Pred. No.: 18.4 Length: 1565
Score: 456.40 Matches: 197
Percent Similarity: 24.95% Conservative: 58
Best Local Similarity: 19.28% Mismatches: 123
Query Match: 15.25% Indels: 645
DB: 1 Gaps: 16

us-09-896-522-1 (1-1624) x US-09-488-725A-5990 (1-1565)
Qy      1622 GGGCCCGCACAAGCTGGGTGTATGCTGGTGTCTTCAGGG-----CAT----- 1578
Db      881 GlyPro-----LeuGly-----ProGlyProGlnHisAlaProPhe 894
Qy      1577 -----
Db      895 TrpSerThrValProProProProLeuProProAlaSerHisGlyArgAlaValProG 914
Qy      1561 -CCTTAAGGCACAGAGGGGG-----GAAAACATCCCTCACTG 1521
Db      914 nPro-LysMetGlnSerArgGlyThrProAlaGlyProProGlnAsnVal----- 930

```

```

QY 1520 CTCCCATATCCGTTAGTGGCCACGCTGACTGACAAACCACTGGGTCAATGAGTTT 1461
    |||:::|||||
Db 931 LeuProLeuSerMet-AlaPro-----ProLeu-----SerLeuGlyLeu 943
QY 1460 GTAGGCCAACAACGCTTGTGTTATGAAACAGAAAACAGAAAACATGAGACATGTAAAC 1401
    |||:::|||||
Db 944 ProGlyHisGlyAlaPro-----GlnThrGlnProThrLeuValGlu----- 957
QY 1400 ATGTAATA-----AGGAAGTACTGTTTCAAAAACCTTTT 1365
    |||:::|||||
Db 958 --ValLysProValProAlaSerProHisProLys-----HisLysValSer 972
QY 1364 GAGTTATGTGTGATGATGTAGAACCAAGTCACTGGAATAAATCTCTCCCACTGT 1305
    |||:::|||||
Db 973 AlaLeu-----ValGlnSerProGlnMet-----LysAlaLeuAla--Cys 985
QY 1304 -----GGTTCACCTGTCAACAAAACATCAGGCCAGCCAGTGTCTAGGCTGTCT 1257
    |||:::|||||
Db 986 ValSerAlaGlyValThrValGluGlu-----ProAlaSer-GluArgLeuLys 1002
QY 1256 CTTCAATTTCCCAATATATGCTCACAATTCCTCACAAGAAAGCTCCCAAGCTTCTGCA 1197
    |||:::|||||
Db 1003 ThrGlnThrGlnGlu-----ThrArgProArgGlnLysProPro--LeuProAla 1018
QY 1196 CATTCGTGTG----- 1188
Db 1019 ThrLysAlaValProThrProArgGlnSerThrValProLysLeuProAlaValHisPro 1038
QY 1188 ----- 1188
Db 1039 AlaArgLeuArgLysLeuSerPheLeuProThrProArgThrGlnGlySerGluAspVal 1058
QY 1187 -----GCATTTCTCAGTACGCTAAGAGGATCTTTAAACCGCAACGAGCTTAAGTGTCTG 1134
    |||:::|||||
Db 1059 ValGlnAlaPheHisSerGluIle--GlyIle-----GluAlaSerAspLeuSer----- 1074
QY 1133 AAAACCTCAGGAAGCGCTGTCAAGTGTCCAGCAAGTTGATGTAGACACATCTGAGT 1074
    |||:::|||||
Db 1075 -----SerLeuLeuGlnGlnPheGlnLys-----SerGln- 1084
QY 1073 TTCCACTCTGAGTGAAGAAAGCGCTGCTTAACACTCCCTGGGGTGGCCGAGAA-- 1017
    |||:::|||||
Db 1085 -----AlaLysLys--GluCys-----ProProProAlaProAlaAsp 1096
QY 1016 -----GGAACGATGGGTGTGGTGGCGCTCCCAAGCTCAAGTCCCTGGAACAC 969
    |||:::|||||
Db 1097 SerLeuAlaValGlyLysSerGly-----GlyVal-----AspIleProGlnGlu 1111
QY 968 ACATGCCGGGGGGAAGACCTGAGCTCGGAGCTCGGAGACCCCTCAATGAGGTGTGCTGTG 909
    |||:::|||||
Db 1112 Lys-----ArgProLeuAspArgLeuGlnAlaProGlnLeuAlaAsnValAlaG 1128
QY 908 GACTCCAAATGTGACCGCTTTGCCAGAGTCAAGATCCCAAGGTGTCCCTGCTCAGAA 849
    |||:::|||||
Db 1128 LysLeuThr-----ProProAlaThrProHisGlnLeu--TrpLysPro----- 1142
QY 848 AAGTCCGCTTGTAGCTCCGCCCATTTGACCTTCCTCGGTGCATTTGGCAGATGTACCA 789
    |||:::|||||
Db 1143 -----LeuAlaAlaValSerLeuLeuAlaLys 1151
QY 788 TTCAGATGCTCTGATGTGCTGACAGATCAGGTGATGCAACATATTGTCCACTCCT 729
    |||:::|||||
Db 1151 SerAlaLysSerProLysSerThrAlaGlnGlyLys-----ThrLeu-----LysPro 1166
QY 728 CGTGGATGATGATCATCGCATATCTTTGTGCGCAGGAGCAACTCTTCCGAAGGC----- 673
    |||:::|||||
Db 1167 GluGly--ValThrGlnAla--LysHisProAlaAlaValArg--LeuGlnGlnGlyValH 1185
QY 672 -----CGGCTTCACGAAGGTGTG-----TACTGCTGAGATATGCT 635
    |||:::|||||
Db 1185 HisGlyProSerArgValHisValGlySerGlyAspHisAspLysCysValArg-----S 1203
QY 634 CCAGTTCCTCTCCCTCGCGGCACTCCCGAGAACTCTTCGAGACAGCTGACCTCGGAGT 575

```

```

Db 1203 eArgThrProProLysLys-MetProAlaLeuLeuIle-----ProLysValGly-- 1219
QY 574 CGGTGTCACGAAGAGCGCGAGGTGGAACATGTCGCCGATCTCTGCTGTAGAACCA 515
    |||:::|||||
Db 1220 -----SerArgTrpAsnValLysArg-----HisGly 1228
QY 514 AGAT----- 511
Db 1228 nAspIleThrIleLysProValLeuSerLeuGlyProAlaAlaProProProCysIle 1248
QY 510 -----GCCCTCAACAGAACCAACGCTCCGAGGTAGACCAACCGTGTCTGTAACTTG 455
    |||:::|||||
Db 1248 eAlaAlaSerArg--GluPro-----LeuAspHisArg-----Thr 1259
QY 454 AGTGTGTCAAAATCATAGTGTGCGACCTTCACCGTTTGC----- 413
    |||:::|||||
Db 1260 SerSerGlnGlnAlaAspProSerAlaPro-----CysLeuAlaProSerSerLeu 1276
QY 412 -----CCTCCA----- 407
Db 1277 LeuSerProGlnAlaSerProCysArgAsnAspMetAsnThrArgThrProProGluPro 1296
QY 406 -----CGATGTTCTTCAGATCTGTGATCATCAATCATTAATCA 368
    |||:::|||||
Db 1297 SerAlaLysGlnArgSerMetArgCysTyArgLysAlaCys-----ArgSerAlaSerP 1315
QY 367 AGGCATCT--GGATGTCAA-----AATTGATCTGTCTTTCAGAGCCT 326
    |||:::|||||
Db 1315 roSerSerGlnGlyTrp--GlnGlyArgArgGlyArgAsn-----SerArg-- 1329
QY 325 TGCCCTTTCGCTGTGCGCGCAGACCTTGTAGAACCTGTCTGCTCAGATATACCACT 266
    |||:::|||||
Db 1330 -----SerAlaSerSerGlySerAsnArgThr----- 1338
QY 265 TCCGTCGCGCTGTTCACCTCGTTCTGTCCCACTCATGATCTTCTCACACAG 206
    |||:::|||||
Db 1339 SerGlnAlaSer--SerSerSer-----SerSerSer--SerSerSerSerArg 1353
QY 205 TCGACTTCCCGCTGCGAGTGCAGCGCGCTCACCCCTATCAGAAAGGCGCGTGG-- 153
    |||:::|||||
Db 1354 SerArgSerArg-----SerLeuSerProHisLys--ArgTrpArgArg 1369
QY 152 -----TGCAGACGCTGTGGCTCTCCGCGCGCGGC 125
    |||:::|||||
Db 1369 eArgSerCysSerSerSerGlyArgSerArgArgCysSerSerSerSerSerSerSers 1389
QY 124 TTCGCAAGCTTTCGCTCCCGCGAGCCATCTCGGCTCCGCTCCGCGCATCGGAGTCC 65
    |||:::|||||
Db 1389 eArgSerSerSerSerSerSerSerSerSer-----ArgSerArgSer----- 1404
QY 64 CCGCGCCCGCCCTTCCCGCGGCGCGCGCGCCGCCAGCGCGAGTCCGAGGCGGA 7
    |||:::|||||
Db 1405 --ArgSerProSerProArgArgArgSerAspArg-----ArgArgArg 1418

RESULT 20
US-09-488-725A-2418
; Sequence 2418, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FlPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450

```



```

Db      541 yglYser-AlaProGlnLeuLeu--ValGlnSerGlnSerLeuAaProProLySerThri 560
QY      513 -----GATGCCCTCAACA----- 500
Db      560 leIleProGlnValLySgluValAlaAspSerLeuLySgluSerGlyThrSerAlaT 580
QY      499 -----GACCAAGCTCCGAGGATGAGACACCGGTGCTGTGTAACCTGAGTGTG 448
Db      580 hThrHisGlnAlaArgPro-----ArgPro-----LeuSerLeuS 592
QY      447 CACAAATATATAGG----- 434
Db      592 ergGluYrArgArgArgGlnGlnArgGlnAlaGluThrGlnGluArgSerProGlnP 612
QY      434 ----- 434
Db      612 roProThrGlyYrProSerSerLeuProGlnThrProThrGlyLeuAlaAspIleProC 632
QY      434 ----- 434
Db      632 ySleuValIleProProAlaProAlaLySThrAlaLeuGlnArgSerProGlnThrP 652
QY      433 -----TCGCACCTCCAC 421
Db      652 roLeuGlnIleCysLeuValProValGlyProSerProAlaSerProSerProGlnProP 672
QY      420 CTTTTGGCCCTCCAGCATGTTCTTCAGAGTCCCTGTCATCAATCATTTCAAGAGCATC 361
Db      672 roValSerLySerPro-----ValAlaSerSerProThrGlnGlnVal----- 685
QY      360 TGGATGTCGAAATGCTACTGCTTCAAGCCTGGCT----- 320
Db      686 --ProSerGlnGlnMetProLeuLeuAlaArgProSerProProValGlnSerValSerP 705
QY      320 ----- 320
Db      705 roAlaValProThrProProSerMetSerAlaAlaLeuProPheProAlaGlyGlyLeuG 725
QY      320 ----- 320
Db      725 lYMetProProSerLeuProProProProLeuGlnProProSerLeuProLeuSerMetG 745
QY      319 -----TCGCTCTGCCGTCAGAGACCTGT----- 296
Db      745 lYProValLeuProAaProPhePheHisTyrAlaProLeuProSerTyrProCysTyrP 765
QY      295 --AGAACTGTGCTGCTCAGATGACCA----- 269
Db      765 roHisValSerPro--SerGlyYrProCysLeuProProProProThrValProLeuV 784
QY      268 -----CCTTCGCTGCCGCTGTCACCTGCTGT----- 237
Db      784 alSerGlyThrProGlyAlaTyrAlaValProProThr--CysSerValProThrAlaPr 803
QY      236 -----CCGAGCAACTCCATGATCTTCTACACACGCTGAGACTTCCC 196
Db      803 oProProAlaProValSerProTyrSerSerThrCys-----ThrTyrGly-----Pr 819
QY      195 GCTGGCAGTCCGCGCTCAGCCCTATCAGAAAGGCGCTGATGGAGGCTGCGGCTC 136
Db      819 oleuGlyTyrGlyPro-GlyPro-----GlnHisAlaProPheThrSerThrVal--ProP 837
QY      135 CG-----GCCGC 130
Db      837 roProProLeuProProAlaSerIleGlyArgAlaValProGlnProLySMetGlnSerA 857
QY      129 GGGGCTTCGCGAGTCTTCGCTCC-----GCCGAAGCCT 94
Db      857 rGgly--ThrProAlaGlyProProGlnuAnValLeuProLeuSerMetAlaProProle 876
QY      93 CTCGCGCTCCGCTCCGCGCATGGGTCGCCG----- 62

```

```

Db      876 uSerLeuGlyLeuProGlyHis-GlyAlaProGlnThrGluProThrLySValGluVal 896
QY      62 ----- 62
Db      896 yAProValProAlaSerProHisProLySHisLySValSerAlaLeuValGlnSerProG 916
QY      62 ----- 62
Db      916 lMetLySAlaLeuAlaCysValSerAlaGluGlyValThrValGluGluProAlaSerG 936
QY      61 -----CGCCCGCCCTTCCCGGG 43
Db      936 lAArgLeuYsProGluThrGlnGluThrArgProArgGluLySProProLeuPro--A 955
QY      42 CCGCGCGCGCGCGCGCGAGCGCGAGTCCGAGGCGACCCCA 2
Db      955 lAThrLySAlaValProThrProArgGlnSerThrValPro 968

RESULT 21
US-09-488-725A-2188
; Sequence 2188, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: HySeq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PC_FL_genes_b Versions 1.0
; SEQ ID NO 2188
; LENGTH: 4619
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2188

Alignment Scores:
Pred. No.: 345 Length: 4618
Score: 451.30 Matches: 208
Best Local Similarity: 21.48% Conservative: 50
Best Local Similarity: 17.32% Mismatches: 146
Query Match: 14.87% Indels: 797
DB: 1 Gaps: 27

us-09-896-522-1 (1-1624) x US-09-488-725A-2188 (1-4618)
QY      10 CCTCCGACCTCGCGCTGAGCGCGCGCGCGCGCGG----- 48
Db      682 ProProAlaSerAlaCysProGlyGlyCysGlyProArgGluLeuCysArgAlaGlyGln 701
QY      49 -----GAGGCGCGCGCGCGCGGAGCC----- 70
Db      702 CysValCysValGluGly-----PheArgGlyProAspCysAlaIleGlnThrCysProG 720
QY      71 GATCGCGCGAGCGCGAGCG-----CGAGTGGCTTCG 102
Db      720 yAspCysArgGlyArg-GlyGlnCysHisAspGlySerCysValCysLySAspGlyTyr- 739

```







```

Db      1362 AspSerPheVal1IegIntYLyAspArgAspGlyGlnProGlnValValProValGlu 1381
QY      1300 ACCCAAGGAGGAGAGATTTTTCAGTCTG-----ATCTGTTCTTA 1344
Db      1382 GlyProGlnArgSerAlaVal1IethSerLeuAspProGlyArgLySTyLyAsPheVal 1401
QY      1345 CACACTCACACATACATAAAGTTTGTGAACAGTACTTTCCTTTTTCAT----- 1400
Db      1402 -----LeuTyrlYpHeValIGlyLySlys-----ArgHisGlyP 1413
QY      1401 -----GTTACATGTCCTC 1413
Db      1413 roLeuValAlaGlnAlaLyAlleuPProGlnSerAspProSerProGlyThrProProH 1433
QY      1414 ATGTTTCTGTTTCTGTTTCATACACAGGCTGTTGTG-----CCACAAAC 1464
Db      1433 IsLeu-----GlyAsnLeuTyVal1ThrAspProThr----- 1443
QY      1465 CTATTTCATACCCAGTGTGTCAGTCCAGCGTGCCTTACACGATATGGAGGCAC 1524
Db      1444 -----ProAspSerLeuHisLeuSer-----TrpThrValPr 1454
QY      1525 TGAGGATGTTTTCCTCCCTTCTGCTTGTAAAGGACAGAAAGCGAGCGGATGCCCT 1584
Db      1454 oGIuGIyGlnPheAspThrPheMetValGlnTyTArgAspArg-----Asp----- 1469
QY      1585 GGAAGCAACCCAGATCACACCCAGGCTTGCGCGGCCCA 1623
Db      1470 Gly-ArgProGlnValValPro-----ValGluGlyPro 1480

RESULT 22
US-09-488-725A-3457
; Sequence 3457, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 3457
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3457

Alignment Scores:
Pred. No.: 17.7 Length: 1409
Score: 450.70 Matches: 207
Percent Similarity: 20.39% Conservative: 46
Best Local Similarity: 16.68% Mismatches: 125
Query Match: 14.85% Indels: 863
DB: 1 Gaps: 25

```

```

QY      10 CTTCCGACCTCGGCG-----CTGGCGGCGCGCGCGGCC 45
Db      532 ProProThrAlaAlaGlnGlnGlnLeuAspArgLeuLeuGlyGly-----CysGlyVal 550
QY      46 GGGGAAAGGCGCGGCGCGGAGCCGATGCGCGGAGCGGAGCGGAGATGCTTCGGCG 105
Db      551 Alaser--GlyGlyArgGly-----AlaGlyArgGlnThr-----AlaIleLeu 564
QY      106 GAGGCGAAGACTCGGAGACCCCGCGGAGGCCGACCGTCCGAC----- 153
Db      565 AspAspGlnGlu-----GlnProThrValGlyGly-----GlyProHisLeuGlyValTyx 581
QY      154 -----CAGCGCGCTTCCTGATAGGGGTGAGGGGCGCACTGCGAC----- 194
Db      582 ProGlyHisArgPro-----GlyLeuSer--ArgHisCysSerCysArgGlnGlyT 598
QY      195 --CGGAAAGTGCACCGTGTGTGAGAAATCATGATGATGCTGGGACAGAAAGAGTTGA- 251
Db      598 yrnArgGlu-----ProCys-----GlyValProAsnGlyGlyT 609
QY      252 -----ACAGCGGACGCGGAAAGGTGTGATCTTGAGC 282
Db      609 yTyrArgProGlnGlyThrLeuGlnArgArgLeuAlaTyrglyGlyTyr----- 626
QY      283 CAGGACAGGTTTACAAAGTCTGACGCGAGACGAGA----- 320
Db      627 ----GluGlySer-----ProGlnGlyTyrAlaGlnAlaSerMetGlnyAsArgyl 643
QY      321 -----GGCAAGGCTTGAAGAGCAGTCAATTTTGAACATTCAGATGCC 366
Db      643 euCyAsrSerLeuSerGlnGlyLeu-----TyrProTyr--Pro-ProGlu-- 657
QY      367 TTTGATTAATGATTGATTCACAGAGACTTGAGAAATCGTGGAGGCGAAACGTTGAG 426
Db      658 -----Met-----GlyysProAla-- 662
QY      427 GTGCGACCTATGATTTTGTGACACATCAAGTTTACAGAGCAACGGTGTCTACCT 486
Db      663 ----ThrGlyAspHe-----GlyTyTArgAlaPro--Gly-Tyr-- 673
QY      487 GCGAGCGTGTCTGTTTGAAGGACATCTGTGTTTACAGCCAGAGATCCGAGA----- 542
Db      674 ArgGlnValValIleLeuGlu-----AspProGlyLeuP 665
QY      543 -----CATGTTCCACTGCGCTCTTC 564
Db      685 roAlaLeuTyTProCysProAlaCyGluGlnGlyLeuAlaLeuProThrAlaAlaLeuT 705
QY      565 GTGGAACAGCATCCGACGTCAGGCTGTCTCGAAGATTCTCCGGGACGTCGCCGAGGG 624
Db      705 yrdLyLeuArgLeuGlnArgGlnAla-----Gly-----G 715
QY      625 AGGCACTGAGAGATTTGACAGCA-----GTACACACACTTGTGAAAGCG 672
Db      715 IuGly--TrpAla-----SerGlnAlaGlyLyserProLeuLeuHis--Pro--ValArgPro 731
QY      673 GCCTTCAGAGA-----GTTCTGCTGCGGACAAAGAGATATGCGCATGTG 717
Db      732 -----GlyHisPProLeuPProLeuLeuProAla-----CysG 743
QY      718 ATCAT-----CCACAGAGAGTGGACAAATATGTTGCCATCAACTGATC 762
Db      743 LyHisHisAlaProMetPro-----AspTyTserCysLeuLyserProProL 759
QY      763 GTGCAAGCATCCAGGACATTTGATGTGATGTGACATGTGCAATG----- 807
Db      759 yeaIaGlyGlnGlnGlnHis-----GluGly-----CysSerTyThrMetCysProGlu 775
QY      807 ----- 807
Db      776 GlyArgTyGlyHisPProGlyTyTProAlaLeuValThrTySerTyGlyGlyAlaVal 795
QY      808 -----CACCGAGAGAGGTTCATATGGCGCGAGC 834

```

```

Db      796 ProSerTyrCySProAlaIyRgIyAArgValProHisSerCySglYSerProGlyGlnGly 815
Qy      835 TACAGGGAGCCTTTTCTGAGCCAGGGAGCAC----- 867
Db      816 -----ArgGlyTyrProSerProGlyAlaHisSerProAlaGlySerIleSerPro 833
Qy      867 ----- 867
Db      834 GlySerProProTyrProGlnSerAArgLysLeuSerTyrGluIleProThrGlnGlnGly 853
Qy      868 -----CCTGGGATCTGACCTCTGGCAACGGTCACATTTGGAGTCC 909
Db      854 GlyAspArgTyrProLeuProGly-----HisLeuAlaSer 865
Qy      910 AGCAGCAGACCCCACTGAGGGGCTGCCGAG----- 939
Db      866 AlaGly-----ProLeu-AlaSerAlaGlySerLeuGlnProValSerTyrAArgGlnGly 883
Qy      940 CCTCAGGGC-----AGTCTCCCGCCCGCATGTGTGTTCAGGAGCTGAG 984
Db      884 ProSerGlyHisSerThrLeuProAArgSerProAArgAlaProCySeralAserSer 903
Qy      985 -----CCTGGGAGCGCCACCAACCCACCTGCTTCTCT 1019
Db      904 GluLeuSerGlyPro-SerThrProLeuHisThr-----SerSerProValGlnGly 921
Qy      1020 -----CGCGCGCA 1026
Db      921 yGlnSerThrAArgAArgGlnAAspThrAArgSerProThrSerAlaProThrGlnAArgLeu 941
Qy      1027 CCCAGAGGAGTGTATGACGAGGAGCGCTTCTCTACCTACAGAGTGAAGTCAAGTGTGTC 1086
Db      941 erProGlyGln-----AlaLeuPro-Pro-----Val 949
Qy      1087 ACTGACTCAACTGCTGGGAGCACTGACAGCGCTTCTCTGAGTTTTCAGCCACTTAGGC 1146
Db      950 SerGln-----AlaGlyThr-----GlyLysAlaProGlnLeuProSerGlySerGly 965
Qy      1147 -----TCGTTGGCGTTTAAAGATCCCTTAGGCTCACTG 1179
Db      966 ProGlnProLeuAlaProSerProValSerProThrProSerProSerProSer--- 984
Qy      1180 AGAATGCCACAGATGTCAGAGAGCGCTTCTCTGAGATGTGAGGC----- 1235
Db      985 -AspTrpProGlnGln-----ArgSerPro-GlyGlyHisSerAsp-----GlyAlaAs 1000
Qy      1236 -----ACATTATTGGGAAATTGAGAGACAGCCTAGACACT 1272
Db      1000 erProAArgSerProValProThrThrLeuProGly-----LeuAArgHisAlaPro----- 1016
Qy      1273 GGCTGG----- 1278
Db      1017 -----TrpGlnGlyProAArgGlyProProAAspSerProAAspGlySerProLeuThrProVal 1035
Qy      1279 -----CCTGATGTTTGTTCACAGTGC 1239
Db      1036 ProSerGlnMetProTrpLeuValAlaSerProGlnProPro-----GlnSerS 1052
Qy      1300 AACCCAGTGGGAGAGAGATTTCAGTGTGATCTGTTTACACACTCAGACACAT 1359
Db      1052 erProThrProAla-----PheProLeu-AlaAlaSerTyrAspThrAAsnglyLe 1068
Qy      1360 AACTCAA----- 1366
Db      1068 uSerGlnProProLeuProGlnLysAArgHisLeuProGlyProGlyGlnGlnProGlyPr 1088
Qy      1366 ----- 1366
Db      1088 OTripGlyProGlnGlnAlaSerSerProAlaAArgGlyIleSerHisValThrPheAl 1108
Qy      1366 ----- 1366

```

```

Db      1108 aProLeuLeuSerAspAsnValProGlnThrProGlnProProThrGlnGlnSerGlnSe 1128
Qy      1367 -----AAGTTTGGACAAGTACTTCTTTTACATGTTACATGCTCATGTTT 1419
Db      1128 rAnValLysPheValGlnAspThrSerLysPheTrp-----TyrLys-ProHisLeuS 1146
Qy      1420 TC-----TCGTTCTGTTCATTA 1437
Db      1146 erAArgAspGlnAlaIleAlaLeuLeuLysAspLysAspProGlyAlaPheLeuIleAArg 1166
Qy      1438 ACACAAG-----CTGTTGGCGCTTACAACTTAATT 1470
Db      1166 sPheHisSerPheGlnGlyAlaTyrGlyLeuAlaLeuLysValAlaThrProPro----- 1184
Qy      1471 TCATGACCAAGTGTTCAGTCCAGCGGCTTACACGGAATGAGGAGCCACTGAGG 1530
Db      1185 -----ProSer-AlaGlnPro-TripLys-----GlyAspProValGlnG 1197
Qy      1531 ATGTTTCCCTCTGCTGTG-----CCTTAAGCAGAG 1566
Db      1197 Ln-----LeuValAArgHisPheLeuIleGlnThrGlyPro-LysGlyValI 1212
Qy      1567 AAGCAGCGCGATGCCCT-----GGAAGC-----ACCCAG 1596
Db      1212 yAlleLys-GlyCySProSerGlnProTyrPheGlySerLeuSerAlaLeuValSerGln 1231
Qy      1597 CAT----- 1599
Db      1232 HisSerIleSerProIleSerLeuProCySLeuAArgIleProSerIysAspProLeu 1251
Qy      1599 ----- 1599
Db      1252 GluGlnThrProGlnProProValProThrAsnMetSerThrAlaAlaAspLeuAArg 1271
Qy      1600 -----CACACCAAGGTTTGCGCGG 1620
Db      1272 GlnGlyAlaAlaCySerValLeuTyrLeuThrSerValGlnThrGlnSerLeuThrGly 1291
Qy      1621 CCA 1623
Db      1292 Pro 1292

RESULT 23
US-09-488-725A-2440
: Sequence 2440, Application US/09488725A
: GENERAL INFORMATION:
: APPLICANT: Hyseq Inc
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
: FILE REFERENCE: 784FLPCT
: CURRENT APPLICATION NUMBER: US/09/488,725A
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US/09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: US09/620,312
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: US09/653,450
: PRIOR FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: US09/662,191
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: US09/693,036
: PRIOR FILING DATE: 2000-10-19
: PRIOR APPLICATION NUMBER: US09/727,344
: PRIOR FILING DATE: 2000-11-29
: NUMBER OF SEQ ID NOS: 7144
: SOFTWARE: pt_fl_genes_b Versions 1.0
: SEQ ID NO 2440
: LENGTH: 1589
: TYPE: PRT
: ORGANISM: Homo sapiens

```



Db	613	laleuGlnGluValArgSerCysaenGluHleProCysThValThyHleTrpGlnThrG	633
QY	773	-----	773
Db	633	lyProTrpGlyGlnCysillegluAerThnSerValSerSerPheanThrThrThrt	653
QY	773	-----	773
Db	653	rpaeNGlyGluAlaSerCysSerValGlyMetGlnThrArgLysValIleCysValaArgV	673
QY	773	-----	773
Db	673	alaenValIGlyGluValGlyProLysCysPheProGluSerLeuArgProGluThrValA	693
QY	774	-----	792
Db	693	rgProCysLeuLeuProCysLysLysAerCysIleValThrPro---TyrSerAerTrp-	711
QY	793	GACATCT-----	799
Db	712	-ThSerCysPheSerSerCysLysGluGlyAspSerSerIleArgLysGlnSerArgHl	731
QY	800	-----GCAAATGGACCGAGAGAGGTCCAAATGGAGCG-----	831
Db	731	aArgValIleIleGlnLeuProAlaasnLys-----GlyArgAerCys	745
QY	832	-----AGCTACAG	840
Db	746	ThraPProLeuTyrGlnGluLysValaCysGluAlaProGlnAlaCysGlnSerTyrArg	765
QY	841	CGGACCTTTTCTGACCCAGGAGGACCACTCGGAGCTGACCTCTGG-----CAAA	891
Db	766	-----TrrLysThrHlLysLysTrpArgArgCysGlnL	776
QY	892	CGGTCAATTTGGAGTCCAGACAGACCCCACTGAGGGCTGCCAGCTCAGGAGCAG	951
Db	776	eulAlaProTrpSerValGlnGlnAspSerPro---GlyAlaGlnGlu---GlyCys	792
QY	952	TCTCCGCCCGG-----	963
Db	793	GlyProGlyArgGlnAlaArgAlaIleThrCysArgLysGlnAspGlyGlnAlaGly	812
QY	964	---CATGTGTG-----TCAGGAGACTGAGCCT-----	987
Db	813	lIleHlsGluCysLeuGlnTyrAlaGlyProValProAlaLeuThrGlnAlaCysGlnIle	832
QY	988	-----GGGAGC	993
Db	833	ProCysGlnAspAerCysGlnLeuThnSerTrpSerLysPheSerSerCysaenGlyAerP	852
QY	993	-----	993
Db	853	CysGlyAlaValArgThrArgLysArgThnLeuValIGlyLysSerLysLysLysLys	872
QY	994	-----GCCCACCACACCCACTGCTT-----	101
Db	873	CysLysAsnSerHlSerLeuTyrProLeuIleGluThnGlnTyrCysAerProCysAerLysTyr	892
QY	1015	-----CCCTCTGAGC-----GCACCCGAGGAGTGTTTACAGC	104
Db	893	AsnAlaGlnProValaGlyAsnTrpSerAerCysIleLeuProGlnGlyLysVal	910
QY	1048	GAGGCTTCTCTCACTCAGAGAGTGGAAACTAG-----	107
Db	911	GluValLeuLeu-----GlyMetLysValaGlnGlyAspIleLysGluCysGlyGlnGlyT	929
QY	1079	-----	107
Db	929	yrArgTyrGlnAlaMetAlaCysTyrAerPglAsnGlyArgLeuValGluThnSerArgC	949
QY	1079	-----	107
Db	949	ysAsnSerHlSerGlyTrrIleGlnGluAlaCysIleIleProCysPheSerAerCysLysL	969

[illegible]

```

QY 1290 -----GTTGAC----- 1295
Db 1310 heserlyvalValaspGluGluPheCysalaAspIleGluLeuIleAspGlyAsnL 1330
QY 1296 -----AGTAACCCACAGTGGAGAGAGATTTCACACT 1329
Db 1330 ysaAnetValleuGluGluSerCysSerGlnProCysProGlyAspCysTyrLeuLysa 1350
QY 1330 CTGATCTGTTCTTACACTACACATACACT----- 1363
Db 1350 sp--TTPSerSerTTPSerLeuGluLeuThrCysValaAsnGlyGluAspLeuGlyPh 1369
QY 1364 -----CAAAAGTT 1371
Db 1369 eglYgIyIleGluValArgSerArgProValIleIleGluGluLeuGluAsnGlnHisLe 1389
QY 1372 TTGT--GAACAAGTACTTCTTTTTCATGTTACATGTTCTCATGTTTCTGTTTC 1428
Db 1389 uCysProGluGluMetLeuGluThrLysSerCysTyrAspGlyGluCysTyrGluTyrLys 1409
QY 1429 TGTTCATACACACAGGCTGTTGTGGCCACAAACCTATTTTCATGACCCAGTGTTCG 1488
Db 1409 s--TTPMetAlaSerAlaTTP-----LysGlySerSerArgThrValTTP--Cy 1424
QY 1489 CAGTCCAGCGT-----GGCCTACACGAGATATGAGAGCAGTACAGGATGTTT----- 1537
Db 1424 s--GlnArgSerArgGlyIleAsn-----ValThrGlyGlyCysLeuValMe 1439
QY 1538 -----CCCCCTTGCTTGTC----- 1554
Db 1439 tSerGlnProAspAlaAspArgSerCysAsnProPro--CysSerGlnProHisSer 1457
QY 1554 ----- 1554
Db 1458 TyrCysSerGluThrLysThrCysHisCysGluGluGlyTyrThrGluValMetSerSer 1477
QY 1555 -----TTAAAGCAGAG 1566
Db 1478 AsnSerThrLeuGluGlnCysThrLeuIleProValValValLeuProThrMetGluAsp 1497
QY 1567 AAGCGAGCGGATCCCTTGAGG-----CACCCAGATCACCACCGAGCT 1611
Db 1498 LysArgGly-AspVal--LysThrSerArgAlaValHisPro-----ThrGlnPro 1513
QY 1612 TGAGCGGGGCCA 1623
Db 1514 SerSerAsnPro 1517

RESULT 24
US-09-488-725A-5469
; Sequence 5469, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29

```

```

; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PL FL_genes_b Versions 1.0
; SEQ ID NO: 5469
; LENGTH: 839
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-5469

Alignment Scores:
Pred. No.: 4.84 Length: 839
Score: 447.50 Matches: 190
Percent Similarity: 19.09% Conservative: 65
Best Local Similarity: 14.22% Mismatches: 111
Query Match: 14.95% Indels: 972
DB: 1 Gaps: 20

us-09-896-522-1 (1-1624) x US-09-488-725A-5469 (1-839)
QY 1614 ACAAGCCTGGGTGTATGCTGGGTGCTTCAGAGGACATCCGCTTCCTGCTTAA 1555
Db 6 ThrSerLeu-----ValProThrHis-----LeuProMet- 15
QY 1554 GGCAACAGCAAGGAGGAAACATCCCTCAGTGGCTC-----CCCAT 1513
Db 16 -----Gly-----ThrLeuCysSerGlyLeuLeuPheProva 26
QY 1512 ATCCGTGTAGGCCACCTGAGCTGCAACACCTGGCTCATGAATTAGTTGTAGGCCA 1453
Db 26 1Ser-Cys--LeuValLeu--LeuGlnValAlaSerSer-----Gly-- 38
QY 1452 CAACAGCCTGTGTATGAAACAGAAACAGAAACAGAGACATGTAATGTAATAA 1393
Db 39 -----AsnMetLys-----ValLeu 43
QY 1392 AAGAAAGTACTGTGTTCACAAACTTTTGATGTTAGTGTAGTGTAGAACACAGAT 1333
Db 44 GlnGluProThrCysValSerAspTyr-----MetSerIleSerThr--C 58
QY 1332 CAGACTGGAAAAAATCTTCTCCCATCTGGGTGCTCACTGCAACAAA----- 1286
Db 58 yegLutRpySweLAsnGlyProThr--AsnCysSerThrGluLeuArgLeuLeuT 76
QY 1285 -----CATCAGGCCAGCAGTGCTA----- 1265
Db 76 yrgLInLeuValPheLeuLeuSerGluAlaHisThrCysValProGluAsnAnGlyGlyA 96
QY 1264 --GGCTGTCTCTCAATTCCCAATATGTCCTCACAATTCCTCAGAGA----- 1216
Db 96 lagLYCys-----ValCys--HisLeu--LeuMetAspAspValVal 108
QY 1215 -----GCTCCAGAGCTTCTGCAATTTCTGTGTC 1186
Db 109 SerAlaAspAsnTyrThrLeuAspLeuThrAlaGlyGln-----GlnLeuLeuTTP- 125
QY 1185 ATTTCTCAGTACCTAGAGGATCTTTAAACCGCAACGACTTAAGTGGCTGAAAACTTC 1126
Db 126 -----LysGlySerPheLysPro-----SerGlnHisVal 135
QY 1125 AGAAAGCCTGCTCAGTGTCCCGAAGTGAAGTGAAGTGAACATCTGAGTTCCACATC 1066
Db 136 Lys--Pro--ArgAlaProGlyAsnLeuThrVal-----HisThr 147
QY 1065 CTGAGTGAAGAAAGCCTGCTGCTTAACCTCCCTGGGGTGGCGGAG----- 1018
Db 147 rAsnValSerAspThrLeuLeuLeuThr-----TrpSerAsnProTyrProProAspAs 165
QY 1018 ----- 1018
Db 165 nTyrLeuTyrAsnHisLeuThrTyrAlaValAsnIleTrpSerGluAsnAspProAlaAs 185
QY 1018 ----- 1018
Db 185 pPheArgIleTyrAsnValThrTyrLeuGluProSerLeuArgIleAlaAlaSerThrLe 205

```

QY	1018	-----	1018
Db	205	uLysSerGIylIeSerTYrATGAlaArgValATGAlaTrrAlaGInCYsTYrAenTh	225
QY	1018	-----	1018
Db	225	rTrpSerGIuTrpSerProSerThrTrpHisAenSerTYrATGInProPheGIuGI	245
QY	1018	-----	1018
Db	245	nHleuLeuLeuGIuValSerValSerCYsIleValIleuAlaValCYsLeuLeuCY	265
QY	1017	-----	980
Db	265	sTYrValSerIleThrIleTYrIleLeuLYsLeuGIuTrp---TrpAenGIuIlePro-----As	282
QY	979	TCCTGAACACACATCCGGCGGGAGACCTGCCCTGAGGCTC-----	937
Db	282	nPro-----AlaArgSer-----ArgLeuAlaIleIleIleGI	294
QY	936	-----GGACGCCCTCAGTGGGGnCTGCTGTGAGTCCAAATGTGACCTGTTC	887
Db	294	nAspAlaGInGlySer---GInTrp-----GIuLYs---Arg--Se	305
QY	886	CAGAGTCACAGATCCCCAGAGTGGTCCCTGCTCAGAAAAGGTCCGCTTGACTCCGCC	827
Db	305	rArgGIyGIuGIuPro-----AlaIeCYs---Pro--	314
QY	826	CATTGG-----ACCTCGCGGTGCATTGGCAGATGTGCACCATTCAGAAATG	780
Db	315	HIeTrpLYsAenCYsLeuThrLYsLeu--LeuPro--CYsPheLeuGIuHIeAsn--MetL	333
QY	780	-----	780
Db	333	ySArgAspGIuAspProHIeLYsValAlaLeuGIuMePProPheGInGlySerGIuLYs	353
QY	779	--TCTTGATGTGCTGCACGATCAGGTGATGGCAACCATATTGTTCACCTCCTCGTGGG	722
Db	353	eAlaTrp---CYsProValGIuIleSerLYsThrValLeu-----TrpTr	367
QY	721	TGATCACAATCCGATTACTCTTGTTCGGCAGCAGCAAACTCTCCGAA-----	676
Db	367	oGIuSerIleSerValValArgCYs-----ValGIuLeuPheGIuAlaProValGIuCY	385
QY	676	-----	676
Db	385	sGIuGIuGIuGIuValGIuGIuGIuLYsGIuSerPheCYsAlaSerProGIuSerSe	405
QY	675	-----GGCGGGCTTCACGAA-----	661
Db	405	rATGAspAspPheGInGIuValArgGIuGIuIleValAlaArgLeuThrGIuSerLeuPh	425
QY	660	-----GGTGGTGTACTGCTCAGAAAT-----	640
Db	425	eLeuAspLeuLeuGIuGIuLaandGIuLYsPheCYsGInGIuAspMetGIuLYsSerCY	445
QY	639	-CTGCTCCAGGTCCTCCCTCC-----TCGGGACAGTCCTCCG-----	607
Db	445	hLeuLeu-----ProProSerGIuSerThrSerAlaHIeMetProTrpAspGIuPheDr	463
QY	607	-----	607
Db	463	oSerAlaGIuProLYsGIuAlaProProTrpGIuLYsGIuGInProLeuHIeLeuGIuTr	483
QY	607	-----	607
Db	483	oSerProProAlaSerProThrGIuSerProAspAenLeuThrCYsThrGIuTrpProLe	503
QY	606	-----GAGAACTCTTGACAGCAGCTGACGT	581
Db	503	uValIleAlaGIuAsnProAlaTYrATrGSerPheSerAenSerIleuSerGIh-----	520

QY	580	CGAGTGGAGTGTCCAGAAAGAGCGGAGAGTGAACATATGTCGCGATCTTCGGTGTAGA	521
Db	521	---SerProCyvProArg-----GluLeuGlyProAerProLeuLeuAlaArg	535
QY	520	ACACCAAGATGCGCTCAACAGAACCAAGT-----	491
Db	535	gHiIleuGlu-----GluValGluProGluMetProCyValProGluIleuSerGluPro	553
QY	490	-----CGCAGAGGTAGACCAACCGGTGGTGTGGTGAACCTTGAGTGTGCACAAAT	440
Db	554	ThiThrValProGlnProGluProGlu-----ThiTrp-----GluGlnI	567
QY	439	CATAGTGCAGGACCCACCGCTTTTGCCCTGCACAGATGTCTTCAGAGTCCGTGCATCA	380
Db	567	eleuArgTrgArgen-----ValLeuGln--HiIleGluAlaAlaAlaProValSer--	583
QY	379	AATCATTTTCAAGGACATGTGATGTGCAAAATTG-----	345
Db	584	-----AlaProThiSerGlyGlyGlnGluPheValHiAlaValGluGlnGlyGlyT	601
QY	345	-----	345
Db	601	hrgIAlaSerAlaValAlaGlyLeuGlyProProGluGluAlaGlyTyrValaIaPheS	621
QY	345	-----	345
Db	621	erSerLeuLeuAlaSerSerAlaValSerProGluCyValGlyPheGluAlaSerSerG	641
QY	344	-----TACGTGCTTTTCAAGAGCTTTGGCTGTGCTGTGCTGCCTGCAGACCTTGT	296
Db	641	IyGluGluGlyTyrTyrSerProPheGlnAerLeu-----IlePro--Gly-----	654
QY	295	AGAACTGTCTGTGCTGCAGATGACCAACCTTCGCTGCCGCTGTGCA-----	248
Db	655	-----CyvProGly-----AerProAlaProValaPro--ValProIleuPheThiRhe	669
QY	247	-----CCTGCTGTCTGTCCAGCAACTCATATCTTGCACACACGCGATTCGCCG	194
Db	670	GlyLeuAerPArgGluProProArgSerProGlnSerSerHis-----LeuProSe	686
QY	193	TGGCAGTG-----	184
Db	666	rSerSerProGlnHiIleuGlyLeuGluProGlyValAlaGluAerMetProIuAer	706
QY	183	GCGGCTTCAACCCCTATCAGAAAGG-----CGCTGTGTCCGAGCGGTCCGCTCCGCGC--	132
Db	706	oProLeu--ProGlnGluGlnAlaThiAerProLeuValAerSerLeuGly--SerGlyT	725
QY	132	-----	132
Db	725	eValTyrSerAlaLeuThiCyvHiIleuCyValHiIleuGlyGlnGluGlnGluGlnI	745
QY	121	-----GCGGCGCTTC	121
Db	745	uAerGlyGluGlnThiProValMetAlaSerProCyvGlyCyvGlySerGly--As	764
QY	120	GCAAGTTCGCGCTCCCGCGGAGCAACCATTCGCGCTCCGCTCCGCGAGATCGGCTCCCGC	61
Db	764	ParGluAerProProThi-----ThiProLeu-----Arg-----Al	775
QY	60	GCGCGCCCTTCCCGGCGCGCGCGCGCGC-----	31
Db	775	aProAerProSerProGly--GlyValProLeuGluAlaSerLeuCyvProAlaSerLeu	794
QY	31	-----	31
Db	795	AlaProSerGlyIleSerGluCyvSerLeuSerSerSerSerPheHiProAlaProGly	814
QY	30	---GCCCAGCGCGGAGTGCAGAGCGACCCCA	2
Db	815	AerAlaGln-----SerSerSerGlnThiPro	823

RESULT 25

## RESULT 25

```

US-09-488-725A-6059
; Sequence 6059, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PC FL_genes_b Versions 1.0
; SEQ ID NO 6059
; LENGTH: 1222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6059

```

## Alignment Scores:

```

Pred. No.:      13,6      Length:      1213
Score:          447.30     Matches:      207
Percent Similarity: 18.92%  Conservative: 71
Best Local Similarity: 14.09%  Mismatches: 126
Query Match:      14.94%   Indels:      1066
DB:              1        Gaps:        33

```

```

us-09-896-522-1 (1-1624) x US-09-488-725A-6059 (1-1213)

```

```

QY      1619 CCGGCAAGCGCTGGTGATGCT----- 1595
DB      26  ProGlnLeuSerTrpVal-----AlaSerSerProSerSerLeuSerValAlaSerProth 44
QY      1594 -----GGGCTCTTCAGGGCATCGGCTGCTTCTGCGCTTTAAGCA 1551
DB      44  rGlnMetIleGlyAspGlyCysAspLeuGlyLeu-----GlyG 57
QY      1550 CAAGCAAGGGGGAAAAACATCCCTCAAGTGGTCCCATTCCTGT----- 1505
DB      57  InGlnGlnGlyGly-----ThrGlyLeuProGlyProCysGlnPheCysAsp 73
QY      1505 ----- 1505
DB      73  sSerPheIleArgLeuSerTrpLeuGlyAspGlnIleGlnIleHisSerAspLeuP 93
QY      1504 -----AGGCCACG 1497
DB      93  oPheLysCysThrTrpCysSerArgLeuPheLysHisLeuArgSerArgAspArg-His 113
QY      1496 CTGCACTGCAAAACCATCGGCTCATGAATTAAGTTGTAGGCCAACAACGCTTGTT 1437
DB      113  LeuLysLeuHisThr-----GlyAspLys-----LysTr-----CysH 125
QY      1436 ATGAAACAGAA-----AACAGAAACATGAGCATGTAAATGATTAATAAAG 1389
DB      125  IsGlnCysGlnAlaIaIaPheSerArgSerAspHisLeuLysIle-----HisLeuLysThrH 144
QY      1388 AAGACTTGTTCAAAAACCTTTGAGTTATGTGTGTAGTGTGTAGAAC----- 1338
DB      144  IsSerSer-----SerLysProPheLys-----CysThr-ValCysLysAspGlyPheSer 160

```

```

QY      1338 ----- 1338
DB      161  SerThrSerSerLeuGlnSerHisMetGlnAlaHisLeuLysAsnLysGlnHisLeuAla 180
QY      1338 ----- 1338
DB      181  LysSerGlnLysGlnAlaLysLysAspAspPheMetCysAspArgTrpCysGlnAspThrPhe 200
QY      1337 -----CAGATCAGATGGA 1323
DB      201  SerGlnThrGlnLysGlnLysLysHisValLeuThrArgHisProGlnLeuSer-----Gln 219
QY      1322 AAAAATCTCTCCCACTGTGGGTTCACGT----- 1294
DB      220  LysAlaAspLeuGlnCys-----IleHisCysAspProGlnValPheValAspGlnAsnThrLeu 239
QY      1293 -----CAACAAACATCAGGCCAGCGAGTGT 1268
DB      239  euAlaHisIleHisGlnAlaHisAlaAsnGln-----LysHisLysCysArgMetCysArg 258
QY      1267 -----CTAGGCTGTCTCTCAATTCCCAATTAATGTCCTCAATT-----CTTCACAGAA 1215
DB      258  uGlnPhe-----SerSerValGlnLysValTrpCys-----HisLeuAspSerHisArgG 275
QY      1214 CTTCCCAAGCTTCTGACATTTCTGTGGCATTTCTGACATTAAGGAGGATCTTTAAC 1155
DB      275  n--ProAspSerSerAsnHisSerValSer-----ProAspProValLeuGlnGlySerVal 292
QY      1154 CGCAACGAGCGCTTAAGTGGTGAATAAAGCTTCAGAAAGCGCTGTCAAGTCCAGCAAGTTGA 1095
DB      293  -----AlaSerMetSer-----SerAlaThrProAspSer-SerAlaSerValG 307
QY      1094 GTCTGAGTGCACACATGTAAGTTTCACTCTCTGATGAGAAAGGCTGTGCTTAACATC 1035
DB      307  uArgGly-----SerThrProAsp-----SerThrLeu-LysP 318
QY      1034 CCTGGGAGTGGCGCGAGAGA-----AGCATGGGTGGTGGTGG----- 995
DB      318  roLeu-----ArgGlyGlnLysLysMetArgAspAspGlyGlnGlyTrpThrLys 334
QY      995 ----- 995
DB      335  ValValLysSerCysAspProGlyCysSerLysArgAspPheAsnSerLeuAlaValLeuGln 354
QY      994 -----CGTCCCAAGCTCAATGCTCCCTGGAACACACATGCCC 962
DB      355  IleHisLeuLysThrIleHisAlaAspLysProGln-----GlnSer-----HisThrCys- 371
QY      961 GGGCGGAGACCTGC----- 947
DB      372  -----GlnLysCysLeuAspSerMetProThrLeuTrpAsnLeuAsnGlnHisValArg 389
QY      947 ----- 947
DB      390  LysLeuHisLeuAsnHisAlaTrpProValMetGlnPheGlyAsnLysSerAlaPheHis 409
QY      947 ----- 947
DB      410  CysAsnTrpCysAspProGlnMetPheAlaAspIleAsnSerLeuGlnGlnHisIleArgVal 429
QY      946 -----CTGAGGCTCGGACAGCCC----- 928
DB      430  SerHisCysGlyProAsnAla-----AsnProSerAspGlyAsnAsnAlaAspPheCysAs 448
QY      928 ----- 928
DB      448  nGlnCysSerMetGlyPheLeuThrGlnLysSerSerLeuThrGlnHisIleGlnGlnAlaHis 468
QY      927 -----TCAGTGGGCTGTGCTGTGAGCTCCAA----- 900
DB      468  eCysSerValGlySerAla-----LysLeuGlnSerProValValGlnProThrG 485

```

OY	899	-----TGACCGGTTGGC-----		886
Dd	485	InserPheMetGluValTyrSerCys--ProTyrCyThrAenSerProIlePheGlyLeu		504
OY	885	-----AGAGTCAGCATCCCGAGGTATGCCCTCGACTCA		851
Dd	504	rIleLeuLysLeuThrLysHisIleLeuSerGluAenHisIleValAenIle--ProLeuAlaHis		523
OY	851	-----		851
Dd	524	SerLysLysSerLysAlaGluInserProValSerSerAspValGluValSerSerPro		543
OY	851	-----		851
Dd	544	LysValArgLysLeuSerAlaSerAlaAenSerIleSerAenGlyLutTrpProCysAen		563
OY	851	-----		851
Dd	554	GlnCysAspLeuLysPheSerAenPheGlnSerPheGlnThrHisIleLeuLysLeuHisIleLeu		583
OY	850	-----AAAAGTCCGCTGTAGACTCCGCCAATTGCACCCTCGGTGC----		807
Dd	584	GluLeuLeuLeuArgLysGlnAlaCys-----ProGlnCysLysLeuG		597
OY	806	-----CATTGCAGATGTAC-----		791
Dd	597	IuaSrpPheAspSerGlnGlnInserLeuLeuGlnHisIleThrVal-HisTyrMetThrThr		616
OY	790	-----CATTGAGAATGT-----		779
Dd	617	SerThrHisIleTyrValCysGlnSerCysValSrpLysGlnPheSerSerValAlaAspLeuGln		636
OY	778	-----CTGGATGTGCTGCACGATCAGGTGATGGACAACA		743
Dd	637	LysHisIleLeuLeuAspMetProHisPro-LeuCysCysThr-----His		650
OY	742	T-----AT		740
Dd	650	ECySthrLeuCySGlnGluValAPheAspSerLysValSerIleGlnValHisLeuAlaVal		670
OY	729	TGTCGCACTCC-----TCGGGGAT-----		721
Dd	670	LlysHisSerAenGlnLysLeuMetTyrArgCysThrAlaCysAenThrAspPheArgLys		690
OY	720	-----GATCACATCGGCAATCTTTGTGCGCA		692
Dd	690	eGlnAlaAspLeuGlnValHisIleValLysHisSerHisIleGlnLys-----		704
OY	691	GGCAGAACTCTGGAAGCGCGGCTTACACCAAGGTGGTACTCTGTCAGAACTGCTCCA		632
Dd	705	-----AsnProAlaLysVal----His-LysCysLysIlePheCys-----		715
OY	631	GGTCCCTCCCTCGGCGCACGATCCCGGAGAACCTCTGCAGACAGCTGACACTGCGAG-		576
Dd	716	-----GlyGlnThrPheSerThr-----GluVal-GluLeuG		726
OY	575	-----TCGGTGTCCAGGAAGCGCGCAGGTGAACAATGT-----		542
Dd	726	IncysHisIleIleThrThrHisSerSerLysLysValAen-CysValSrpPheCysSerLysAlaPhe		745
OY	542	-----		542
Dd	746	HisAlaIleIleLeuLeuGlnLysHisIleLeuArgGluLysHisCysValAPheAspAlaAla		765
OY	542	-----		542
Dd	766	ThrGluAenGlyThrAlaAenGlyValProProMetAlaThrLysLysValAlaGluProAla		785
OY	541	-----CCCGATCTCTGACTGTGAACAACCA-----		514
Dd	786	AspLeuGlnGlyMetLeuLeuLysValAsnProGluAlaLeuAen-----SerHisGluAlaSer		800
OY	514	-----		514

```

Db      804  rgluaaerValaaAsraAlaSerGurProMeTyrGluCyuaaPrlleCyseGluAlaIaIaTyr 822
QY      513  -----GATGCGCTCAAAAGAAACAACCGCTCCGAGGGTATGACCA----- 475
Db      824  rThMeGlValleuLeuGlnaenHis--ArgLeuAlaAspHisValaenlleaGrProI 843
QY      474  -----CGAGCTCTCGTAACTTAGT 452
Db      843  ygluaaerAaPrlySerArglyvlyuAlaGluPheIleuGly----- 857
QY      451  GTGTCAACAAATATCAAGTGGACATCCACCGTTTTCCTCCACGATGTCTTCAAG 392
Db      858  -SerHisbys-----CyaaenValCySerArgThrPhePhe-SerGlu 871
QY      391  TCTGTGTCATCAATCATATTACA-----AGGCACTGCAGATGGCA 350
Db      872  AaenIyLeuArgGluIleGlnIThrIlaArgIyProAlaIuVHis-TyrMet----- 889
QY      349  AATTGTATGTGCTTTCAAGGCTTGAGCTTCT----- 317
Db      890  ---CyvProIleCyvGluGluArgPheProSerIleuThrIleuThrGlnIleVal 908
QY      316  -----GCTGTGCGGTCAAGACCTTGGAACCTGTCTGTGCTCAAGATG--- 273
Db      909  ThrHisSerIySerIleuAerPhrGlyThrCyuaArgIleCyS-----LysMetProI 926
QY      273  ----- 273
Db      926  euGlnSerGluGluPheIleGluIHisCyvGlnMetHisProAerPheuArgAaSerI 946
QY      272  --ACCACTTCCGCTGCGGTGTTTCAACCTGTCTGTGTCACCAACATCCATGATCTTCT 215
Db      946  eutInGlyPheArgCyS-ValValCyaaeGlnIThrValIThrSerThr-LeuGluIleu 965
QY      214  CACACACCGT-----CAACTTCCCGCTGGACATGTCGCGCTGCAC----- 175
Db      965  sIleHisGlyThrPheHisMetGlnIyLeu--AlaGlySerSerAlaIaIaSerSerPr 984
QY      175  ----- 175
Db      984  aaenGlyGlnIyLeuGlnIyLeuTyrGlyCyuaIaLeuCyuaIySeGluPheIaGrSe 1004
QY      174  -----CCTATGACGAAGGCGCGTGT 152
Db      1004  rlyeGlnAaerPheuValIyLeuAaerValaenGlyLeuProTyr--GlyLeuCyuaIaGly 1023
QY      151  -----GGGACCGGTCCGCTCCGAC-----GGGGGCTTCGCAAGTCTTCGCGTCCG 104
Db      1024  CyaaeAla--ArgSerAlaAaenIyGlnIValaGlyGlyLeuAla-----Pro 1038
QY      103  CCGAAGCCATCT--CGGCT----- 86
Db      1039  ProGluProAlaAaerArgProCyuaIaGlyLeuArgCySProGluCySerValIyPhe 1058
QY      85  -----CCGCTC 80
Db      1059  GluSerAlaGluAaerPheGluSerHisMetGlnIValaAspHisArgAaerPheuThrPro--- 1077
QY      79  CCGGCAATCGGGTCCCGCGCGCGCTTCCCGGCGCGGCGCGCGCGCGCGCGCGCG 20
Db      1078  -GluThrSerGlyProArg-----LysGlyThrGlnIThrSerProValPro 1092
QY      19  AGGTGCGAG 11
Db      1093  ArgIyAlyS 1095

RESULT 26
US-09-488-725A--2638
; Sequence 2638, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

```



```

FILE REFERENCE: 784FLIPCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US/09/488, 725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US/09/552, 317
PRIORITY FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: US09/598, 042
PRIORITY FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: US09/620, 312
PRIORITY FILING DATE: 2000-07-19
PRIORITY APPLICATION NUMBER: US09/653, 450
PRIORITY FILING DATE: 2000-08-31
PRIORITY APPLICATION NUMBER: US09/662, 191
PRIORITY FILING DATE: 2000-09-14
PRIORITY APPLICATION NUMBER: US09/693, 036
PRIORITY FILING DATE: 2000-10-19
PRIORITY APPLICATION NUMBER: US09/727, 344
PRIORITY FILING DATE: 2000-11-29
NUMBER OF SEQ. ID NOS: 7144
SOFTWARE: pc_fl_genes_b_versions 1.0
SEQ. ID NO 2638
LENGTH: 1122
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-2638

```

```

Db 619 VALLEUCYGLINLEUCYCY--GLYVALA----- 629
QY 742 TATGTCACTCTCTGGATGATCATCGGCATCTTTGTGGCAGCAGAACT 683
Db 630 --LEUSERTHRPROGLYGLY-----ALAARGPHE-----GLYGLYGLYASN- 642
QY 682 CCTCGAAGCCGGCTTCAGAAAGTGG-----TGTACTGGCTGAGAA----- 641
Db 643 -----GLYGLINLE-----TPARGHIEMERPHENHISCYSTRHGLYTHGLIN 657
QY 641 ----- 641
Db 658 HISMETGLYASPCYSPROVALTHRALAENGLYALASERLEUCYSPROSERGLUGLINAL 677
QY 640 -----TCTGCT 635
Db 678 ALASERVALLEUCYSERGLYAENGLINSEGLINTHRLEUSERSERCYASNSERSE 697
QY 634 CCAAGTCCCTCCCTCGGCGACGTCGGAGAACTTCAGACAGCTGACCTCGAGT 575
Db 698 LEUGLYPROTHR-ARGPROTHRILEPROGLUGLINSERALA-----VALALA-- 712
QY 574 CGGTGTCACAGAAAGGC-----GCAGTGAACATGTCGGAGTCT 533
Db 713 --CYSLLEGLUSERGLYGLINLEUARGLEUVALASNDLYGLYGLYARGCYBALAGLYARG 731
QY 532 CTTGGCTGTGAACACCA----- 514
Db 732 -VALGLINLETHYHISGLYGLYSETRGLYTHRILECYASAPSPSETRPAPLEUSE 751
QY 513 -----GATGCCCTCAAGAACAGAACGCT 491
Db 751 TPAPALANLEVALVALCYASARGLEULEUGLYCYSEGLYGLINALLE-ASNALATHRILYS 771
QY 490 CCGGAGGGTAGACCAACCGTGGT----- 469
Db 771 ERALA-----HISHEGLYGLYGLYTHRGLYPROILETRIPLEUASRGLEUCLYSY 788
QY 468 -----CTTGTAACCTTGAGTGTGCACAAATCAT----- 437
Db 788 SAENGLYLYSEGLUSERARGILETR-----GLNCYENHIS--SERHISGLYTRGLY 804
QY 437 ----- 437
Db 805 GLINGLINANCYSARGHISLYSGLUASPRALAGLYVALLECYSERGLUPHEMETSERLEU 824
QY 436 -----AGGTCCGACCTCCACCGCTTTTGCCTCCACGA----- 404
Db 825 ARGLEUTHRSERGLUALASERARGLUALA-----CYBALAGLYARGLEUGLU 840
QY 404 ----- 404
Db 841 VALPHERYHARGNGLYATRPGLYTHRVALGLYSSERSEMETSERGLUTHRTHRVAL 860
QY 403 -----TGTTCACAGACTCCGTGACATCAATCATTTATCAAGGC----- 364
Db 861 GLYVALVALCYASARGLEULEUGLYCYBALAASP-----LYSGLYLYSILEASMPR 877
QY 364 ----- 364
Db 877 CALASERLEUASPRYBALAMETSETRILEPROMETTRYPALASPRANVALGINCYSPROLY 897
QY 363 -----ATCTGATGCTCAAAATTTACTGTCTTCCTTCAGAGCCTTGCTTCT 317
Db 897 SGLYPROASPRHLEUTRGLIN-----CYSPRO--SERSEPROTRPGGLUYS 912
QY 316 GCTTCCCGCTCA----- 305
Db 913 ARGLEUALASERPROSEGLUGLINTHRTRIPLETHRACYASPRANLYSILEARGLEUGLIN 932
QY 304 ---GGACCTTGAGAACCTGTCTCGTCCAGAGT----- 273

```

```

Db 933 GLUGLYPRO---THRSERCYSESRGLY--ARGVALGLINLETRHISGLYGLYSETRPG 951
QY 272 --ACCACCTTCGGCGCGCCGCTGTCACCTGCTC----- 240
Db 951 LYTHRVAL-----CYASAPSPSETRTPAPLEUASPRALAGLINALVALALC 967
QY 240 ----- 240
Db 967 YSEGLINLEULEUGLYCYSEGLYPROALALEUVALAPHELYSGLUALAGLUPHAGLYGLIN 987
QY 239 -----TGTCACAGCAACTCCAGATCTTCTAC 212
Db 987 LYTHRGLYPROILETRIPLEUANGLYVALLYSCYSLYSGLYASN----- 1001
QY 211 ACACGGTGCACCTCCCGCTGCGACGTGCCCGCTCACCCCTTCAGAGAGCCGCTG- 153
Db 1002 ---GLUSERSETRLEUTRASPYS-----PROALARG-----ARGTRPG 1014
QY 153 ----- 153
Db 1014 LYHISERGLUCYSEGLYHISLYSGLUASPRALALAVALAANCYSTRHAPRILESERVALG 1034
QY 152 -----TGCGACGCTCGGCTCCGCGCGGGGCT----- 124
Db 1034 INLYTHRPROGLINLYSALATHRTHRGLYARGSESR--ARGGLINSESRPHEILEAL 1053
QY 123 -----CTCGACGCTTCGCTCC----- 106
Db 1053 AVALGLYILEULEUGLYVALLEULEUALATHRPHENIVALALALEUPHETHEUTHRLY 1073
QY 105 -----CGCGAAGCCATCTCGGCTCCGCTCCCGC----- 76
Db 1073 SLYSARGARGLARGGLNARGGLNARGLEUALAVALSERSETRARGLYGLUASNLEUVALHISGL 1093
QY 75 -----GC 74
Db 1093 NLEGLINTYARGGLUMETASNSERCYSELEUASNALAPAPRLEUASPRLEUMETASNSE 1113
QY 73 ATCGGGTCCCGCGCGCCGCTTCCCGGAGCCGCGCGCCAGCGCCAGGCTGCG 14
Db 1113 RSERGLY-----GLYH 1117
QY 13 GAGCGCACCCAC 1
Db 1117 SSERGLUPROHIS 1121

```

RESULT 27  
 US-09-488-725A-6210  
 / Sequence 6210, Application US/09488725A  
 / GENERAL INFORMATION:  
 / APPLICANT: Hyseq, Inc  
 / TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 / FILE REFERENCE: 784FLPCT  
 / CURRENT APPLICATION NUMBER: US/09/488, 725A  
 / PRIOR FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: US/09/488, 725  
 / PRIOR FILING DATE: 2000-01-21  
 / PRIOR APPLICATION NUMBER: US09/552, 317  
 / PRIOR FILING DATE: 2000-04-25  
 / PRIOR APPLICATION NUMBER: US09/598, 042  
 / PRIOR FILING DATE: 2000-06-20  
 / PRIOR APPLICATION NUMBER: US09/620, 312  
 / PRIOR FILING DATE: 2000-07-19  
 / PRIOR APPLICATION NUMBER: US09/653, 450  
 / PRIOR FILING DATE: 2000-08-31  
 / PRIOR APPLICATION NUMBER: US09/662, 191  
 / PRIOR FILING DATE: 2000-09-14  
 / PRIOR APPLICATION NUMBER: US09/693, 036  
 / PRIOR FILING DATE: 2000-10-19  
 / PRIOR APPLICATION NUMBER: US09/727, 344  
 / PRIOR FILING DATE: 2000-11-29  
 / NUMBER OF SEQ ID NOS: 7144  
 / SOFTWARE: pt\_fl\_genes\_b Versions 1.0

SEQ ID NO 6210  
 LENGTH: 1124  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-488-725A-6210

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
11.4	1124	195	63	146	996	26
Score:	446.40					
Percent Similarity:	18.44%					
Best Local Similarity:	13.94%					
Query Match:	14.91%					

us-09-896-522-1 (1-1624) x US-09-488-725A-6210 (1-1124)

```

QY 1623 TGGCCCCGACAAAGCTGGGTG-----GATGCTGGG-----TGCTTCAGG 1582
DB 138 TrrgLylyshisSer--AsnCysThrHisGlnGlnAspAlaGlyValThrCysSerAapG 157
QY 1581 GCATCCGCGCTGCTGCTGCTTAAAGCACAAGCAGGGGGGAAA----- 1534
DB 157 Ly-----SerAsnLeuGlnMetArg-LeuThrArgGlyGlyAsnMetCysSerGly 173
QY 1534 ----- 1534
DB 174 ArgGlnLeuLeuSerPheGlnGlyArgGlyThrValCysAspAspAspPheAsnIle 193
QY 1533 ---CATCCCTGAGTGGCTCCCATATCCGTGAGGACGCTGAGCTGCAAACTGAGG 1477
DB 194 AspHisAlaSerValIle-----CysArg-GlnLeuGlnCys-----Gln 206
QY 1476 TCATGAATTAAGTTGTAGG----- 1455
DB 206 ySerAlaValSerPheSerGlySerSerAsnPheGlyGlnGlySerGlyProIleTrrpH 226
QY 1455 ----- 1455
DB 226 eAspAspLeuIleCysAsnGlyAsnGlnIleLeuTrrpAsnCysGlyHisGlnGlyTrr 246
QY 1454 ---CACACCAAGCTTGTGTATGAACAGAAAAGAAAACATGAGACATGTAA 1402
DB 246 rGlyLyshisAsn-----CysAspHisAlaGlnAspAla-----Gly--ValI 260
QY 1401 CATGTAAAAAAGAAAGTACTTGTTCACAAACTTTTGAATATGCTGTGAATGT--- 1346
DB 260 IecysSerLyshisGlyAlaAspLeuSerLeuArgLeuValAspGlyValThrGlnCysSerG 280
QY 1345 ---GTAGACCAAGATCAGACTGAAAAAATCTCTCCCACTGGG----- 1303
DB 280 LyArgLeuGlnValAlaGrrPheGlnGlyGlnTrrp-GlyThrIle-----CysAspAspG 297
QY 1302 ----- 1265
DB 297 yTrrpAspSerLyAspAlaAlaValAlaCysGlySerGln-LeuGlyCysProThr----- 314
QY 1264 GGTGTCTCTCTCAATTTCCCAATATGAGCTCAATCTCTCAAGAAAGCTCCAGAG 1205
DB 315 -AlaValThrAlaIleGlyArgVal-----AsnAlaSerLyS----- 327
QY 1204 TTCCTGCACATCTGTGAGCATTTCTAGTACCTAGAGGAGTCTTAAACCGCAAGAG 1145
DB 328 PheGlyHisIleIle---TrrpLeuAspSerVal-----SerCysGlnGlnGlyAsn 343
QY 1144 GT-----AAGTGG----- 1137
DB 343 roAlaValAlaTrrpGlnCysLyshisAsnIleGlyTrrpGlyLyshisIleTrrpCysAsnHisAsnGln 363
QY 1137 ----- 1137
DB 363 ePAlaGlyValAlaThrCysSerAspGlySerAspLeuGlnLeuArgLeuArgGlyGlyS 383
QY 1137 ----- 1137

```

```

DB 383 eArgCysAlaGlyThrValGlnValGlnIleGlnArgLeuLeuGlyLyValCysAspA 403
QY 1136 -----C 1136
DB 403 rGlyTrrpGlyLeuLyshisGlyAlaAspValAlaCysArgGlnLeuGlyCysGlySerAla 423
QY 1135 TGAAAACCTCAGGAAGCGCTGTCAAGTGTCCACAGAAAGTGAAGCTGAGTACATCTGA 1076
DB 423 euLyshisSer-----TrrpGlnValLyshisGlyValIleGlnAlaThrAsnThrTrp 440
QY 1075 GTTTCACATCTGTGAGTGAAGAAAGCTCCGTGCTAACTCCCTGGAGGTCGCCAGAG 1016
DB 440 urPhe---LeuSerSerCysAsnGlyAsnGlnu---ThrSerLeuTrrp-----AspC 455
QY 1015 GAAGCAGTGGGTGG----- 1000
DB 455 sLyAsnTrrpGlnTrrpGlyGlyLeuThrCysAspHisTrrpGlnGlnAlaLyshisThrCys 475
QY 999 -----CTGGGCGTCCCAAGGCTCAGTCCCTGGAACACAT 965
DB 475 sSerAlaHisArgGlnProArgLeuValGly-----GlyAspIlePro-----C 490
QY 964 GCCGGCGGGAACCTGCGCTGAGGCTGCGAGCCCTCAGTGGAGGCTGTGCTGAGT 905
DB 490 yS--SerGlyArgValGlnValLyshisGlyAsp---ThrTrrpGlySerIleCysAspS 508
QY 904 CCAA----- 900
DB 508 eAspPheSerLeuGlnAlaAlaSerValLeuCysArgGlnLeuGlnCysGlyThrVal 528
QY 900 ----- 900
DB 528 aIsSerIleLeuGlyGlyAlaHisPheGlyGlnGlyAsnGlyGlnIleTrrpAlaGlnL 548
QY 900 ----- 900
DB 548 heGlnCysGlnGlyHisGlnSerHisLeuSerLeuCysProValAlaProArgProGln 568
QY 899 -----TGTACCGTTTCCAGAGTCAACA 875
DB 568 LyThrCysSerHisSerArgAspValGlyValAlaCysSerArgTrrpThrGlnIle--- 586
QY 874 TCCCAAGGTGTC----- 862
DB 587 ---ArgLeuValAsnGlyLyshisProCysGlnGlyArgValGlnLeuLyshisThrLeuG 605
QY 861 -CCCTGCTCAGAAAAGTCCGCTGTAGCTCCGACATTTGACCTCCCTCGGTGCAT 803
DB 605 yAlaTrrp-----GlySerLeuCysAsnSer---HisTrrpAspIleGlnAspAlaHis 621
QY 802 TGCAGATGTCAACATTCAGAAATGTCTGTGATGTCTGCACATCAGTGTGATGGCAACA 743
DB 622 ValLeuCysGlnGlnLeuLyshisCys---GlyValAla----- 632
QY 742 TATGTTCACCTCTGTGAGGATGATCATCGGCATACTTTTGTGCGCAGAGCAACT 683
DB 633 -LeuSerThrProGlyGly-----AlaArgPhe-----GlyLyshisGlyAsn- 645
QY 682 CCTCGAAGCGGCTTCACAGAAAGTGG-----TGTACTCCGTCAGAA- 641
DB 646 -----GlyGlnIle-----TrrpArgHisMetPheHisCysThrGlyThrGln 660
QY 641 ----- 641
DB 661 HisMetGlyAspCysProValThrAlaLeuGlyAlaSerLeuCysProSerGlnVal 680
QY 640 -----TGTGCT 635
DB 681 AlaSerValIleCysSerGlyAsnGlnSerGlnThrLeuSerSerCysAsnSerSerSer 700
QY 634 CCAAGTCCCTCCCTGCGGCGACATCCCGAGAAACTTTTGAAGACAGCTGAGTGGAGAT 575

```

```

Db      701 LeuGlyProThr-ArgProThrIleProGluIleSerIle-----ValAla-- 715
QY      574 CGGPTGCCAGAAAGAGC-----GCAGGTGACATGTCGGAGTCT 533
Db      716 ---CysIleGluSerGluIleuValuValaIleuGlyIleGlyArgCysAlaGlyArg 734
QY      532 CTTGGCTGTAGAACACCA-----CTCCAGTCTTCGGCTCC----- 514
Db      735 -ValGluIleTyrHisGluIleGlySerTrpGlyThrIleCysAspAspSerTrpAspLeu 754
QY      513 -----GATGCCCTCAACAGAACCAAGT 491
Db      754 rAspAlaHisValaValaCysArgGluIleuGlyCysGlyGluAlaIle-AsnAlaThrGlyS 774
QY      490 CCGGAGGAGTACACCACTGGT-----GATGCCCTCAACAGAACCAAGT 469
Db      774 etAla-----HisPheGluGluGlyThrGlyProIleTrpLeuAspGluMetCys 791
QY      468 -----CTTGGTAACTTGAAGTGTGCACAAATCAT----- 437
Db      791 sAsnGlyLysGluSerArgIleTrp-----GlnCysHis--SerHisGlyTrpGly 807
QY      437 ----- 437
Db      808 GlnGlnAsnCysArgHisLysGluAspAlaGlyValIleCysSerGluPheMetSerLeu 827
QY      436 -----AGGTGGGACCTGCACCGTTTGGCCCTCCACGA----- 404
Db      828 ArgLeuThrSerGluAlaSerArgGluAla-----CysAlaGlyArgLeuGlu 843
QY      404 ----- 404
Db      844 ValPheTyrAsnGlyAlaTrpGlyThrValGlyLysSerSerMetSerGluThrThrVal 863
QY      403 -----TGTTTTCAGAGCTCTGTGCATCAATATTCATAAGCC----- 364
Db      864 GluValValaCysArgGluIleuGlyCysAlaAsp-----LysGlyLysIleAsnPr 880
QY      364 ----- 364
Db      880 AlaSerLeuAspLysAlaMetSerIleProMetTrpValaAspAsnValGlnCysProly 900
QY      363 -----ATCTGATGTGTCAAATTTACTCTCTTCAAGCCCTTGGCTTCT 317
Db      900 sGlyProAspThrLeuTrpGln-----CysPro-SerSerProTrpGluLys 915
QY      316 GCTTGGCCGCTA----- 305
Db      916 ArgLeuAlaSerProSerGluGluThrTrpIleThrCysAspAsnLysIleArgLeuGln 935
QY      304 ---GACCTGTAGAACCTGTCTGGCTCAGAGATG----- 273
Db      936 GluGlyPro--ThrSerCysSerGly--ArgValGluIleTrpHisGlyIleSerTrpG 954
QY      272 --ACCACCTTCCGCTGCTGCTTCACCTGCTC----- 240
Db      954 LysThrVal-----CysAspAspSerTrpAspLeuAspAspAlaGluValaValC 970
QY      240 ----- 240
Db      970 YsGlnGlnLeuGlyCysGlyProAlaLeuLysAlaPheLysGluAlaGluPheGlyGln 990
QY      239 -----TGTCCAGAGAACTCCATGATCTTCTTCAC 212
Db      990 LysThrGlyProIleTrpLeuAsnGluValLysCysLysGlyAsn----- 1004
QY      211 ACACGCTGACCTCCGCTGCGACAGTGCAGCGCTCACCCCTATGACGAAGGCGCGTGG- 153
Db      1005 ---GluSerSerLeuTrpAspCys-----ProAlaArg-----ArgTrpG 1017
QY      153 ----- 153
Db      1017 LysIleSerGluCysGlyHisLysGluAspAlaAlaValaAsnCysThrAspIleSerValG 1037

```

```

QY      152 -----TGCGAACGTGGCTCCGGCGCGGAGCT----- 124
Db      1037 LysThrProGlnLysAlaThrThrGlyArgSerSer--ArgGlnSerSerPheIleAl 1056
QY      123 -----CTCCAGTCTTCGGCTCC----- 106
Db      1056 aValGlyIleLeuGlyValaValaLeuLeuAlaIlePheValaIleuPhePheLeuThrly 1076
QY      105 -----CGCGAAGCCATCTCGAGCTCCGCTCCGCGC----- 76
Db      1076 sLysArgArgGlnArgGlnArgLeuAlaValaSerSerArgGlyGluAsnLeuValHisG 1096
QY      75 -----GC 74
Db      1096 nIleGlnTyrArgGluMetAsnSerCysLeuAsnAlaAspAspLeuAspLeuMetAsn 1116
QY      73 ATCGGTCCTCCGCGCGCGCGCTTCCCGGCGCGCGCGCGCGCGAGAGTGC 14
Db      1116 rSerGly-----GlyHis 1120
QY      13 GAGCGGACCCCGAC 1
Db      1120 sSerGluProHis 1124

RESULT 28
US-09-488-725A-6211
Sequence 6211, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: PL FL_genes_b Versions 1.0
SEQ ID NO 6211
LENGTH: 1124
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-6211

Alignment Scores:
Pred. No.: 11.4 Length: 1124
Score: 446.40 Matches: 195
Percent Similarity: 18.44% Conservative: 63
Best Local Similarity: 13.94% Mismatches: 146
Query Match: 14.91% Indels: 996
DB: 1 Gaps: 26

us-09-896-522-1 (1-1624) x US-09-488-725A-6211 (1-1124)
QY      1623 TGGCCCGGCAAGCCTGGGT-----GATGCTGGG-----TGCTTCAGG 1582
Db      138 TrpGlyLysHisSer--AsnCysThrHisGlnGlnAspAlaGlyValaThrCysSerAsp 157
QY      1581 GCATCCGCTCGCTTCTCTGCTTAAAGGACAAAGGCGGGA--- 1534

```

```

Db      157  ly-----serAenleuGluMetArg-LeuthrtrgGlyGlyAanMetCysSerGly 173
QY      1534  -----
Db      174  ArgIleGluIleuYspheGInGlyArgItrpGlyThrValCysAerAerAenPheAenIle 193
QY      1533  ----CATCCCTCAGAGGCTCCCATATCCGTGTAGCCACGCTGACCAACACAGCTGGG 1477
Db      194  AsphIleAlaSerValIle-----CysArg-GlnleuGluCys-----GI 206
QY      1476  TCATGAATTAGGTTGTAGGC-----
Db      206  ySerAlaValaSerPheSerGlySerSerAenPheGlyGluGlySerGlyProIleTrpH 226
QY      1455  -----
Db      226  eaerAerPheuIleCysAenGlyAenGluSerAlaIleuTrpAenCysAlyAenGInGlyTr 246
QY      1454  ----CACACACGCTTGTGTATGAAACAGAAACAGAAACATGAGCAGCTAA 1402
Db      246  pGlyAlyAenAen-----CysAerPhIleAlaGluAerAla-----Gly--ValI 260
QY      1401  CATGTAAAGAAAGAACTACTGTTCACAAACTTTGAGTTATGTGTGAGTGT---- 1346
Db      260  leCysSerIyGlyAlaAerPheuSerleuAerGlyAerGlyValThrGluCysSerG 280
QY      1345  -----GTAGAACCAATCAGACTGTGAAACAACTCTCTCCACGTGTG-- 1303
Db      280  IyAtrGleuGlyAtrGpHeGInGlyIuTrp--GlyThrIle-----CysAerAerG 297
QY      1302  -----GTTCACGTGTCAACAAACATCAGGCGACGACCTGTCTA 1265
Db      297  yTrpAerSerTyAerAlaAlaValAlaCysAlyAenLeuGlyCysProthr-- 314
QY      1264  GAGTGTCTCTCAATTTCCCAATATGTGCTCAGCTCTCAAGAAACCTCCAGG 1205
Db      315  -AlaValThrAlaIleGlyAerGly-----AenAlaSerIys-----Gly 327
QY      1204  TTCTGTCAACTTGTGTGCAATTTCTCAGTACGACCTAGAGGATCTTTAAACCGCAAGC 1145
Db      328  PheGlyPhIleIle---TrpIleAerSerVal-----SerCysGInGlyPhIleIuP 343
QY      1144  CT-----AAGTGC-----
Db      343  roAlaValItrGInCysAlyAenIleGlyIuTrpGlyAlyAenIleCysAenIleAenGluA 363
QY      1137  -----
Db      363  sprAlaGlyValThrCysSerAerPdySerAerPheuGluAerGlyAerGlyGlyS 383
QY      1137  -----
Db      383  eaArgCysAlaGlyThrValGluValGluIleGlnAtrGleuAerGlyAlyValCysAerA 403
QY      1136  -----C 1136
Db      403  rGlyIuTrpGlyAlyAerValAerValValCysAerGlnIleuGlyCysGlySerAlaI 423
QY      1135  TGAACCTCAGAGGCTGTGATGTCCAGCAAGTTGAGTGTGACACATCTGA 1076
Db      423  euIySerThrSer-----TyGlnIValTyGlySerIyAlyIleGlnAlaThrAenPhrI 440
QY      1075  GTTTCACCTCTGAGTGAAGAGGCTCGCTGTAAACATCCCTGGAGGTGCGCCAGAG 1016
Db      440  uPhe---LeuSerSerCysAenGlyAenGlu---ThrSerLeuTrp-----AerCy 455
QY      1015  GAAGCAGTGGGTGTG--
Db      455  slyAenAenTrpGlnIuTrpGlyAlyAerThrCysAerPhIeTyGlnGluAlaAlyAlyIleThrCy 475
QY      999  -----GTGGGCTGCCAGGCTCAGTCCCTGAAACACAT 965

```

```

Db      475  sSerAlaIleArgGluuProAerGleuValGly-----GlyAerIlePro-----C 490
QY      964  GCCGAGCGGAGACCTGCTCCTGAGGCTCGGACGCTTCAAGGCTGTCTGTGACT 905
Db      490  ys--SerGlyAtrGlyAlaGluValAlyAenIyAenAer---ThrTrpGlySerIleCysAerS 508
QY      904  CCAA-----
Db      508  eaerPheSerleuGluAlaAlaSerValleuCyAerGlyAerGluAerGlnCysGlyThrValI 528
QY      900  -----
Db      528  alSerIleleuGlyGlyAlaIlePheGlyGluGlyAenGlyGlnIleTrpAlaGluIuP 548
QY      900  -----
Db      548  heGInCysGluGlyAlyAenGluSerPhIleuSerleuCyAerProValAlaProAerProGlu 568
QY      899  -----TGTCACGTTTCCAGAGCTCAGCA 875
Db      568  IyThrCysSerPhIleSerAerAerValGlyValValCysSerAerGlyTrThrGluIle--- 586
QY      874  TCCAGGCTGTGTC-----
Db      587  -ArgleuValAenGlyAlyThrProCysAlyGluAtrGlyAtrGluAlyAenIyThrleuG 605
QY      861  -CCCTGCTCAAGAAAGCTCCGCTGTGAGTCCGCGCATGTGACCTCTCGGTCCATT 803
Db      605  yAlaTrp-----GlySerleuCyAenSer---HisTrpAerIleGluAerAlaIle 621
QY      802  TGCAATGTGCACATTCAGAAATGCTCGATGTGTGCACAGTTCAGTTGATGGCAACA 743
Db      622  ValleuCyAerGlnIleuIyAenCys---GlyValAla----- 632
QY      742  TATGTTCACCTCTCGTGGATGATGACATCCGACATCTTTTCGCGAGGACAGACT 683
Db      633  -leuSerThrProGlyGly-----AlaArgPhe-----GlyAlyGlyAen 645
QY      682  CTTGAAAGCCGGCTTCAAGAGTGTG-----TGATCTGCTCAGAA-- 641
Db      646  -----GlyGlnIle-----TrpArgIleMetPheHisCysAerPhIeGlyThrGlnGln 660
QY      641  ----- 641
Db      661  HisMetGlyAerCyAerProValIleAlaIleuGlyAlaSerleuCyAerProSerGluIuVal 680
QY      640  -----TCTGCT 635
Db      681  AlaSerValIleCysSerGlyAenGlnSerGlnThrleuSerSerCyAenSerSerSer 700
QY      634  CAGAGTCCCTCCTCGGCGACGCTCCGAGAACTTTGAGACACGCTGACGTCGAGT 575
Db      701  leuGlyProThr--ArgProThrIleProGluGlnSerAla-----ValAla-- 715
QY      574  CGGTGTCCAGAAAGAGC-----CGAGGTGGAACATGTCCCGATCT 533
Db      716  ---CysIleGluSerIyGlnIleuAerGleuValAenGlyGlyAtrGlyAerCysAlaGlyAtr 734
QY      532  CTTGCTGTAGAACCA----- 514
Db      735  -ValGluIleTyGlnleGluGlySerTrpGlyThrIleCysAerAerSerTrpAerleuSe 754
QY      513  -----GATGCCCTCAACAGAACACAGT 491
Db      754  rAerAlaIleValaIleCysAerGlnleuGlyCysGlyGluAlaIle--AenAlaThrGlyS 774
QY      490  CGCAGAGTAAACACCCGTGT----- 469
Db      774  etAla-----HisPheGlyGluGlyAlyThrGlyProIleTrpAerAerGluMetIyAerCy 791
QY      468  -----CTGTGTAACTTGTGAGTGTCAAAATCAT 437
Db      791  sAenGlyAlyGluSerAerGlyIleTrp-----GlnCyAenIle---SerHisGlyTrpGly 807

```





```

QY 1459 A-----CAACCTAAATTGATGACCCAGT 1482
DB 1553 ICysGluAlaProAlaMetValMetAlaValHisSerGlnThr--IleGlnIleProPro 1572
QY 1483 GATTGACATCCAGCGCGCTACACGATATG-- 1516
DB 1573 ----CysProSerGlyThr--SerSerLeuThrIleGlyTyrSerPheValMethIsth 1590
QY 1517 -----GAGACCACTAGAGGAGTGTTCCTCCCTGCTTGTGCTTAAAGCAGAGAG 1569
DB 1590 rSerAlaGlyAla--GluGlySerGlyGlnAlaLeuAlaSerPro----- 1604
QY 1570 CGAGCGCGGATCCCTGGAA-----GCACCCAGCATCACACCCAGGCTTGCG 1617
DB 1605 ---GlySerCys-LeuGlnGluPheArgSerAlaProPheIle-----GluCysHis 1620
QY 1618 GGG 1620
DB 1621 Gily 1621

RESULT 30
US-09-488-725A-2487
; Sequence 2487, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLECT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: Pf FL_genes_b Versions 1.0
; SEQ ID NO 2487
; LENGTH: 1225
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2487

Alignment Scores:
Pred. No.: 14.6 Length: 1224
Score: 446.20 Matches: 204
Percent Similarity: 18.95% Conservative: 73
Best Local Similarity: 13.95% Mismatches: 129
Query Match: 14.91% Indels: 1057
DB: 1 Gaps: 27

us-09-896-522-1 (1-1624) x US-09-488-725A-2487 (1-1224)

QY 1619 CCGGCAAGCCTGGGTGTGATGCT----- 1595
DB 38 ProGlnLeuSerTrpVal-----AlaSerSerProSerSerLysAspValAlaSerProth 56
QY 1594 -----GGGTGCTTCCAGGGCATCCGCTCGCTTCTTGCTTTAAGCA 1551
DB 56 rGlnMetIleGlyAspGlyCysAspLeuGlyLeu-----GlyG 69
QY 1550 CAAGCAAGGGGGAACATCCCTCAGTGGCTCCCATATCCGCT----- 1505

```

```

DB 69 IuGIuGIuGIuGly-----ThrGlyLeuProTyrProCysGlnPheCysAspLys 85
QY 1505 ----- 1505
DB 85 sSerPheIleArgLeuSerTyrLeuLysArgHisGluGlnIleHisSerAspLysLeuP 105
QY 1504 -----AGGCCACG 1497
DB 105 orPheLysCysThrTyrCysSerArgLeuPheLysHisLysLysArgSerArgAspArg-HisI 125
QY 1496 CTGAGCTGCAGAACCCATGGGTGATGAATTAAGTTGTGTAAGCCACACAGCCTTGTT 1437
DB 125 IeLysLeuHisThr-----GlyAspLys--LysTyr-----His-----CysH 137
QY 1436 ATGAAACAGAA-----AACAGAAACATGAGGACATGTAACATGTAATAAAG 1389
DB 137 IeGluCysGluAlaAlaPheSerArgSerAspHisLeuLysIle--HisLeuLysThrH 156
QY 1388 AAGTACTTGTTCAACAACCTTTGAGTTATGTGTGAGTGTGTAAGAAC----- 1338
DB 156 IsSerSer-----SerLysProPheLys-----CysThr-ValCysLysArgGlyPheSer 172
QY 1338 ----- 1338
DB 173 SerThrSerSerLeuGlnSerHisMetGlnAlaHisLeuLysValnLysGlnHisLeuAla 192
QY 1338 ----- 1338
DB 193 LysSerGlyLysGlnAlaLysLysAspAspPheMetCysAspTyrCysGluAspThrPhe 212
QY 1337 -----CAGATCAGACTGGA 1323
DB 213 SerGlnThrGluGluLeuGlnLysHisValLeuThrArgHisProGlnLeuSer--Glu 231
QY 1322 AAAACTCTCTCCACATCTGGGTGCTCACT----- 1294
DB 232 LysAlaAspLeuGlnCys--IleHisCysProGluValPheValAspGluAsnThrLeuL 251
QY 1293 -----CAACAAACATCAGGCCAGCCAGT----- 1268
DB 251 euAlaHisLysIleHisGlnAlaHisAlaAsnGln--LysHisLysCysProMetCysProG 270
QY 1267 -----CTAGCGTGTCTCTCAATTTCCCAATTAATGTCCTCAAT-----CTCAGAGAG 1215
DB 270 uGlnPhe-----SerSerValGluGlyValTyrCys--HisLeuAspSerHisAspG 287
QY 1214 CTTCCAGGCTCTCGACATCTGTGAGCATTTCTCAGTACGACCTAGAGGATCTTTAAC 1155
DB 287 n--ProAspSerSerAsnHisSerValSer--ProAspProValLeuGlySerVal-- 304
QY 1154 CGCAACGAGCTTAAGTGGCTGMAAAACCTCAGAACGCTGTCAGTGCCAGCAAGTTGA 1095
DB 305 -----AlaSerMetSer-----SerAlaThrProAspSer-SerLysSerValG 319
QY 1094 GTCTGATGACACATCTGAGTTCCACTCTGAGTGAAGAAAGGCTCGCTTAACATC 1035
DB 319 uArgGly-----SerThrProAsp-----SerThrLeu--LysP 330
QY 1034 CCTGGGGGTGGCGGAGAGAA-----AGCAGTGGGTGGGTGGG----- 995
DB 330 rGluLeu-----ArgGlyGlnLysLysMetArgAspArgGlyGlnGlyTyrThrLys 346
QY 995 ----- 995
DB 347 ValValTyrSerCysProTyrCysSerLysArgAspPheAsnSerLeuAlaValLeuGlu 366
QY 994 -----CGTCCCAAGGCTCAGTCCCTGAAACACATGCGC 962
DB 367 IleHisLeuLysThrIleHisAlaAspLysProGln--GlnSer-----HisThrCys- 383
QY 961 GAGCGGAGACCTGC----- 947
DB 384 -----GlnIleCysLeuAspSerMetProThrLeuTyrAsnLeuAsnGlnHisValArg 401

```



```

QY 947 ----- 947
Db 402 LysLeuH1bLysAsnH1sAlaTyrProValMetGlnPheGlnLysAsnL1SerAlaPheH1s 421
QY 947 ----- 947
Db 422 CysAsnTyrCysArgProGlnMetPheAlaAspL1LeuAsnSerLeuGlnGlnH1sL1LeuArgVal 441
QY 946 ----- 946
Db 442 SerH1sCysGlyProAsnAla-----AsnProSerAspGlyAsnAlaAsnAlaPhePhe-----C 459
QY 898 GTACAGCTTTGC-----CAGAGG 881
Db 459 ysAsnGln-CysSerMetGlyPheLeuThrGlnSerSerLeuThrGlnH1sL1LeuGln 478
QY 880 TCAGCATCCGAGGATGTCCTGTCAGAAAAGTCGCTGTAGATCCGTCAGATTCG 821
Db 479 Ala-H1s-----CysSerValGlySerAlaLys-----LeuGlnSerProValValG1 494
QY 820 ACCCTCC----- 814
Db 494 nProThrGlnSerPheMetGlnValTyrSerCysProTyrCysThrAsnSerProL1Phe 514
QY 813 ----- 800
Db 514 eGlySerL1LeuLysLeuThrLysH1sL1LeuGlnAsnH1bLysAsnH1bLeuLysL1 534
QY 799 AGATGTCACCATTCAGAA----- 782
Db 534 a-----HisSerLysLysSerLysValAlaGlnGlnSerProValSerSerAspValGln 551
QY 782 ----- 782
Db 552 ValSerSerProLysArgGlnArgLeuSerAlaSerAlaAsnSerL1LeuSerAsnGlnLys 571
QY 782 ----- 782
Db 572 TyrProCysAsnGlnCysAspLeuLysPheSerAsnPheGlnSerPheGlnThrH1sLeu 591
QY 781 ----- 760
Db 592 LysLeuH1bLeuGlnLysLeuLeuArgLysGlnAlaCysProGlnCysLys-GlnAspH1 611
QY 760 ----- 760
Db 611 eAspSerGlnGlnSerLeuLeuGlnH1sLeuThrValH1sTyrMetThrThrSerThrH1 631
QY 760 ----- 760
Db 631 sTyrValCysGlnSerCysAspLysGlnPheSerSerValAspAspLeuGlnLysH1sLe 651
QY 760 ----- 760
Db 651 uSerMetH1sThrPheValLeuTyrH1sCysThrLeuCysGlnGlnValPheAspSe 671
QY 760 ----- 760
Db 671 rLysValSerL1LeuValH1sLeuAlaValLysH1sSerAsnGlnLysLeuMetTyrAr 691
QY 759 ----- 743
Db 691 gCysThrAlaCysAsnTyrAspPheArgLysGlnAlaAspLeuGlnVal-----H1 708
QY 742 TATTCGTCATCTCTCGGATGATGATCATCGCATATCTTTGTGCGCAGGACAGACT 683
Db 708 sValLysH1sSer-----HisLeuGly-----AspH1 717
QY 682 CCGTCGAAGCCGAGCTTCAGAAAGTGGTGTACTGCGTCAGAAATCTGTCAGAGTCCCTCC 623
Db 717 rAlaLysAla-----His-LysCysL1LeuPheCys----- 726

```

```

QY 622 CTCGCGCAGCTCCGAGAACTCTTCAGACAGACTGATCGGAG-----TCGG 572
Db 727 -----GlyGlnThrPheSerThr-----GlnVal-GlnLeuGlnCysH1sL1 740
QY 571 TGTTCAGAAAGAGCCGAGGTGGAACATGT----- 542
Db 740 lThrThrH1sSerLysLysTyrAsn-CysLysPheCysSerLysAlaPheH1sAlaL1Le 759
QY 542 ----- 542
Db 760 lLeuLeuGlnLysH1sLeuArgGlnLysH1sCysValPheAspAlaAlaThrGlnAsn 779
QY 542 ----- 542
Db 780 GlyThrAlaAsnGlyValProProMetAlaThrLysLysAlaGlnProAlaAspLeuGln 799
QY 541 ----- 514
Db 800 GlnMetLeuLysLysAsnProGlnAlaProAsn-----SerH1sGlnAlaSerGlnAspAs 818
QY 513 -----GA 512
Db 818 pValAspAlaSerGlnProMetTyrGlyCysAspL1CysGlyAlaAlaTyrThrMetG1 838
QY 511 TGCCCTCAAAACAGAACACGTCGCGAGGTAGACAC 475
Db 838 uValLeuLeuGlnAsnH1s-----ArgLeuArgAspH1sAsnL1LeuArgProGlyGlnAspAs 857
QY 474 -----CGTGTCTCTGTGTAACCTTGATGTGCACA 443
Db 857 pGlySerArgLysValAlaGlnPheL1LeuGly-----SerH1sLys 871
QY 442 AATCATAGTCCGACACTCAGCGTTTGCCTCCACAGATGTTCTTCAGATCTGTGCA 383
Db 871 s-----CysAsnValCysSerArgThrPhePhe-SerGlnAsnGlyLeu 885
QY 382 TCMAATCATTTACAA-----AGCATGTGATGTCAAAATGTGACT 341
Db 886 ArgGlnH1sLeuGlnThrH1sArgGlyProAlaLysH1s-TyrMet-----CysPro 902
QY 340 GTCCCTTCAAGGCTTGAGCTCT----- 317
Db 903 lLeuGlyGlnArgPheProSerLeuLeuThrLeuThrGlnH1sLysValThrH1sSer 922
QY 316 -----GCTTCGCGCAGGACTGTGAGACCTGCTGCTGTCAGATG----- 273
Db 923 LysSerLeuAspThrGlyThrCysArgL1Cys-----LysMetProLeuGlnSerG 940
QY 272 -----ACCACT 266
Db 940 lGlnGlnPheL1LeuH1sCysGlnMetH1sProAspLeuArgAsnSerLeuThrGlyP 960
QY 265 TCCGCTGCGGCTGTTCACCTGTTCTGTCCAGACAGCTCATGATCTTTCACACAGG 206
Db 960 heArgCys-ValValCysMetGlnThrValThrSerThr-LeuGlnLeuLysL1LeuH1sG1 919
QY 205 T-----CGACTTCGCTGCGAGTGCCTGCGCTCAC----- 175
Db 979 yThrPheH1sMetGlnLysLeu-----AlaGlySerSerAlaAlaSerSerProAsnGlyG1 998
QY 175 ----- 175
Db 998 nGlyLeuGlnLysLeuTyrLysCysAlaLeuCysLeuLysGlnPheArgSerLysGlnAs 1018
QY 174 -----CCCTATCAGAAAGGCGCGCTGT-----GCG 149
Db 1018 pLeuValLysLeuAspValAsnGlyLeuProTyr--GlyLeuCysAlaGlyCysMetAla 1037
QY 148 GACGTGCGCTCCGAGC-----GCGGAGCTTTCGAGTCTTGCGCTCCGCGAAAGCA 95
Db 1038 --ArgSerAlaAsnGlnGlnValGlyGlyLeuAla-----ProProGlnPro 1052
QY 94 TCT-----CGGCT----- 86

```



QY	574	AAATCTCCGAACGTCAAGCTGTCTCCGAAGAGTTCTCCGGAGACGTGCCCGGAGGAGGACTG	633
Db	556	-----SerSerAlaGluCysIle-----LeuSerGlyAlaAlaAlaHis-----Tr	609
QY	634	GAGCAGATTCTGCACCGCACTACACACACTTCCTGTGAAGCCGGCTTCGAGGAGTTCTGCCTG	693
Db	609	pSer-----ThrIleProPro-----IleCys-----	616
QY	694	CCGACAAAGAACTATCCGAGTGTATCATCCACAGAGGTGACAAATATGGTCCCATC	753
Db	617	-----GlnArg-----IleProCysGly-----LeuProBr	625
QY	754	AACTCGATTCTGCACACATCCAGGACATTCTGAATGTGGACATC-----	798
Db	625	oThr-----IleAlaAlaGlyAspPheIleSerThrAsnArg	637
QY	799	-----TGCAATATGGACCCGAGAGAGTCC	822
Db	638	GluAsnPheHieIleTyrGlySerValValThrTyrAlaArgCys-Asn---Pro---GlySer	654
QY	823	AATGGCCGAGCTACACAGCGACCTTTCTTGAGCCAGGGGACAC-----	867
Db	655	GlyGlyArgGlyValPheGluIleuValGlyGluProSerIleTyrCysThrSerAsnAsp	674
QY	867	-----	867
Db	675	AspGluValGlyIleTyrSerGlyProAlaProGlnCysIleIleProAsnIlyCysThr	694
QY	867	-----	867
Db	635	ProProAsnValGluAsnGlyIleLeuValSerAspAsnAspSerLeuPheSerLeuAsn	714
QY	868	-----CTGGGAGTGTACCTCTGGCAAAAGGTCAATT--	901
Db	725	GluValValGluPheArgCysGlnProGlyPheValMetIyGlyProArg-ArgValIly	734
QY	901	-----	901
Db	734	sCysGlnAlaLeuAsnIlyStrGluProGluIleuProSerCysSerArgValCysGlnBr	754
QY	901	-----	901
Db	754	oProProAspValIleuHisAlaGluArgThrGlnArgAspIlyAspAsnPheSerProGly	774
QY	901	-----	901
Db	774	YGlnGluValPheTyrSerCysGluProGlyTyrAspLeuArgGlyAlaAlaSerMetArg	794
QY	902	-----TGAGTCTCCAGCAGACCCCACT--	925
Db	794	gCysThrProGlnIlyAspTrpSerProAlaIa---ProThrCysGluValIlySerCys	813
QY	925	-----	925
Db	813	sAspAspPheMetGlyGlnLeuLeuAsnGlyArgValIleuPheProValAsnLeuGlnIle	833
QY	926	-----GAGGCGCTGCCAGCTCAGAGCGAGCTGCC	957
Db	833	uGlyAlaIysValAspPheValCysAspGlnIlyPhe--GlnLeuIyGlySerSerAla	852
QY	958	GCCCGGCATGTGTTCACGAGCATGAG-----	984
Db	853	serTyrCysValIleuAlaGlyMetGluSerLeuTrpAsnSerSerValProValCysGlu	872
QY	985	-----CCTGGGACGCCCAAC-----	999
Db	873	GlnIlePheCysProSerProProValIleProAsnGlyArgHisThrGlyIlyAspIleu	892
QY	1000	-----CCACACCACTGCTCTCT	1017
Db	893	GluValPheProPheGlyIlyAlaIaValAsnTyrThrCysAspProHisPro-----Asp	910
QY	1018	CTCGGCGCA-----CCCGAG	1032

Dd	911	ArgGlyThrSerPheAspLeuIleGlyGluSerThrIleArgCysThrSerAspProGln		930
Qy	1033	GGGAGTGTTCACGACGAGCCCTCTCTACAGAGTGAAGAACTGCATGCTACAG		1092
Dd	931	GlyAsn-----GlyVal-----Trp-----SerSerProAlaProArg		941
Qy	1093	ACTCAACTGCTGGACACATGACAGCGCTCTGACGTTTC-----		1134
Dd	941	GCysGlyIleLeuGlyHisCysGlnAla--ProAspHisPheLeuPheAlaIleLeuLys		960
Qy	1134	-----		1134
Dd	961	ThrGlnThrAsnAlaSerAspPheProIleGlyThrSerLeuLysTyrgLysArgPro		980
Qy	1134	-----		1134
Dd	981	GluTygTyrgLysArgProPheSerIleThrCysLeuAspAsnLeuValTrpSerSerPro		1000
Qy	1134	-----		1134
Dd	1001	LysAspValCysLysArgLysSerCysLeuSerThrProProAspProValAsnGlyMetVal		1020
Qy	1135	-----AGCCAC		1144
Dd	1021	HisValIleThrAspIleGlnValGlySerArgIleAsnTygSerCysThrThrGlyHis		1040
Qy	1141	TTAGGCTGCTGGCGGTTAAAGATCCCTAGTGCATGAGAAATGCCAGCAAAATGCA		1200
Dd	1041	--ArgLeuIle--GlyHis--SerSerAlaGlyCysIle		1051
Qy	1201	GGAAGCCTGGAGAGCCTTCTGTGAGAAATGTGAGGCACATTAATGCG--		1245
Dd	1052	--LeuSerGly--AsnThrAlaHis--TrpSerThrLysProPro		1064
Qy	1246	-----GGAATTGAGAGACACCTA		1266
Dd	1065	IleCysGlnArgIleProCysGlyLeuProProThrIleAlaAsn--GlyAspPheIle		1083
Qy	1267	GACACT-----		1272
Dd	1084	SerThrAsnArgGluAsnPheHisTyrgLysSerValValThrTygCysAsnLeuGly		1103
Qy	1273	-----GGCTGAGCTGATGCTTTGTTGTCACAGTGAAC		1302
Dd	1104	SerArgGlyArgLysValPheGluLeuValGlyIleProSerIleTyrgCysThrSerAsn		1123
Qy	1303	-----CCACAG--		1308
Dd	1124	AspAspGlnAlaGlyIleTrpSerGlyProAlaProGlnCysIleIleProAsnLysCys		1143
Qy	1308	-----		1308
Dd	1144	ThrProProAsnValGluAsnGlyIleLeuValSerAspAsnArgSerLeuPheSerLeu		1163
Qy	1308	-----		1308
Dd	1164	AsnIleValValGluPheArgCysGlnProGlyPheValMetLysGlyProArgArgVal		1183
Qy	1309	-----TGGAGAGAGTTTTCGA--		1327
Dd	1184	LysCysGlnAlaLeuAsnLysTyrgLs-----ProGluLeuProSerCysSerArg		1200
Qy	1328	-----GTCGATCTGCTTTCACACTGCACACTGCACACTGCAC		1365
Dd	1200	GValCysGlnProProGluIleLeuHisGlyGln--HisThrProSerHisGln--As		1219
Qy	1366	AAAGTTT-----TGTGAACAAGTACTTCTCT-----		1391
Dd	1219	PAsnPheSerProGlyGlnGluValPheTygSerCysGln-----ProGlyTygAs		1236
Qy	1392	-----TTTTCATGTTTACA-----		1406



```

Db      787 ProGlyLeuProGly-----SerValGlySerProGlyValProGlyTleGlyProProGly 805
Qy      612 ----CCTGGCCCGAGGAGGACCTGAGACAGATTCTGACGACGTACACCACTTCTGCGTA 667
Db      805 yAlaAArgGlyProProGlyGlyGlnGlyProProGly--LeuSerGlyProPro----- 822
Qy      668 AGCCGGCCTTCGAGAGATTCTGCCTCGCAAAAGAGTATGCGATGATCATCCAC 727
Db      823 ----GlyIleLeuGly-----GlnuysGlyPhePro--GlyPhePro-- 834
Qy      728 GAGAGCTGACCAATATGTTGCATCACT-----GATCGTCAGACAT-----CC 775
Db      835 --GlyLeuAsp-----MetProGly--ProLysGlyAspLysGlyAlaGlnGlyLeuPr 851
Qy      776 AGGACATTCGAAATGCTGACATCTGCAATGGCAC----- 811
Db      851 ogly-----IleThrGlyGlnSerGlyLeuProGlyLeuProGlyGlnGlnGly 867
Qy      811 ----- 811
Db      868 AlaProGlyTleProGlyPheProGlySerLysGlyGlnuMetGlyValMetGlyThrPro 887
Qy      812 ----GAGAGGCTCCAAATGGCGGAGCTACAAAGGACCTTTCTGAGCCAG 859
Db      888 GlyGlnProGlySerProGlyPro--Trp--GlyAlaProGlyLeuPro--GlyGlnuysG 906
Qy      860 GGGACCAAC-----CCTGGAGTCTGACCTCTGCGAAACGGTCAATTTGAGTCCAGCA 913
Db      906 yAspHisGlyPheProGly--SerSerGly-----ProArg 917
Qy      914 GCAGACCCC----- 922
Db      918 GlyAspProGlyLeuLysGlyAspLysGlyAspValGlyLeuProGlyLysProGlySer 937
Qy      922 ----- 922
Db      938 MetAspLysValTyrMetGlySerMetLysGlyGlnuysGlyAspGlnGlyGlnuysGly 957
Qy      922 ----- 922
Db      958 GlnIleGlyProIleGlyGlnuysGlySerArgGlyAspProGlyThrProGlyValPro 977
Qy      922 ----- 922
Db      978 GlyLysAspGlyGlnAlaGlyGlnProGlyGlnProGlyProLysGlyAspProGlyTle 997
Qy      923 ----ACTGAGGGGCTGCCGAGCTC----- 943
Db      998 SerGlyThrProGlyAlaProGlyLeuProGlyProLysGlySerValGlyGlyMetGly 1017
Qy      943 ----- 943
Db      1018 LeuProGlyThrProGlyGlnuysGlyValProGlyTleProGlyProGlnGlySerPro 1037
Qy      944 -----AGGCGAGGTCTCCGCGCCGCGC 964
Db      1038 GlyLeuProGlyAspLysGlyAlaLysGlyGlnuysGlyGlnAlaGly--ProProGly 1056
Qy      965 ATGTGTGTTCAAGGAGCTG----- 982
Db      1057 IleGlyTleProGlyLeuArgGlyGlnuysGlyAspGlnGlyTleAlaGlyPheProGly 1076
Qy      983 ----AGCTGGGAGCGCCCA----- 998
Db      1077 SerProGlyGlnuysGlyGlnuysGlySerIleGlyTle--ProGlyMetProGlySerPr 1096
Qy      998 ----- 998
Db      1096 oglyLeuLysGlySerProGlySerValGlyTyrProGlySerProGlyLeuProGlyGly 1116
Qy      998 ----- 998

```

```

Db      1116 uysGlyAspLysGlyLeuProGlyLeuAspGlyTleProGlyValLysGlyGlnuAlaGly 1136
Qy      999 ----CCCAACCCCACTGCTTCTCTCCGCG----- 1023
Db      1136 yLeuProGlyThrProGlyProThrGly--ProAlaGlyGlnuysGlyGlnProGlySera 1156
Qy      1023 ----- 1023
Db      1156 spGlyTleProGlySerAlaGlyGlnuysGlyGlnuProGlyLeuProGlyArgGlyPheP 1176
Qy      1023 ----- 1023
Db      1176 roGlyPheProGlyAlaLysGlyAspLysGlySerLysGlyGlnuValGlyPheProGlyTle 1196
Qy      1024 -----G 1024
Db      1196 euAlaGlySerProGlyTleProGlySerLysGlyGlnuGlnGlyPheMetGlyProProG 1216
Qy      1025 CACCCGAGGAGATGTAGCAGGAGGCTTCTCACTCAGAGTGGAACTCAGATGTG 1084
Db      1216 yProGlnGly-----GlnProGlyLeuProGlySer--ProGlyHisAla----- 1230
Qy      1085 TCACAGACTCAACTGCTGGAGCACTGACAGCGCTTCTGAGGTTTTCAGCCACTTAG 1144
Db      1231 --ThrGlnuGlyPro--LysGly--AspArgGlyProGlnGly--GlnPro----- 1244
Qy      1145 GCTCGTTGGGCTTTAAAGATCCCTCTAGGTCAGTGAAGAAATGCCACAGAAATGTCAGGAA 1204
Db      1245 GlyLeuProGlyLeuProGlyPrometGly-----Pro----- 1255
Qy      1205 GCCTGGAGAGCTTCTGAGGAGATGTAGGACACATTATTTGGGAAATTTGAGAGACAGCC 1264
Db      1256 -ProGly--LeuProGlyTleAspGlyVal-----Lys--GlyAspLysG 1269
Qy      1265 TAGACACTGCGTGGCT----- 1281
Db      1269 yAsnProGlyTrpProGlyAlaProGlyValProGlyProLysGlyAspProGlyPheG 1289
Qy      1281 ----- 1281
Db      1289 GlnuMetProGlyIleGlyGlySerProGlyTleThrGlySerLysGlyAspMetGlyP 1309
Qy      1281 ----- 1281
Db      1309 roProGlyValProGlyPheGlnGlyProLysGlyLeuProGlyLeuGlnGlyTleLysG 1329
Qy      1281 ----- 1281
Db      1329 yAspGlnGlyAspGlnGlyValProGlyAlaLysGlyLeuProGlyProProGlyPPro 1349
Qy      1282 ----GATGTTTGTGACAGTGA----- 1301
Db      1349 roGlyProTyrAspIle--IleLysGlyGlnuProGlyLeuProGlyProGlnuGlyProPr 1368
Qy      1301 ----- 1301
Db      1301 ----- 1301
Db      1368 oglyLeuLysGlyLeuGlnGlyLeuProGlyProLysGlyGlnGlnGlyValThrGlyLe 1388
Qy      1301 ----- 1301
Db      1388 uValGlyTleProGlyProProGlyTleProGlyPheAspGlyAlaProGlyGlnuysGly 1408
Qy      1301 ----- 1301
Db      1408 yGlnuMetGlyProAlaGlyProThrGlyProArgGlyPheProGlyProProGlyProAs 1428
Qy      1302 -----CCCAAGTGGAGAGAGATTTTTC 1327
Db      1428 pGlyLeuProGlySerMetGlyProProGlyThrProSerValAspHisGlyPhe----- 1446
Qy      1328 GTCTGATCTGTTCTTACACTCACACACA----- 1358
Db      1447 ----LeuValThrArgHisSerGlnThrIleAspAspProGlnGlnCyProSerGlyThr 1464

```

```

QY 1358 ----- 1358
Db 1464 rLysIleLeuTyRHisGlyTyRSerLeuLeuTyRValGlnGlyAsnGlnArgAlaHisGly 1484
QY 1359 -----TAACTCAAAAGTTTGTGAAACAAGTACTTTCCTTT 1393
Db 1484 yGlnAspLeuGlyThRAlaGlySerCysLeuArgGlyPheSer-ThrMetProPheLeuP 1504
QY 1394 TTTCACATGTTACATGCTCCATGTTTCTGTTTCTGT 1431
Db 1504 he-CysAsnIleAsnAsn-----ValCysAsnPheAlaSerArgAsnAspT 1519
QY 1431 ----- 1431
Db 1519 yRserTyRTrPLeuSerThRProGlnProMetProMetSerMetAlaProIleThRGlY 1539
QY 1432 -----TTTCATAACACAGAGCTGTGTGACCTA----- 1459
Db 1539 IuAsnIleArgProPheIleSerArg-----CysAlaValCysGlnAlaProAlaMet 1556
QY 1460 -----CAACCTAATTTCATGACCCAGTGTTCGACTTCAGCGTGG 1501
Db 1557 ValMetAlaValHisSerGlnThr-IleGlnIleProPro-CysProSerGlyTrp 1574
QY 1502 CCTACAGCAGTATGCG-----GGAGCCACTGAG 1528
Db 1575 --SerSerLeuTrpIleGlyTyRSerPheValMetHisThrSerAlaGlyAla--Glu 1592
QY 1529 GGAATGTTTCCCTGCTGTGCTTAAAGCAGAGAAAGCAGCGAGTGCCTCGAA 1588
Db 1593 GlySerGlyGlnAlaLeuAlaSerPro-----GlySerCys-LeuGln 1606
QY 1589 -----GCACCCAGCATACACCCAGGCTTGTGCGGGG 1620
Db 1607 GluPheArgSerAlaProPheIle-----GluCysHisGly 1618

RESULT 33
US-09-488-725A-6012
/ Sequence 6012, Application US/09488725A
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq Inc
/ TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
/ FILE REFERENCE: 784PLPCT
/ CURRENT APPLICATION NUMBER: US/09/488,725A
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US/09/488,725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: US09/598,042
/ PRIOR FILING DATE: 2000-06-20
/ PRIOR APPLICATION NUMBER: US09/620,312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: US09/653,450
/ PRIOR FILING DATE: 2000-08-31
/ PRIOR APPLICATION NUMBER: US09/662,191
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: US09/693,036
/ PRIOR FILING DATE: 2000-10-19
/ PRIOR APPLICATION NUMBER: US09/727,344
/ PRIOR FILING DATE: 2000-11-29
/ NUMBER OF SEQ ID NOS: 7144
/ SOFTWARE: PL_FL_genes_b Versions 1.0
/ SEQ ID NO 6012
/ LENGTH: 1557
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-488-725A-6012

Alignment Scores: 31.7 Length: 1551
Pred. No.: 443.40 Matches: 219
Score:

```

```

Percent Similarity: 17.67% Conservative: 58
Best Local Similarity: 13.97% Mismatches: 145
Query Match: 14.81% Indels: 1146
DB: 1 Gaps: 38

us-09-896-522-1 (1-1624) x US-09-488-725A-6012 (1-1551)
QY 1623 TGGCCCCGACAAAGCTGGGTGTGATGTGCTGCTCCAGAGGACATCCGCTGCTTC 1564
Db 321 TrpArgThrThRGlU-TrpThRGlUcysArgValAspPro-----LeuLeuSerG 337
QY 1563 TGCCTTAAAGCACAAGCAAGGGGGGAAAAATCCTCCAGTGCCTCCCATATCCGTGA 1504
Db 337 InGlnAspLys--ArgArgGlyAsnGlnThrAlaLeuCysGly----- 350
QY 1503 GGGCAGCTGGAGTGTGAACCACTGGGTGATGAATTAAGTTGTGAAGCACAACAGCC 1444
Db 351 -----GlyGlyIleGlnThr-----ArgGluValIlyr----- 359
QY 1443 TTGTGTTATGAACAAGAAAAACAGAAAAAC-----ATGAGACATGTATACATGA 1396
Db 360 -CysVal-----GlnAlaAsnGlnLeuLeuSerGlnLeuSerThr--HisLys 375
QY 1395 AAAAAGAAAGTACT----- 1381
Db 376 AsnLysGlnAlaSerLysProMetAspLeuLysLeuCysThrGlyProIleProAsnThr 395
QY 1381 ----- 1381
Db 396 ThrGlnLeuCysHisIleProCysProThrGlnCysGlnValSerProTrpSerAlaTrp 415
QY 1380 -----TGTTCACAAAAATTGAGTTATGTGTGAGTGTGTGAAGACCAATCAGACT 1327
Db 416 GlyProCys-----ThyTrpGlnAsnGly-----Asn--AspGlnGln 427
QY 1326 GGA AAAAATCTCTCCACTGTGGGTTCACTGCACAA----- 1287
Db 428 GlyLysLys-----GlyPheLysLeuArgLysArgArgIleThrAsnGlnPur 443
QY 1286 -ACATCAGCGCAGCAGCTGTCTAGGCTGTCTCCTCAATTTCCCAATTAATGTGCTACA 1228
Db 443 oThrGlyGlySerGlyValThr-----GlyAsnCysProHis- 455
QY 1227 TTCTCACAAGAACCTCCAGGCTTCCTGCACATTCGTGTGCAATTT----- 1182
Db 456 --LeuLeuGlnAla-----IleProCysGlnGlnProAlaCysLysTrpAspTrpLysAl 472
QY 1181 -----CTCAGTGACCTTAAGGGAGATCTTAAACCGCACAG----- 1146
Db 472 aValArgLeuGlyAspCysGlnProAsp--AsnGlyLysGlnCysGlyProGlyThrGln 491
QY 1146 ----- 1146
Db 491 nValGlnGlnValAlaCysIleAsnSerAspGlyGlnGlnValAspArgGlnLeuCysArg 511
QY 1145 -----CTTAAG----- 1140
Db 511 GAspAlaIlePheProIleProValAlaCysAspAlaProCysProLysAspCysValLe 531
QY 1139 -----TGCTGA AAACCTGAGAACGCTGT----- 1114
Db 531 uSerThrTrpSerThrTrpSerSerCysSerHisThr--CysSerGlyLysThrThRGlU 550
QY 1113 -----CAG 1111
Db 551 GlyLysGlnIleArgAlaArgSerIleLeuAlaTyRAlaGlyGlnGlnGlyLysLeuArg 570
QY 1110 TGTCCAGCAAGTTGAGCTG----- 1090
Db 571 CysProAsnSerSerAlaLeuGlnGlnValArgSerCysAsnGlnHisProCysThrVal 590
QY 1089 -----AGTACACATGTGAGTTTCCACT- 1067

```

```

Db      591 TyrHisTrpGlnThrGlyProTrpGlyGlnCysIleGluAspThrSer--ValSerSerp 610
Qy      1067 -----
Db      610 heanThrThrThrThrTrpAsnGlyGlnAlaSerCysSerValGlyMetGlnThrArgL 630
Qy      1067 -----
Db      630 yValIleCysValArgValAsnValGlyGlnValGlyProLysCysProGluSerL 650
Qy      1066 ----CCTGAGTAAAGAGGCTT-----
Db      650 euArgProGluThrValArgProCysLeuLeuProCysLysLysAspCysIleValThrP 670
Qy      1049 -----
Db      670 rofYrSerAspTrpThrSerCysProSerSerCysLysGlnLysAspSerSerIleArgL 690
Qy      1049 -----
Db      690 yGlnSerArgHisArgValIleIleGlnLeuProAlaAsnGlyGlyArgAspCysThrA 710
Qy      1049 -----
Db      710 sPrProLeuYrGlnGlnLysAlaCysGlnLysAlaProGlnAlaCysGlnSerYrArgTrpL 730
Qy      1048 ----CGCTGCTAACATC-----CGCTGGGGT-----GGGCC 1021
Db      730 yThrHisLysYrTrpHisArgCys--GlnLeuValProTrpSerValGlnGlnAspSerPr 749
Qy      1020 GAGAGGAGAGAGAGTGGGTGGGTGGGCTGCC-----CAGGCTCAGCTCCGTAACACAC 967
Db      749 oGlyAlaGlnGlnGlyCysGly-----ProGlyArgGlnAlaArgAlaIle-----Th 765
Qy      966 ATGCCGG-----CGGAGAGA 952
Db      765 rCysAspGlyGlnAspGlyGlyGlnAlaGlyIleHisGlnCysLeuGlnIntyrAlaGlyPr 785
Qy      951 CCGGCCCTGAGGCTCGAGCCCTCAGTGGGAGTGGCTGGCTGACTCCAAATGT----- 897
Db      785 ovalPro-----AlaLeuThrGln-----AlaCysGlnIlePro--CysGlnAs 799
Qy      896 -GACCGTTTGCCAGAGTCCAGATCCAGGGGTGGTCCCGCTGCTCA----- 852
Db      799 pAsp-----CysGln-----LeuThrSerTrpSerLysPheSerSerCysAsnGlyAs 815
Qy      851 -----GAAA 847
Db      815 pCysGlyAlaValArgThrArgLysArgThrLeuValGlyLysSerLysLysGlyGly 835
Qy      846 GGTCCCGCTTGAGCTCCGCCCAT----- 824
Db      835 s-----CysLysAsnSerHisLeuYr--ProLeuIleGluThrGlnYrCysProCysA 853
Qy      823 -----TGAC----- 818
Db      853 sPlsYrTrpAsnAlaGlnProValGlyAsnTrpSerAspCysIleLeuProGluGlyLysV 873
Qy      817 ----CTCCTCGGT----- 809
Db      873 aIGlnValLeuLeuGlnMetLysValGlnGlyAspIleLysGlnCysGlyGlnGlyTyrA 893
Qy      809 ----- 809
Db      893 xGlyTrglnAlaMetAlaCysYrAspGlnAsnGlyArgLeuValGluThrSerArgCysA 913
Qy      808 ----GCAATTTGCAGATGTCCATTCAGATTCGCT- 776
Db      913 snSerHisGlyYrIleGlnGlnAlaCysIleIleProCys--Pro-SerAspCysLysLys 932
Qy      775 ----GGATGTGCTGCAC 763
Db      932 euSerGluTrpSerAsnTrpSerArgCysSerLysSerCysGlySerGlyValLysValA 952

```

```

Qy      762 GATCAGGTTGATGG-----CAACCATAT-----TGTCCACTCCTCG 727
Db      952 rGserLys--TrpLeuArgGlnLysProYrAsnGlyArgProCysProLysLeu- 970
Qy      726 TGGGATGATCATCATCGCATACTTCTTGTTCGACAGACAGAACTCTCGAAGCCGGCTT 667
Db      971 ----AspHisVal-----AsnGlnAlaGlnValTyrGlu----- 980
Qy      666 CACGAAGTGTGTACTCGCTCAGAAATCTGCTCCAGGCTCCCTCGGCGCACGTCC- 608
Db      981 ----ValValProCysHisSerAspCysAsnGlnTyrLeu--TrpValThrGluProT 998
Qy      607 ----GGAGAACTCTCGACA 592
Db      998 rPserIleCysLysValThrPheValAsnMetArgLysLeuLysCysGlyGlnGlyValGlnT 1018
Qy      591 CACCTGACGTCCGAGTGGGTGTCCACGAAGAGCCAGGTGGAACATGTCC----- 539
Db      1018 hr-----ArgLysValArgCysMetGlnAsnThrAlaAspGly-----ProSerGluH 1034
Qy      538 ----GGATCTCTGCTGTAGAA 520
Db      1034 iValIGlnAspTyrLeuCysAspProGluGlnLysMetProLeuGlnGlySerArgValCysLysL 1054
Qy      519 CACCAAGATGCCCTCA----- 503
Db      1054 euPro--CysProGluAspCysValIleSerGluTrpGlyProTrpThrGlnCysValL 1073
Qy      502 ----ACGAACACAGTCC 490
Db      1073 euProCysAsnGlnSerSerPheArgGlnArgSerAlaAspProIleArgGlnProAlaA 1093
Qy      489 CCGAGGCTGAA----- 479
Db      1093 sPlGlnLysArgSerCysProAsnAlaValIGlnLysGluProCysAsnLeuAsnLysAsnC 1113
Qy      479 ----- 479
Db      1113 yEfYrHisYrAspYrAsnValThrAspTrpSerThrCysGlnLeuSerGlnLysAlaV 1133
Qy      479 ----- 479
Db      1133 aICysGlyAsnGlyLysLysThrArgMetLeuAspCysValArgSerAspGlyLysSerV 1153
Qy      479 ----- 479
Db      1153 aLAspLeuYrYrCysGlnAlaLeuGlyLeuGlnLysAsnTrpGlnMetAsnThrSerC 1173
Qy      478 -----CCACCGTGGTCTCTGGTAA 460
Db      1173 yMetValGlnCysProValAsnCysGlnLeuSerAspTrpSerProTrpSer- 1190
Qy      459 CCTTGAGTGTGCACA-----AATCATAGGTGGGCAC 427
Db      1191 ----GlnCys--SerGlnThrCysGlyLeuThrGlyLysMetIleArgArgArgThrValT 1209
Qy      426 CTCACCGTTT-----T 415
Db      1209 hrGlnProPheGlnGlnLysAspGlyArgProCysProSerLeuMetAspGlnSerLysProC 1229
Qy      414 GGCCT-----CCAGATGTCTTCAGA----- 393
Db      1229 yAsProValLysPro--Cys--TyrArgTrpGlnTyrGlnGlnTrpSerProCysGlnVa 1247
Qy      392 ----GTCTGTGTCATCAATCATT 373
Db      1247 lGlnGlnAlaGlnCysGlyGlnGlyThrArgThrArgAsnIleSerCysValValSerAs 1267
Qy      372 ATCAAGGCACTGATGCTCAAAATTGTAC----- 342
Db      1267 pGlySerAlaAspAspPheSerLysValValAspGlnGluPheCysAlaAspIleGluLe 1287

```

```

QY 341 -----TGTCTTTCAAGGCTTGGC 322
Db 1287 uilleleargglyAsnlysaenmetValleugluserCys---SerGlnProCysP 1306
QY 321 CTTCTGCTCCCGCTCAGACCTTGT----- 296
Db 1306 ro-----GlyAspCysrlyleuysaerTpserserTpsrleucysg 1321
QY 295 -----AGAA 292
Db 1321 InleuThrCysValaenGlylnaAspleuglyPhegllylleglnValArgserArg- 1340
QY 291 CCGTCTCGGCTCAGATGACCACTTCGCTCGCTGTTCCACTCTGTTCTGCCAG 232
Db 1341 Provallellelleglnlu-----LeuGlnaenGlnhisleu---CysPro-- 1354
QY 231 CAATCCATGATCTTCTCACAACGCTCG----- 203
Db 1355 -GluGlnMetleu---GluThrlyserCysrlyraerGlylnCysrlyGlnlyrlyr 1373
QY 202 -----ACTTCCCGCTGGCAG-----TGCCGCCGCTCA----- 176
Db 1373 rPmetalaSerAlatrllysglySerSerArgThrValTrpCysGlnArgSerArglyT 1393
QY 175 -----CCCTATCAGAAAGGCGCGCTGGTGC 151
Db 1393 leaenValThrGlyGlyCysleuValmetSerGlnProAspAlaAspArgSer-----Cy 1411
QY 150 CGGAGCGTCCGCTCCGCGCG----- 131
Db 1411 s-----AsnProProCysSerGlnProHisSerTrpCysSerGluThrlyserCysH 1429
QY 131 ----- 131
Db 1429 IscYsglGlnGlyTrpThrGlnValmetSerSerAsnSerThrLeuGlnGlnCysThrL 1449
QY 130 -----CGGCGCTCTCGACATCTTCCGCC 109
Db 1449 eulleProvalValaValleuProThrmctGlnaAspArgGlyAsp-----VallyThr 1467
QY 108 TCCCGCGGAAGCCATCTCGGCTCCGCTCCGCGCATCGGCTCCCGCGCGCGC----- 55
Db 1468 SerArgAlaValHis-----ProThrGlnPro-SerSerAsnProAlaGlyArgGlyArg 1485
QY 54 -----CCCTTCCCGCGCGC----- 42
Db 1486 ThrTrpPheLeuGlnProPhe-----GlyProAspGlyArgleuylThrTrpValTyrG1 1504
QY 42 ----- 42
Db 1504 YValAlaAlaGlyAlaPheValleuLeullePheleValSerMetIleTyrleuAlaCy 1524
QY 41 -----CCGCGCGCGCGCGCGCGCGCGCGAGTCCGAGCGCA 7
Db 1524 slyeLysProLysPro--GlnArgArgGlnaenAsnArg 1537

RESULT 34
US-09-488-725A-2653
; Sequence 2653, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLEPT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19

```

```

; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_PL_genes_b Versions 1.0
; SEQ ID NO 2653
; LENGTH: 752
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2653

Alignment Scores:
Pred. No.: 4.5 Length: 751
Score: 442.20 Matches: 184
Percent Similarity: 22.90% Conservative: 59
Best Local Similarity: 17.34% Mismatches: 140
Query Match: 14.57% Indels: 678
DB: 1 Gaps: 18

us-09-896-522-1 (1-1624) x US-09-488-725A-2653 (1-751)
QY 2 TGGAGTCCGCTCCGACCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 61
Db 71 trpGlyGlnGlnlyrArgArgArg-----ProGlyPro----- 81
QY 62 CGGAGACCCGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGT 99
Db 82 -----CysAlaGlyIleTyrAlaGlnHisValleuAspProLysAsnLeuGlyL 98
QY 100 -----TCGG 103
Db 98 eulAlaHisGlnArgGlnGlnGlnleuGlnPheSerArgGlnSerPheGlnSerAspThrA 118
QY 104 CGGAGCGCGAAGACTCGGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 163
Db 118 laGlnGlyGlnGlnlyrGlnlyrSerThr-----LysProMetAlaPheSerSerP 135
QY 164 TCCT-----GA 169
Db 135 oProLeuArgHisAlaValSerSerArgArgArgSerValValGlnleuGlnSerSe 155
QY 170 TAGCGGTGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 229
Db 155 rGlnGlyGlnArgGlnaen--ProThr-GluIleAspLysVal-----Le 169
QY 230 TGCCTGGAGACAGACGAGTGAACAGCGCGCGCGCGCGCGCGCGCGCGCGCG 289
Db 169 uLySgLyIleGln-----Amser-----ArgTrpGlyAla----- 179
QY 290 GATTTCACAGAGTCTCGACCGACAGACGAGCGCGCGCGCGCGCGCGCGCGCG 349
Db 180 -----PheLys-----CysAlaGlnArg--GlyGlnAspPheSerArg----- 191
QY 350 TTGACCATCCAGATCGCTTGATATGATATTGATGACACAGACTTGAAACATCG 409
Db 192 -----LysMetMetValIle-----IleHisLys-----LysAlaHisSer- 203
QY 410 AGGCGAAGACGAGGAGTGCAGCTATGATTTGTGACACACTCAAGTTACACAGA 469
Db 204 ArgGlnLysLeuPheThrCysArgGln-----Cys-----His-GlnGlyPhe-ArgAs 219
QY 470 CCAAGTGTCTTACCTCGGACGCTGCTGTTGAGAGGCGCATCTTGTTCTACAGCC 529
Db 219 pGlnSerAlaLeu-----LeuLeuHisGlnaen-----ThrHisThrGly 232
QY 530 AGGAGATCCGAGACATTTCCACTCGCGCTTCTTGAGACACCGAGTCCGAGCTC 589
Db 233 GlnLysSerTrpValCysSerValCysGly-----ArgGlyPheSerLeuLys----- 248

```



```

QY 590 TGTCTGGAAGATTCTCCGGGACGTGGC----- 618
Db 249 -----AlaMetLeuLeuArgHisGlnArgThrHisSerGlyGlyProPheLeuGly 267
QY 619 -----CGAGGAGGAGACCTGAGACAGATTCTGACGACATAC-----CA 658
Db 267 ValAlaGlyGlyArgGlyThrSerLeuSerGlyLeuThr-----ValHisGlnArgThrHis 286
QY 659 CCTTCGGAAGCGGCTTCGAGAGATTTCGCTCGGACAAAGAGTATGCGGATGTA 718
Db 286 ValArgGlyGly-----LysProGlyGlyGlyGlnGlyGlyArgGly-----PheAsnAsp----- 303
QY 719 TCATCCGACGAGGAGTGACAAATATGTTGTCATCAATGATGTCGACAGACGAG 778
Db 304 -----LysSerSerGlyAsnGlyHis-----LeuValAlaHisSerGly 316
QY 779 ACATTCTGAATGTGACATCTGAAA-----TGACACCGAGAGGAGGTCCAAATGAGCGAGACT 835
Db 316 ValGlyLysProPhe-----ValGlyGlyGlnGlyGlyArgGlyGlyThrAsn-----LysSerGly 334
QY 836 AC-----AAGCGACCTTTTCTGACGAGGAGGACACCT----- 870
Db 334 ValPheValAlaHisLysArgGlnLeuHisSer-----GlyGlyLysProGlyArgGlyGlnG 352
QY 871 -----GGGATGCTGACCTTCGCAAAAGGTCAATTTGAGTCCAGACGAGAC 919
Db 352 ValGlyGlyArgGlyPhe-----SerAsnLys-----SerHisLeuLeuLeuHisGlnArg 369
QY 920 CCCACTGAGGAGGCTGCGGACGCTCAGGAGGAGTCTCCGCGGACGATGTT----- 970
Db 369 HisHis-----SerGlyGly-----LysProPheAlaCysArgGlnGly 381
QY 971 -----GTCAGGAGCTGACCTTCGCAAGGCTGGGAGCGGACCCACACCTGCTTC 1015
Db 382 LysGlnSerPheSerValLysGly-----SerLeuLeuArgHisGlnArgThrHis 398
QY 1016 CTCTCGCGCCACCCCGGAGAGTGT----- 1040
Db 399 -SerGlyGlyLysProPheValCysLysAspCysGlnArgSerPheSerGlnLysSerThr 418
QY 1041 -----TAGACCGGAGGCTTCCTCACTGACAG----- 1067
Db 418 rLeuValTyrHisGlnArg-----ThrHisSerGlyGlyLysProPheValCysArgGly 436
QY 1068 -----GTGAACTCAAGTGTGCTGACAG----- 1093
Db 436 ValGlyGlnGlnArgPheLeuGlnLysSerThrLeuValLysHisGlnLeuThrHisSerGly 456
QY 1094 C-----TCAACT----- 1100
Db 456 ValGlyLysProPheValCysLysAspCysGlnArgGlyPheLeuGlnLysSerThrPheAla 476
QY 1101 -----TGCTGAGACACTGACGAGCG----- 1120
Db 476 AlaLeuHisGlnArgThrHisSerGlnGlyLysProGlyGlyCysArgGlnGlyArgGly 496
QY 1121 TTCCTGAGGTTTTC-----AACCACTTAGGCT 1147
Db 496 G-----PheArgAspLysSerSerGlyAsnLysHisLeuArgAlaHisLeuGlyG 513
QY 1148 CGTTGGCGTTTAAAGATCCCTAGAGTCACTGAAATCCACAGATGTGACAGAGCC 1207
Db 513 ValLysArgPhe-----PheCys-----ArgAspCysGlyArg----- 523
QY 1208 TGGAGGCGTTTC----- 1218
Db 524 -----GlyPheThrLeuLysProAsnLeuThrHisGlnArgThrHisSerGlyGly 542
QY 1219 -----TGTCAGCAATGTGAGGACATTTATTTGGGAAA----- 1250
Db 542 ValProPheMetCysValGlnGlyGly-----LysSerPheSerLeuLysAla 557

```

```

QY 1251 -----TTGAGGAGACAGCTTAGACACTGCTGAGCTGATGTTTGTGACAGTGAACC 1303
Db 557 AlaMetLeuLeuArgHisGln-----Trp-----Thr 565
QY 1304 CACAGTGGAGAGAGATTTTTC-----CAGTTC 1330
Db 566 HisSer-GlyGlyLysArgProPheHisLysValAspCysGlyArgGlyPheLeuLeuLysSe 585
QY 1331 TGATTGCTTTTCACTACACTGACACACATTAAGTAAAGTTTGTGACAAAGTATTC 1390
Db 585 rThrLeuLeu-PheHisGlnLysThrHisSerGlyGly-----Lys-----Pr 599
QY 1391 TTTTTCATGATGTTACATGCTCCATGTTTTCGTTTTCGTTTTCATTAACAGAGGCTGT 1450
Db 599 OrnHisLeu-Cys-----SerGlyCys-----GlyGlnGlyPhe 610
QY 1451 TGTGCTTCAAAACCTAATTTCAATGACACGAGTGTGACATGACAGCTGACAGG 1510
Db 610 LeuTrpLysSerHisLeuValLys-----HisGly 619
QY 1511 ATATGGGAGGACCACTGAGGAGATGTTTCCCTTCCTTGTGCTTAAAGGACAGAGAC 1570
Db 619 nLeu-----AlaHisSerGlyLys-----GlnProPheValCys-----LysGlyCysGly 635
QY 1571 GAGGCGGATGCCCTGAGAC-----CACCCAGATCAACCCAGGC----- 1610
Db 635 rGlyLys-PheAsnTrpLysGlyValMetLeuThrHisGlnArgThrHisSerGlyGly 654
QY 1611 -----TTGTGCGCG 1619
Db 654 SerProPheValCysAsnValCysGly 662

RESULT 35
US-09-488-725A-6225
; Sequence 6225, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: HySeq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784F1PCT
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc FL_genes_b Versions 1.0
; SEQ ID NO 6225
; LENGTH: 773
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6225

Alignment Scores:
Pred. No.: 4.88 Length: 773
Score: 442.20 Matches: 184
Percent Similarity: 22.90% Conservative: 59
Best Local Similarity: 17.34% Mismatches: 140
Query Match: 14.57% Indels: 678
DB: 1 Gaps: 18

```

```

us-09-896-522-1 (1-1624) x us-09-488-725A-6225 (1-773)
QY      2 TGGAGTGCCTCCGACCTCGGCGCGGCGCGCGCGCGGAGGAGGCGGCGG 61
Db      |||||
QY      93 TrpGlyGlnGlnArgArgArg-----ProGlyPro----- 103
Db      |||||
QY      62 CGGGAGCCCGATGCGCGGAGCGGAGCGGAGATGCGT----- 99
Db      |||||
QY      104 -----CysAlaGly11etyrAlaGlnHisValLeuArgProLysAsnLeuGlyL 120
Db      -----
QY      100 -----TCGG 103
Db      -----
QY      120 euAlaHisGlnArgGlnGlnGlnLeuGlnPheSerArgGlnSerPheGlnSerAspThr 140
Db      -----
QY      104 CGGAGCGGAGACTCGGAGAGCCCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCT 163
Db      |||||
QY      140 laGlnGlyGlnGlnGlnLysGlnLysSerThr-----LysProMetAlaPheSerSerPr 157
Db      -----
QY      164 TCCT-----GA 169
Db      -----
QY      157 opPLeuArgHisAlaValSerSerArgArgArgAsnSerValValGlnLileGlnSerSe 177
Db      -----
QY      170 TAGGGTGAAGCGCGCGGACTGCGAGCGGAGTGAAGTGAAGTGAAGTGAAGTGAAGT 229
Db      |||||
QY      177 rgInGlyGlnArgGlnLysn--ProThr--GlnLileAspLysVal-----Le 191
Db      -----
QY      230 TGCTGGAGACAGACGAGGTGAGACAGCGGAGCGGAGAGTGTGATCTGAGCCAGACA 289
Db      |||||
QY      191 ulysGly11eGln-----AsnSer-----ArgTrpGlyAla----- 201
Db      -----
QY      290 GGTTCCTCAAGGTCTGACCGGACGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGT 349
Db      |||||
QY      202 -----PheLys-----CysAlaGlnArg--GlyGlnAspPheSerArg----- 213
Db      -----
QY      350 TTGACATCCAGATGCTTTGATATGATGATGATGATGATGATGATGATGATGATGATG 409
Db      |||||
QY      214 -----LysMetMetValIle-----IleHisLys-----LysAlaHisSer-- 225
Db      -----
QY      410 AGGCGAAACCGGTGAGGTGCGGAGCTGATGATTTTGTGACACACTCAAGGTTGACAGA 465
Db      |||||
QY      226 ArgGlnLysLeuPheThrCysArgGln-----Cys-----His--GlnGlyPhe--ArgAs 241
Db      -----
QY      470 CCAAGGTGTCTACCCCTGCGGAGCGGAGTGTGTTTGTGAGGAGCATCTGGTGTCTACAGCC 529
Db      |||||
QY      241 pGlnSerAlaLeu-----LeuLeuHisGlnAsn-----ThrHisThrGly 254
Db      -----
QY      530 AGGAGATCCGGGAGATGTTCCACCTGCGCTCTTGTGAGACACGACTCCGACGCTCAGGC 589
Db      |||||
QY      255 GlnLysSerArgValCysSerValCysGly-----ArgGlyPheSerLeuLys----- 270
Db      -----
QY      590 TGTCTCGAAGTCTCCGGAGCGTGGC----- 618
Db      -----
QY      271 -----AlaAsnLeuLeuArgHisGlnArgThrHisSerGlyGlnLysProPheLeuCysL 289
Db      -----
QY      619 -----CGAGGAGGAGGAGCGGAGGAGATTTGACGACGAGC-----CA 658
Db      -----
QY      289 ysValCysGlyArgGlyLysThrSerLysSerTyrLeuThr--ValHisGlnLysGlnHis 308
Db      |||||
QY      659 CTTTCGTGAAGCGGCTTTCGAGGAGTCTGCTGCTGCGGAGAGAGATGATGCGGATGGA 718
Db      |||||
QY      308 sThrGlyGln--LysProTyrGlnLysGlnGlnLysGlnLysArgGln--PheAsnAsp----- 325
Db      -----
QY      719 TCATCCCAAGAGAGTGAATATGTTGGTCCATACCTGATCTGTGACGACATCCAGG 778
Db      |||||
QY      326 -----LysSerSerTyrAsnLysHis-----LeuLysAlaHisSerGly 338
Db      -----
QY      779 ACATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 835
Db      |||||
QY      338 yGlnLysProPhe-----ValCysLysGlnCysGlyArgGlyLysThrAsn--LysSer 356
Db      -----
QY      836 AC-----AAGCGACCTTTTCTGAGCGGAGGAGCGGAGCGGAGCGGAGCGGAGCGG 870
Db      |||||
QY      356 yPheValValHisValArgHisSer-----GlyGlnLysProTyrArgCysGlnG 374

```

```

QY      871 -----GGAGTGTGACCTTGGCAACGGTCAATTGAGTCCAGACAGAC 919
Db      |||||
QY      374 luCysGlyArgGlyPhe-----SerAsnLys--SerHisLeuIleThrHisGlnArgT 991
Db      |||||
QY      920 CCCACTGAGGGGCTGGCCAGGCTCAGGAGGAGTCTCCCGCGGAGTGT----- 970
Db      |||||
QY      391 hHis-----SerGlyGln-----LysProPheAlaCysArgGlnCys 403
Db      -----
QY      971 -----GTTCAGGACCTGAGCTCCGGGAGCCGACCCAGCCAGCCAGCTGCTTC 1015
Db      |||||
QY      404 LysGlnSerPheSerValLysGly--SerLeuLeuArgHisGlnArgThrHis----- 420
Db      -----
QY      1016 CTCTGCGCGACCCGAGGAGTGT----- 1040
Db      -----
QY      421 -SerGlyGlnLysProPheValCysLysAspCysGlnArgSerPheSerGlnLysSerTh 440
Db      -----
QY      1041 -----TACAGCGAGCGCTTCTGACTCAGGA----- 1067
Db      -----
QY      440 rLeuValTyrHisGlnArg-----ThrHisSerGlyGlnLysProPheValCysArgGly 458
Db      -----
QY      1068 -----GTGAAACTCAGATGCTGCTCAGGA 1093
Db      -----
QY      458 uCysGlyGlnGlyPheIleGlnLysSerThrLeuValLysHisGlnIleThrHisSerGly 478
Db      -----
QY      1094 C-----TCACT----- 1100
Db      -----
QY      478 uGlnLysProPheValCysLysAspCysGlnArgGlyPheIleGlnLysSerThrPheTh 498
Db      -----
QY      1101 -----TGCTGGACACTGACAGCGG 1120
Db      -----
QY      498 rLeuHisGlnArgThrHisSerGlnGlnLysProTyrGlnCysArgGlnCysGlyArg 518
Db      -----
QY      1121 TTCTCGAGTTTC-----AGCAGCTTGGGCT 1147
Db      -----
QY      518 g-----PheArgAspLysSerSerTyrAsnLysHisLeuArgAlaHisLeuGlyG 535
Db      -----
QY      1148 CGTTGCGGTTTAAAGATCCCTAGGTCACCTGAGAAATGCCAGACAGATGTCAGAGAGCC 1207
Db      |||||
QY      535 luLysArgPhe-----PheCys--ArgAspCysGlyArg-- 545
Db      -----
QY      1208 TGGAGGCTTC----- 1218
Db      -----
QY      546 -----GlyPheThrLeuLysProAsnLeuThrIleHisGlnArgThrHisSerGlyGlnL 564
Db      -----
QY      1219 -----TGTGAGGAATGTGAGGACATTAATGGGGAAT----- 1250
Db      -----
QY      564 ysProPheMetCysLysGlnCysGln-----LysSerPheSerLeuLysAl 579
Db      -----
QY      1251 -----TTGAGGAGACAGCTGAGACAGCTGCGCTGATGTTTGTGACAGTGAACC 1303
Db      |||||
QY      579 aAsnLeuLeuArgHisGln-----Trp-----Thr 587
Db      -----
QY      1304 CACAGTGGAGAGAGTTTTC-----CAGTC 1330
Db      -----
QY      588 HisSer--GlyGlnLysProPheAsnLysLysAspCysGlyArgGlyPheIleLeuLysSe 607
Db      -----
QY      1331 TGATCTGTTCTTAACACTCAACACATCAATCAAAAGTTTGTGAACAGTACTTTC 1390
Db      |||||
QY      607 rThrLeuLeu--PheHisGlnLysThrHisSerGlyGln-----Lys-----Pr 621
Db      -----
QY      1391 TTTTTCATGATCATGATGCTGATGTTTCTGTGTTTCTGTTCATTAACAAGGCTGT 1450
Db      |||||
QY      621 oPheIle--Cys-----SerGlnCys-----GlyGlnGlyPheI 632
Db      -----
QY      1451 TGTGGCTCAAAACCTAATTTCATGACCAGTGTGTCAGTCCAGGCTGACAGCG 1510
Db      |||||
QY      632 leryLysSerAsnLeuValLys-----HisGly 641
Db      -----
QY      1511 ATATGGGAGGACCTGAGGAGTGTTCCTGCTGCTGCTGCTGCTTAAAGGACAGAGAGC 1570
Db      |||||
QY      641 mLeu-----AlaHisSerGlyLys--GlnProPheValCys--LysGlnCysGlyA 657

```

QY 1571 GAGCGGATCCCTGAG-----CACCCAGCATCACCCAGC----- 1610  
 ||||| |||||  
 Db 657 rggly--PheAsnTrpYsglyAsnLeuLeuThHISglArghrHisserglyIu 676  
 QY 1611 -----TTGGCGGG 1619  
 |||||  
 Db 676 sPropheValCysAsnValCysgly 684  
 |||||  
 RESULT 36  
 US-09-488-725A-2440  
 / Sequence 2440, Application US/09488725A  
 / GENERAL INFORMATION:  
 / APPLICANT: Hysge Inc  
 / TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 / FILE REFERENCE: 784PLPCT  
 / CURRENT APPLICATION NUMBER: US/09/488,725A  
 / CURRENT FILING DATE: 2000-12-22  
 / PRIOR APPLICATION NUMBER: US/09/488,725  
 / PRIOR FILING DATE: 2000-01-21  
 / PRIOR APPLICATION NUMBER: US09/552,317  
 / PRIOR FILING DATE: 2000-04-25  
 / PRIOR APPLICATION NUMBER: US09/598,042  
 / PRIOR FILING DATE: 2000-06-20  
 / PRIOR APPLICATION NUMBER: US09/620,312  
 / PRIOR FILING DATE: 2000-07-19  
 / PRIOR APPLICATION NUMBER: US09/653,450  
 / PRIOR FILING DATE: 2000-08-31  
 / PRIOR APPLICATION NUMBER: US09/662,191  
 / PRIOR FILING DATE: 2000-09-14  
 / PRIOR APPLICATION NUMBER: US09/693,036  
 / PRIOR FILING DATE: 2000-10-19  
 / PRIOR APPLICATION NUMBER: US09/727,344  
 / PRIOR FILING DATE: 2000-11-29  
 / NUMBER OF SEQ ID NOS: 7144  
 / SOFTWARE: pc\_flt\_genes\_b Versions 1.0  
 / SEQ ID NO 2440  
 / LENGTH: 1589  
 / TYPE: PRT  
 / ORGANISM: Homo sapiens  
 / US-09-488-725A-2440  
 Alignment Scores:  
 Pred. No.: 35.9 Length: 1588  
 Score: 442.00 Matches: 217  
 Percent Similarity: 17.57% Conservative: 59  
 Best Local Similarity: 13.81% Mismatches: 145  
 Query Match: 14.77% Indels: 1150  
 DB: 1 Gaps: 37  
 us-09-896-522-1 (1-1624) x US-09-488-725A-2440 (1-1588)  
 QY 1623 TGGCCCCGACAGCTGGGTGTGATGCTGGTCTCCAGGGCATTCCGCTTCTC 1564  
 ||||| ||||| ||||| |||||  
 Db 358 TTPArghrThrglu-TTPhrghlucYsArghValAspPro-----LeuLeuSerg 374  
 ||||| ||||| ||||| |||||  
 QY 1563 TGGCTTTAAGGACAGGAGGAGAAACATCCCTCACTGGCTCCCATTCGGTGA 1504  
 ||||| ||||| ||||| |||||  
 Db 374 lnglnAspYs--ArgArghValAsnGlnThralauCysgly----- 387  
 ||||| ||||| ||||| |||||  
 QY 1503 GGGCAGCTGAGTGCATGCAACTGGGTCAATGAATTGATTGTAGGCCACACAGCC 1444  
 ||||| ||||| ||||| |||||  
 Db 388 -----GlyGlyIleGlnThr-----ArgIluValTyr----- 396  
 ||||| ||||| ||||| |||||  
 QY 1443 TTGTGTTATGAAACAGAAACAGAAAC-----ATAGAGACATGTAACTGA 1396  
 ||||| ||||| ||||| |||||  
 Db 397 -CysVal-----GlnAlaAsnGluAsnLeuLeuSergGlnLeuSergThr-----HisTys 412  
 ||||| ||||| ||||| |||||  
 QY 1395 AAAAAGAAAGTACT----- 1381  
 ||||| ||||| ||||| |||||  
 Db 413 AsnTysGlnAlaSerYsProMetAspLeuLeuCysThrGlyProIleProAsnThr 432  
 ||||| ||||| ||||| |||||  
 QY 1381 ----- 1381

Db 433 ThrGlnLeuCysHisIleProCysProThrGluCysGluValSerProTTPserAlaTyr 452  
 ||||| ||||| ||||| |||||  
 QY 1380 -----TGTTCACAAAACTTTGAAGTTATGTGTGTGTGTGTGAAGACACAGTCACT 1327  
 ||||| ||||| ||||| |||||  
 Db 453 GlyProCys-----ThyTrgIluAsnYs-----Asn--AspGlnGln 464  
 ||||| ||||| ||||| |||||  
 QY 1326 GAAAAAAATCTCTCCCACTGTGGGTTCACTGTCAAAA----- 1287  
 ||||| ||||| ||||| |||||  
 Db 465 GlyValYs-----GlyPheValYsValGlyValArgIleThrAsnGluP 480  
 ||||| ||||| ||||| |||||  
 QY 1286 -ACATCAGGCGACAGCTGTAGGCTGTCTCTCAATTCCCAATATGTGCTTACA 1228  
 ||||| ||||| ||||| |||||  
 Db 480 oThrGlyGlySerglyValThr-----GlyAsnCysProHis- 492  
 ||||| ||||| ||||| |||||  
 QY 1227 TTCTTCACAGAACCTTCCCAAGGCTTCTGCACTTCTGGCACTT----- 1182  
 ||||| ||||| ||||| |||||  
 Db 493 -----LeuLeuGluAla-----IleProCysGluGluProAlaCysTyrAspTrpYsAl 509  
 ||||| ||||| ||||| |||||  
 QY 1181 -----CTCAGTACCTAGAGGATCTTTAAACCGCAACAGAG----- 1146  
 ||||| ||||| ||||| |||||  
 Db 509 aValArgLeuGlyAspCysGluProAsp--AsnGlyValGlyCysGlyProGlyThrG 528  
 ||||| ||||| ||||| |||||  
 QY 1146 ----- 1146  
 Db 528 nValGlnGluValValCysIleAsnSerAspGlyGluGluValAspArgGlnLeuCysAr 548  
 ||||| ||||| ||||| |||||  
 QY 1145 -----CTTAG----- 1140  
 ||||| ||||| ||||| |||||  
 Db 548 gaPalaIlePheProIleProValAlaCysAspAlaProCysProLysAspCysValle 568  
 ||||| ||||| ||||| |||||  
 QY 1139 -----TGGCTGAAAACCTCAGAGAGCCGT----- 1114  
 ||||| ||||| ||||| |||||  
 Db 568 uSerThrTTPserThrTTPserSergYsSerHisIthr--CysSerglyValThrGlu 587  
 ||||| ||||| ||||| |||||  
 QY 1113 -----CAG 1111  
 ||||| ||||| ||||| |||||  
 Db 588 GlyValGlnIleArgAlaArgSerIleLeuAlaTyrAlaGlyGluGluGlyIleArg 607  
 ||||| ||||| ||||| |||||  
 QY 1110 TGTCCAGCAGATGTGATCTG----- 1090  
 ||||| ||||| ||||| |||||  
 Db 608 CysProAsnSerSergIleLeuGlnGluValArgSergCysAsnGluHisProCysThrVal 627  
 ||||| ||||| ||||| |||||  
 QY 1089 -----AGTACACATCACTGATTTCCACT- 1067  
 ||||| ||||| ||||| |||||  
 Db 628 TyrHisTrpGlnThrGlyProTrpGlyGlnCysIleGluAspThrSer--ValSerSerp 647  
 ||||| ||||| ||||| |||||  
 QY 1067 ----- 1067  
 Db 647 heAsnThrThrThrThrTPAsnGlyGluAlaSerCysSergValGlyMetGlnThrArg 667  
 ||||| ||||| ||||| |||||  
 QY 1067 ----- 1067  
 Db 667 yeValIleCysValArgValAsnValGlyGlnValGlyProLysCysProGluSert 687  
 ||||| ||||| ||||| |||||  
 QY 1066 -----CCTGAGTACGAGAGGCT----- 1049  
 ||||| ||||| ||||| |||||  
 Db 687 euArgProGluThrValArgProCysLeuLeuProCysLysLysAspCysIleValThrP 707  
 ||||| ||||| ||||| |||||  
 QY 1049 ----- 1049  
 Db 707 roTyrSerAspTrpThrSerCysProSerSergCysLysGluGlyAspSerSerIleArg 727  
 ||||| ||||| ||||| |||||  
 QY 1049 ----- 1049  
 Db 727 yeGlnSerArgHisArgValIleIleGlnLeuProAlaAsnGlyArgAspCysThra 747  
 ||||| ||||| ||||| |||||  
 QY 1049 ----- 1049  
 Db 747 sPProLeuTyrGluGluValaCysGluAlaProGlnAlaCysGlnSerTyrArgTrp 767  
 ||||| ||||| ||||| |||||  
 QY 1048 -----CGCTGCTAACACTC--CCCTGGGGGT-----GGCGC 1021  
 ||||| ||||| ||||| |||||  
 Db 767 yeThrHisIserTrpArgArgCys--GlnLeuValProTTPserValGlnGlnAspSerTr 786  
 ||||| ||||| ||||| |||||

```

QY 1020 GAGAGGAGGAGTGGGTGGGTGGGCTCC-----CAGGCTCAGTCCCTGAACAC 967
Db 786 oGtAlaGlInGlucYsGly-----ProGlYArgInAlaArgAlaIle-----Th 802
QY 966 ATGCCGG-----GCGGAGAGA 952
Db 802 rCySbArgLysGlnAspGlyGlyGlnAlaGlyIleHLeGluCyLeuGlnInTrYrAlaGlyPr 822
QY 951 CTTGGCTTGAAGGCTCGGAGAGCCCTCAGTGGGGCTGTCTGGACTCCAAATGT----- 897
Db 822 oValPro-----AlaLeuThrGln-----AlaCySgInIlePro--CySgInAs 836
QY 896 -GACCGTTTGCAGAGGTGACAGATCCAGAGGTGGTGGCTGGCTCAGAAAAGTCCGCTT 838
Db 836 pAsp-----CySgIn-----LeuThrSerTrpSer-----LysPheSerSerC 849
QY 837 GTAGCTCC----- 830
Db 849 yAsnGlnYAspCySgLYAlaValArgThrArgLysArgThrLeuValGlyLysSerLysL 869
QY 830 ----- 830
Db 869 ySlySlySlyCySlyAsnSerHLeuTyrrProLeuIleGluThrGlnTrpCySerProC 889
QY 829 -----GCCCATTTGGAGCC----- 818
Db 889 ySAspLySTyrAsnAlaGlnProValGlyAsnTrpSerAspCySIIleLeuProGluGlyL 909
QY 817 -----CTCTCTCGGT----- 809
Db 909 ySValGluValLeuLeuGlyMetLysValGlnGlyAspIleLysGluCySgLYGlnGlyT 929
QY 809 ----- 809
Db 929 yTrArgTrGlnAlaMetAlaCySTyrYAspGlnAsnGlyArgLeuValGluThrSerArgC 949
QY 808 -----GCCATTTTGAGATGTCAACATTCAGAAATGTC 778
Db 949 yAsnSerHLeGlyTyrrIleGluGluAlaCySIIleIleProCyS--Pro--SerAspCyS 968
QY 777 CT-----GGATGTCTG 766
Db 968 ySLeuSerGluTrpSerAsnTrpSerArgCySerLysSerCySgLYSerGlyValLysV 988
QY 765 CACGATCAGGTTATGC-----CAACGATAT-----TGTCCACTCC 730
Db 988 alArgSerLys--TrpLeuArgGluLysProTyrrAsnGlyGlyArgProCySerProLysL 1007
QY 729 TCGTGGGATGATCAGATCGGATCTTTGTGGCAGGAGAACTCTCGAAGGCCGG 670
Db 1007 eu-----AspHsVal-----AsnGlnAlaGlnValTyrrGlu----- 1017
QY 669 CTTTCAGAGAGGTGGTGTACTGTCGTCAGAAATCTGCTCCAGTCCCTCGGCGCACGTC 610
Db 1018 -----ValAlaProCySIIleSerAspCySAsnGlnInTrpLeu--TrpValThrGlnP 1034
QY 609 CC-----GGAACACTCTTCG 595
Db 1034 rOTrPserIleCySlyValAlaThrPheValaAsnMetArgGluAsnCySgLYGlnGlyValG 1054
QY 594 AGACAGCCTGACGTCGAGTGGGTGTCCAGAGAGGCGGAGTGAACATGTCC----- 539
Db 1054 InTrp-----ArgLysValArgCySmetGlnAsnThrAlaAspGly-----ProSerG 1070
QY 538 -----GGATCTCTCGCTGTA 523
Db 1070 lWhIleValGluAspTrpLeuCySAspProGluGluMetProLeuGlySerArgValCyS 1090
QY 522 GAACACCAAGATGCCCTCAA----- 503
Db 1090 ySLeuPro--CySbProGluAspCySValIleSerGluTrpGlyProTrpThrGlnCySv 1109

```

```

QY 502 -----ACGAAACAC 493
Db 1109 alLeuProCySAsnGlnInsSerPheArgGlnArgSerAlaAspProIleArgGlnProA 1129
QY 492 GTCCGCAAGGTGACA----- 479
Db 1129 lAspGluGlyArgSerCySProAsnAlaValGluLysGluProCySAsnLeuAsnLysA 1149
QY 479 ----- 479
Db 1149 sMcYsTyrrHsTyrrYAspTrpAsnValThrAspTrpSerThrCySgInLeuSerGluLysA 1169
QY 479 ----- 479
Db 1169 lAvalCySgLYAsnGlyIleLysTyrrArgMetLeuAspCySValArgSerAspGlyLys 1189
QY 479 ----- 479
Db 1189 eValAspLeuTyrrCySgLYAlaLeuGlyLeuGlyLysAsnTrpGlnMetAsnThs 1209
QY 478 -----CCACCGTGGCTCTCG 463
Db 1209 eTySmetValGluCySProValAsnCySgInLeuSerAspTrpSerProTrpSer----- 1227
QY 462 TAACTTGAAGTGTGACAA-----AATCATAGTCCG 430
Db 1228 -----GluCyS--SerGlnThrCySgLYLeuThrGlyLysMetIleArgArgArgThrV 1245
QY 429 CACCTCACCCTTT----- 416
Db 1245 alThrGlnProPheGlnGlyAspGlyArgProCySbProSerLeuMetAspGlnSerLysP 1265
QY 415 --TGCCCT-----CCACGATGTTCTTCAGA----- 393
Db 1265 rOCySProValLysPro--CyS--TyrrArgTrpGlnInTyrrGlyGlnTrpSerProCyS 1283
QY 392 -----GTCCCTGTCAATCAATC 376
Db 1283 nValGlnGluAlaGlnCySgLYGlnGlyThrArgThrArgAsnIleSerCySValIse 1303
QY 375 AATTATCAAGGCAATCTGAGTGTCAAAATTTGAC----- 342
Db 1303 rAspGlySerAlaAspAspHeserLysValAlaAspGluGluPheCySAlaAspIleG 1323
QY 341 -----TGTCTTTCAAGCCTT 325
Db 1323 uLeuIleIleAspGlyAsnLysAsnMetValLeuGluGluSerCyS--SerGlnProC 1342
QY 324 GGCCTTGTCTGCTCCGCTCAGAACCTTGT----- 296
Db 1342 ySPro-----GlyAspCySlyrLeuLysAspTrpSerSerTrpSerLeuC 1357
QY 295 -----A 295
Db 1357 ySgInLeuThrCySValAsnGlyGluAspLeuGlyPheGlyGlyIleGlnValArgSerA 1377
QY 294 GAACCTGTCTCGGCTCAGATGACACACTTCGCTGGCGCTGTTCACACTCTGTCTGTC 235
Db 1377 rG--ProValIleIleGlnGlu-----LeuGluAsnGlnHsIleu--CySPr 1391
QY 234 CAGCACTCATGATCTTTCACACACGCTG----- 203
Db 1391 o-----GluGlnMetLeu--GluThrLysSerCySTyrAspGlyGlnCySTyrGluTyrrL 1409
QY 202 -----ACTTCCCGCTGGCAG-----TGCCTCCGCTCA----- 176
Db 1409 ySTrMetAlaSerAlaTrpLysGlySerSerArgThrValTrpCySgInArgSerAspG 1429
QY 175 -----CCCTATCAGAAAGGCGCTG 154
Db 1429 lyIleAsnValThrGlyGlyCySLeuValMetSerGlnProAspAlaAspArgSer----- 1447
QY 153 GTGCGAGCGGTGCGCTCCGCGCG----- 131

```



```

QY 571 ----- 571
Db 356 ArgGluValTyrCysValGlnAlaSerGlnLeuLeuSerGlnLeuSerThrHisLys 375
QY 571 ----- 571
Db 376 AsnLysGlnAlaSerLysProMetAspLeuLysLeuCysThrGlyProIleProAsnThr 395
QY 572 ----- 572
Db 396 ThrGlnLeuCysHisIleProCysProThrGlnCysGlnValSerProTyrPse 413
QY 614 TGGG----- 617
Db 413 rAlaTyrGlyProCysThrTyrGlnAsnCysAsnAspGlnGlnGlyLysLysGlyPheLys 433
QY 618 ----- 649
Db 433 sLeuArgLysAspArgGlyLeuThrAsnGluProThrGlyGlySerGlyValThrGlnAsnCys 453
QY 650 AGTACACCACTTGTGTAAGCC----- 671
Db 453 s----ProHisLeuLeuGlnAlaIleProCysGlnGluProAlaCysAspTyrAspTyrLysAl 472
QY 671 ----- 671
Db 472 aValArgLeuGlyAspCysGluProAspAsnGlyLysGlnCysGlyProGlyThrGlnVal 492
QY 672 ----- 703
Db 492 lGlnGluValValCysIleAsnSerAspGlyGlnGluValAspArgGly 508
QY 704 AGTATGCCGA----- 725
Db 508 nLeuCysArgAspAlaIlePheProIleProValAlaCysAspAlaProCysProLysAs 528
QY 726 ----- 772
Db 528 pCysValLeuSerThrTrpSerThrTrpSerSerSerSerSerSerSerSerSerSerSer 542
QY 773 T----- 773
Db 542 sThrCysSerGlyLysThrThrGlnGlyLysGlnIleArgAlaArgSerIleLeuAlaTyr 562
QY 773 ----- 773
Db 562 rAlaGlyGlnGlnGlyLysIleArgCysProAsnSerSerAlaLeuGlnGluValArgSe 582
QY 773 ----- 773
Db 582 rCysAsnGlnHisProCysThrValTyrHisTrpGlnThrGlyProTyrGlnCysIle 602
QY 773 ----- 773
Db 602 eGluAspThrSerValSerSerPheAsnThrThrThrTrpAsnGlnGluAlaSerCys 622
QY 773 ----- 773
Db 622 sSerValGlyMetGlnThrArgLysValIleCysValArgValAsnValGlyGlnValGly 642
QY 773 ----- 773
Db 642 yProLysLysCysProGlnSerLeuArgProGlnThrValArgProCysLeuLeuProCys 662
QY 774 ----- 799
Db 662 sLysLysAspCysIleValThrProTyrSerAspTrpThrSerCysProSerSer 680
QY 799 ----- 799
Db 681 CysLysGlnGlyAspSerSerIleArgLysGlnSerArgHisArgValIleIleGlnLeu 700
QY 800 ---GCAATGCACCGAGAGGCTCCATGGCGG----- 831

```

```

Db 701 ProAlaAsnGly-----GlyArgAspCysThrAspProLeuTyrGlnG 715
QY 832 ----- 859
Db 715 lndValAcysGlnAlaProGlnAlaCysGlnSerTyrArgAGCTACAAAGGAGACTTTTCGAGCCAG 728
QY 860 GGGACCACTGGAGATGCTGACTCTGG-----CAACGGTACATTTGAGTGCACA 910
Db 729 ----- 963
QY 911 GCACAGACCCCACTGAGGGGCTGCCAGCCTTCAGGCAAGTCTCCCGCCGG----- 963
Db 745 nGlnAspSerProGlyAlaGlnGluGlyCysGlyProGlyArgGlnAlaA 762
QY 964 ----- 972
Db 762 rGAlaIleThrCysArgLysGlnAspGlyGlyGlnAlaGlyIleHisGlnCysLeuGlnT 782
QY 973 ---TCAGGAGCTGAGCCT----- 987
Db 782 yrlaGlyProValProAlaLeuThrGlnAlaCysGlnIleProCysGlnAspAspCysG 802
QY 988 ----- 993
Db 802 lndThrSerTrpSerLysPheSerSerCysAsnGlyAspCysGlyAlaValArgThra 822
QY 994 ----- 1003
Db 822 rglYsArgThrLeuValGlyLysSerLysLysLysGlnLysCysLysAsnSerHisLeuT 842
QY 1004 ACCCACTGCTT-----CCTCTCGGC- 1023
Db 842 yrrProLeuIleGlnThrGlnTyrCysProCysAspLysTyrAsnAlaGlnProValGlyA 862
QY 1024 ----- 1066
Db 862 snTrpSerAspCysIleLeuProGlnGlyLysValGluValLeu-----Gly 878
QY 1067 AGTGGAACTCAG----- 1079
Db 878 yMetLysValGlnGlyAspIleLysGlnCysGlyGlnGlyTyrArgTyrGlnAlaMetAl 898
QY 1079 ----- 1079
Db 898 aCysTyrAspGlnAsnGlyArgLeuValGlnThrSerArgCysAsnSerHisGlyTyrI 918
QY 1079 ----- 1079
Db 918 eGlnGluAlaCysIleIleProCysProSerAspCysLysLeuSerGlnTrpSerAsnTr 938
QY 1079 ----- 1079
Db 938 pSerArgCysSerLysSerCysGlySerGlyValLysValArgSerLysTrpLeuArgGly 958
QY 1079 ----- 1079
Db 958 ulYsProTyrAsnGlnGlyArgProCysProLysLeuAspHisValAsnGlnAlaGlnVal 978
QY 1080 ----- 1114
Db 978 lTyrGluValValProCysHisSerAspCysAsnGlnTyrLeuTyrValThrGly 996
QY 1115 C----- 1115
Db 996 uProTrpSerIleCysLysValThrPheValAsnMetArgGlnAsnCysGlyGlnGlyVal 1016
QY 1115 ----- 1115
Db 1016 lGlnThrArgLysValArgCysMetGlnAsnThrAlaAspGlyProSerGlnHisValGly 1036
QY 1115 ----- 1115

```

```

Db      1036 uaSerTyrLeuCyaspProGluGluMetProLeuGlySerArgValCysIleuProCy 1056
Qy      1115 -----
Db      1056 sProGluuAPCyValIleSerGluTyrGlyProTyrThrGlnCyValIleuProCyAs 1076
Qy      1116 -----AGGCGTTCTTGAGGTTTTCAGCCACTTACAGCTCGGCGGTTT 1159
Db      1076 ngInSerSerPheArgGlnArgSer-----AlaAspProIleArgGlnProIle 1092
Qy      1160 AAGATCCCTAGTCACTGAGAAATGCCACAGAAATGTCAGAGAGCTGGAGGCTTCT 1219
Db      1093 --AspGluGlyArgSerCyPProAsnAlaValGlu-----LysGluPro-----C 1107
Qy      1220 GT-----
Db      1107 ysaAnLeuAnlyAsnCyTyrHisTyrAspTyrAsnValThrAspTyrSerThrCySg 1127
Qy      1221 -----
Db      1127 InLeuSerGluValAlaValCyGlyAsnGlyIleLysThrArgMetLeuAspCyValA 1147
Qy      1222 -----GAGGAATGTGAGGACATTTATTTGGGAAATTGAG 1255
Db      1147 rgsSerAspGlyLysSerValAspLeuLysTyrCySgluAla-----LeuGly----- 1162
Qy      1256 GAGACAGCCTAGACACTGGCTGG-----
Db      1163 -----LeuGluLysAsnTyrGlnMetAsnThrSerCysMetValGluCySProValA 1180
Qy      1278 -----
Db      1180 snCySgluLeuSerAspTyrPsrProTyrPsrGluCySserGlnThrCySgluLeuThrG 1200
Qy      1278 -----
Db      1278 -----
Qy      1279 -----CCTGATGTTT----- 1289
Db      1200 lYlYsMetIleArgArgThrValThrGlnProPheGlnGlyAspGlyArgProCyS 1220
Qy      1279 ----- 1289
Db      1220 roSerLeuMetAspGlnSerLysProCySProValLysPro--CysTyrArgTyrGlnTyr 1239
Qy      1289 ----- 1289
Db      1289 -----
Qy      1290 -----GTTGAC-- 1295
Db      1299 gAnIleSerCyValValSerAspGlySerAlaAspAspPheSerLysValValAspG 1279
Qy      1295 ----- 1295
Db      1279 uGluPheCyAlaAspIleGluLeuIleIleAspGlyAsnLysAsnMetValLeuGluG 1299
Qy      1296 -----AGTGAACCCAGCAGTGGAGAGAGATTTCAGTCGATTCGTTTACACA 1348
Db      1299 uSerCySserGlnProCySProGlyAspCyStryLeuLysAsp--TrpSerSerTyrPsr 1318
Qy      1349 CTCACACACATACT----- 1363
Db      1319 LeuCySgluLeuThrCySValAsnGlyLysAspLeuGlyPheGlyGlyIleGlnValArg 1338
Qy      1364 -----CAAAAGTTTGT--GACACAGTACTT 1387
Db      1339 SerArgProValIleIleGlnGluLeuGluAsnGlnHisLeuCySProGluGlnMetLeu 1358
Qy      1388 TCCTTTTACATGATGTCCTCATGTTTCTGTTTCTGTTTCTATTAACACAGGCT 1447
Db      1359 GluThrLysSerCyStryAspGlyGlnCyStryGluLys--TrpMetAlaSerAla 1378
Qy      1448 GGTGTGGCCTTACAAACCTAATTCATGACCCAGTGGTTTGACGCCGCT-----GG 1501
Db      1378 rp-----LysGlySerSerArgThrValTyr--Cys-----GlnArgSerAspG 1392

```

```

Qy      1502 CCTACAGGATATGGGAGACCTAGAGATGTTT----- 1537
Db      1392 yIleAsn-----ValThrGlyGlyCySLeuValMetSerGlnProAspAlaAsp 1408
Qy      1538 -----CCGCCCTTGCTTGTGCC----- 1554
Db      1409 ArgSerCyAsnProPro-----CysSerGlnProHisSerTyrCySserGluThrLys 1427
Qy      1554 ----- 1554
Db      1427 hrCyHisCySgluGluGlyTyrThrGluValMetSerSerAsnSerThrLeuGluGlnC 1447
Qy      1555 -----TTAAGCAGAGAGAGCGAGCGGATGCCCTG 1585
Db      1447 ystThrLeuIleProValValIleuProThrMetGluAspLysArgGly-AspVal- 1465
Qy      1586 GAAG-----CACCCAGCATCACACCGAGCTTGTGGCGGCGCA 1623
Db      1466 -LysThrSerArgAlaValHisPro-----ThrGlnProSerSerAsnPro 1480

RESULT 38
US-09-488-725A-5941
; Sequence 5941, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784PLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc FL_genes_b Versions 1.0
; SEQ ID NO 5941
; LENGTH: 2045
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5941

Alignment Scores:
Pred. No.: 71.7 Length: 2044
Score: 441.90 Matches: 214
Percent Similarity: 17.68% Conservative: 44
Best Local Similarity: 14.67% Mismatches: 142
Query Match: 14.56% Indels: 1060
DB: 1 Gaps: 33

us-09-896-522-1 (1-1624) x US-09-488-725A-5941 (1-2044)
Qy      4 GGGTGGCCTCCGACCTCGGCGTGGCGGG----- 33
Db      622 GlyLeuProProThrIleAlaAsnGlyAspPheIleSerThrAsnArgGluAsnPheHis 641
Qy      34 -----CGCGCGGCGCGCGGGAAGGGCGGCGCC----- 62
Db      642 TyrGlySerValValThrTyrArgCySAsnProGlySerGly--GlyArgLysValPheG 661
Qy      63 -----GGGAGCCCG----- 71

```

```

Db      661  |||||
        IuLeuValGIyGIuProSerIleTyrCysThrSerAsnAspGlnValGIyIleTrps 681
Qy      71  -----
        71  -----
Db      681  erGIyProAlaProGlnCysIleIleProAsnLysCysThrProProAsnValGIuAsnG 701
Qy      71  -----
        71  -----
Db      701  IyIleLeuValSerAspAsnArgSerLeuPheSerLeuAsnGlnValValGIuPheArgC 721
Qy      72  -----
        72  -----
Db      721  ySGInProGIyPheValMetLysGIy-----ProArgArgValLysCysGlnAlaIle 738
Qy      95  -----
        95  -----
Db      738  uAsnLysTrp-----GluProGIuLeuProSerCysSerArg 750
Qy      148  CCGACACGCGCGCCCTTCCTGAT-----AGGGGTGAGCGCGGCACTGCCAGCGGAG 201
Qy      751  ValCysGlnProPro--ProAspValLeuHisAlaGluArg-----ThrGlnArgAspL 768
Qy      202  TCGACCGGTGTGAGAGATCA-----TGAGATTGCTGGACAGAC 243
Db      768  ySAspAsnPhe-----SerProGIyGlnGlnValPheTyrSerCys-----GluP 783
Qy      244  GAGGT-----GGAACAGCGGAGC-----GGAAGGTGTC 273
Db      783  roGIyTyrAspLeuArgGIyAlaIala--SerMetArgCysThrProGlnGIyAspTrpSe 802
Qy      274  ATCCTGAGCCA-----GACACG 291
Db      802  r-----ProAlaAlaProThrCysGlnValLysSerCysAspAspPheMetGIyGlnL 820
Qy      292  TTCTACAGGT----- 302
Db      820  euLeuAsnGIyArgValLeuPheProValAsnLeuGlnLeuGIyAlaIalValAspPheV 840
Qy      302  ----- 302
Db      840  alCysAspGlnGIyPheGlnLeuLysGIySerSerAlaSerTyrCysValLeuAlaGlyM 860
Qy      302  ----- 302
Db      860  etGIuSerLeuTyrAsnSerSerValProValCysGlnGlnIlePheCysProSerProp 880
Qy      303  -----
        303  -----
Db      880  roValIleProAsnGIyArgHisThrGIyLysProLeuGlnValPheProheGIyLysA 900
Qy      340  CAGTACAAATTT-----GACCATCCAGAT-----GCCTTGATATAG- 376
Db      900  laVal--AsnTyrThrCysAspProHisProAspArgGIyThrSerPheAsp--LeuIleGI 919
Qy      377  -----
        377  -----
Db      919  yGIuSerThrIleArgCysThr--SerAspProGlnGIyAsnGIyVal-----TrpSe 936
Qy      425  -----
        425  -----
Db      936  rSerProAlaProArgCysGIy-----IleLeuGIyHisCysGlnAla--Pro--AspH 953
Qy      472  ACGGTGCTTAC----- 483
Db      953  is--PheLeuPheAlaIalLeuLysThrGlnThrAsnAlaSerAspPheProIleGIyThr 972
Qy      483  ----- 483
Db      973  SerLeuLysTyrGIuLysArgProGIuTyrTyrGIyArgProPheSerIleThrCysLeu 992
Qy      484  -----
        484  -----

```

```

Db      993  AspAsnLeuValTrpSerSerProLysAspVal-----CysLysArgLysSer--CysLy 1010
Qy      523  TACAGCCAGAGATCCG----- 539
Db      1010  sThr--ProProAspProValAlaAsnGIyMetValHisValIleThrAspIleGlnValGIyS 1030
Qy      540  -----
        540  -----
Db      1030  erArgIleAsnTyrSerCysThrThrGlyHis-----ArgLeuIle--GlyHis- 1045
Qy      574  GACTCCGACGTCAAGGCTGTCTCGAAGATTCTCCGGAGACGTGCGCGAGAGAGACCTG 633
Db      1046  -----
        1046  -----
Qy      634  GAGCAGATTCTGACGACGTACACCTTGTGTGAAGCGGCGCTTCGAGAGATTCTGCTG 693
Db      1059  pSer-----ThrLysProPro-----IleCys-- 1066
Qy      694  CCGACAAAGAGTATGCCGATGTGATCATCCACGAGAGTGGACAATATGTTGCCATC 753
Db      1067  -----
        1067  -----
Qy      754  AACCTGATCGTGAGACATCCAGACATTCTGAATGTGACATCTGC----- 801
Db      1075  oThr-----IleAlaAsnGIyAspPheIleSerThrAsnArg 1087
Qy      802  ---AAATGCCACCGAGA-----GGGTCCATGCGCGG 831
Db      1088  GIuAsnPheHisTyrGIySerValValThrTyrArgCysAsnLeuGIySerArgGIyArg 1107
Qy      832  AGCTACAAAGCGACCTTTCTGAGCCA----- 858
Db      1108  LyValPheGlnLeuValGIyGIuProSerIleTyrCysThrSerAsnAspGlnVal 1127
Qy      859  -----
        859  -----
Db      1128  GIyIleTrpSerGIyProAlaProGlnCysIleIleProAsnLysCysThrProProAsn 1147
Qy      871  -----
        871  -----
Db      1148  ValGIuAsnGIyIleLeuValSerAspAsnArgSerLeuPheSerLeuAsnGlnValVal 1167
Qy      897  ----- 897
Db      1168  GIuPheArgCysGlnProGIyPheValMetLysGIyProArgArgValLysCysGlnAla 1187
Qy      898  -----
        898  -----
Db      1188  LeuAsnLysTrpGIuProGIuLeuProSerCysSerArgVal-----Cys--Gln 1203
Qy      940  CTTGAGGCGAGTCTCCCGCGCGCATGTGTTCACAGGACTGAGCTTGGGAGCGCCAC 999
Db      1204  Pro-----ProPro--GluIleLeuHisGIyGluHis-----ThrProSe 1216
Qy      1000  CCAC----- 1003
Db      1216  rHisGlnAspAsnPheSerProGIyGlnGlnValPheTyrSerCysGIuProGIyTyrAs 1236
Qy      1004  -----
        1004  -----
Db      1236  pLeuArgGIyAlaAlaSerLeuHisCys-----ThrProGlnGIyAspTrpSer 1252
Qy      1045  AGCGAGGCTTCTCTCACTCAGAGATGAGAACTCAGATGTGTCACTCAGACTCAACTGTCT 1104
Db      1253  ProGlnAla--Pro-----ArgCysAlaValLys-----SerCysA 1264
Qy      1105  GGACACTGACAGAGGCTTCTGAGGTTTCAGCCACTAGAGCTGTGCGGTTTAAGAT 1164
Db      1264  sPAsp-----Phe-----LeuGIyGlnLeu----- 1270
Qy      1165  CCTCTAGTCACTGAGAAATGCCACAGAAATGTGACAGAAAGCTGGAGGC----- 1215
Db      1271  ProHisGIyArgValLeuPheProLeuAsnLeuGln-----LeuGIyAlaLysValSer 1288

```



```

QY 1216 ---TTGTGAGGA----- 1227
Db 1289 PheValCysaspGluGlyPheArgLeuGlySerSerValSerHisCysValLeuVal 1308
QY 1228 -----TGAGGACATATT----- 1243
Db 1309 GlyMetArgSerLeuTrpAsnAsnSerValProValCysGlu-HisIlePheCysProAs 1328
QY 1244 -----GGGAAATTGAGGAGAC 1260
Db 1328 nProProAlaIleLeuAsnGlyArgHisThrGlyThrProSerGlyAspIle----- 1345
QY 1261 AGCCT-----AGACATGGCTGCTGATGTTTG 1290
Db 1346 --ProTyrGlyLysGluIleSerTyrThrCysAspProHis-----ProAspArgGly 1362
QY 1291 TTGACAGTGAACCCACAGTGGAGAGATTTTTC----- 1325
Db 1363 MetThrPheAsn--LeuIleGlyIleSerThrIleArgCysThrSerAspProHisGlyA 1382
QY 1326 -----CAGTCTGATCTGTTCTTACACACTCACACACAT 1359
Db 1382 snGlyValTrpSerSerProAlaProArgCysGluLeuSerValArgAlaGlyHisCys- 1401
QY 1360 AACTCAAAAGTTTGTGACAGACTTCTCTTTTACATGTTACATGTCCTC----- 1413
Db 1402 -----LysThrProGluGln-----PheProPheAlaSerProThrIleProIleAsnA 1418
QY 1413 ----- 1413
Db 1418 spbheGluPheProValGlyThrSerLeuAsnTyrGluCysArgProGlyTyrPheGlyL 1438
QY 1414 --ATGTTTCTGTTTCTGTTTCAATAACACAGGCTGCTGTG----- 1455
Db 1438 yMetPheSerIleSerCysLeu-----GluAsnLeuValTrpSerSerValGluAspA 1456
QY 1456 -----CCTACAAAC----- 1464
Db 1456 snCysArgAlaGlySerCysGlyProProProGluProPheAsnGlyMetValHisIleA 1476
QY 1464 ----- 1464
Db 1476 snThrAspThrGlnPheGlySerThrValAsnTyrSerCysAsnGluGlyPheArgLeuI 1496
QY 1464 ----- 1464
Db 1496 IeGlySerProSerThrThrCysLeuValSerGlyAsnAsnValThrTrpAspLysA 1516
QY 1465 -----CTAATTTCATGACCCAGTGTTCAGTCCAGGCTGCGCTAC- 1507
Db 1516 IabProIleCysGluIleIleSer-----CysGluProPro--ProThrIle 1530
QY 1507 ----- 1507
Db 1531 SerAsnGlyAspPheTyrSerAsnAsnArgThrSerPheHisAsnGlyThrValValThr 1550
QY 1507 ----- 1507
Db 1551 TyrGlnCysHisThrGlyProAspGlyGluGlnLeuPheGluLeuValGlyGluArgSer 1570
QY 1508 -----CGGATATGGGGAGCCACTGAGGATGTTT 1537
Db 1571 IleTyrCysThrSerLysAspAspGlnValGlyValTrpSerSer----- 1585
QY 1538 CCCCCTTGCTTGCTT----- 1556
Db 1586 --ProProProArgCysIleSerThrAsnLysCysThrAlaProGluValGluAsnAlaI 1605
QY 1556 ----- 1556
Db 1605 earGValProGlyAsnArgSerPhePheSerLeuThrGluIleIleArgPheArgCysG 1625

```

```

QY 1557 -----AAAGCAGAGAGC 1570
Db 1625 nProGlyPheValMetValGlySerHisThrValGlnCysGlnThrAsnIlyArgTrpG 1645
QY 1571 GAGCGGAGTCCCTGGAAGCACCAGCATCACCCAGGCTTGTGCGGGCCA 1623
Db 1645 yProLysLeuPro-----HisCysSerArgValCysGlnProPro 1658

RESULT 39
US-09-488-725A-1897
; Sequence 1897, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hysag Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784PI/PT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 1897
; LENGTH: 826
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-1897

Alignment Scores:
Pred. No.: 6.73 Length: 825
Score: 439.00 Matches: 184
Percent Similarity: 18.808 Conservative: 66
Best Local Similarity: 13.838 Mismatches: 113
Query Match: 14.674 Indels: 969
DB: 1 Gaps: 19

us-09-896-522-1 (1-1624) x US-09-488-725A-1897 (1-825)
QY 1608 CTGGGTGTGATGCTGGGTGCTCTCCAGGCGATCCGCTGCTTCTGCTTAAAGCACA 1549
Db 1 MetGly-----TriLeuCysSerGly-----LeuLeu----- 9
QY 1548 AGCAAGGGGGAACAATCCCTCAGTGGCTCCCATATCCGTGTAGGACACGCTGACTG 1489
Db 10 -----PheProValSer-Cys--LeuValLeu--Leu 18
QY 1488 CAACACACTGGGTCATGAATATTAGTTTGTAGGCCACAACACAGCCTTGTTATGAACA 1429
Db 19 GlnValAlaSerSer-----Gly----- 24
QY 1428 GAAACAGAAACATGAGACATGTAAATGAAAAAGAAAGTACTTGTTCACAAAC 1369
Db 25 -----AsnMetLys-----ValLeuGlnGluProThrCysValSerAsp 37
QY 1368 TTTTGAGTTATGTGTGTAGTGTGTAAAGAACAGATCAACTGGAATAAACTCTCCCA 1309
Db 38 Tyr-----MetSerIleSerThr-----CysGluTrpLysMetAsnGlyProI 52
QY 1308 CTGTGGTTCACGTGCACAAAC-----CATC 1282

```

```

Db      52 hr-----AsnCyseSerThrGluLeuArgLeuLeuTyrGlnLeuValPheLeuLeuSerG 70
QY      1281 AGCCGACCGACAGTGTCTA-----GGCTGTCTCTCAATTCCCA 1243
Db      70  IuAaHisThrCysIleProGluAsnAsnGlyIalGlyCys-----84
QY      1242 ATATGTGCTTCACATTCCTTCACAGAA-----1216
Db      85 -----ValCys--HisLeu--LeuMetAspAspValValSerAlaAspAntYrThrLeuAsp 102
QY      1215 -----GCTTCCGAGGCTTCTGTGACATCTGTGGCATTTCTCACTGACCTAGAGGATC 1162
Db      103 LeuTrpAlaGlyGln-----GlnLeuLeuTrp-----LysGlySer 114
QY      1161 TTTAAACCGCAACAGCCTTAAGTGGCTGAAACCTCAGAGAACGCTGTGACGTGCCAGC 1102
Db      115 PheLysPro-----SerGlnHisValLys-----Pro--ArgAlaProGly 127
QY      1101 AAGTTAGTCTGAGTGCACATCTGAGTTTCACCTCCGATGAGAGAGCCTGCTGCT 1042
Db      128 AsnLeuThrVal-----HisThrAsnValSerAspThrLeuLeu 141
QY      1041 AACATCCCTCCCTGGGAGTGGCCGAG-----1018
Db      141 uThr-----TrpSerAsnProTyrProProAspAsnTyrLeuTyrAsnHisLeuThrTy 159
QY      1018 -----1018
Db      159 rAlaValAsnIleTrpSerGluAsnAspProAlaAspPheArgIleTyrAsnValThrTy 179
QY      1018 -----1018
Db      179 rLeuGluProSerLeuArgIleAlaAlaSerThrLeuLysSerGlyIleSerTyrArgAl 199
QY      1018 -----1018
Db      199 aArgValArgAlaTrpAlaGlnCysTyrAsnThrThrTrpSerGluTrpSerProSerTh 219
QY      1018 -----1018
Db      219 rLysTrpHisAsnSerTyrArgGluProPheGluGlnHisLeuLeuGluValSerVa 239
QY      1017 -----AG 1016
Db      239 lSerCysIleValIleLeuAlaValCysLeuLeuCysTyrValSerIleThrLysIleLy 259
QY      1015 GAACGACGTGGTGGTGGCGGCTGCCAGGCTCACTGCTGAACACACATGCCGGGCGG 956
Db      259 sLysGluTrp--TrpAspGlnIlePro--AsnPro-----AlaArgSer 272
QY      955 GAGACCTGCTGAGGCTC-----GGCAGCCCTCAGT 923
Db      273 -----ArgLeuValAlaIleIleIleGlnAspAlaGlnGlySer--GlnT 287
QY      922 GGGGTGCTGCTGCTGACCTCAATATGTGACCGTTGGCAGAGTCAGCATCCCGAGGTGGT 863
Db      287 rp-----GluLysArg-----SerArgGlyGlnGluPro--296
QY      862 CCCCTGCTCAGAAAAGTCCGCTTGTAGCTCCGCCCATTTG-----ACCCTC 815
Db      297 -----AlaLysCys--Pro--HisTrpLysAsnCyLeuThrLys 308
QY      814 CTCGGTGCATTTGTGAGATGTACACATTCAGAAATC-----780
Db      309 Leu--LeuPro--CysPheLeuGlnHisAsn--MetLysArgAspGluAspProHisLysVa 327
QY      779 -----TCTGAGATGTGTCAGCATCA 758
Db      327 lAlaAlaLysGluMetProPheGlnGlnLysSerGlyLysSerAlaTrp-----CysProValG 345
QY      757 GGTGATGGAACCAATATGTTCACCTCTCGTGAGATGACATCGGATCACTTCTTTG 698
Db      345 lLieserLysThrValLeu-----TrpProGluSerLieserValValArgCy 361

```

```

QY      697 TCGGACGACAGACTCTCTCGAA-----676
Db      361 s-----ValGluLeuPheGlnAlaProValGluCyGluGluGluGluValGluG 379
QY      676 -----676
Db      379 uGluLysGlySerPheCysAlaSerProGluSerSerArgAspAspPheGlnGluLysAr 399
QY      675 -----GGCCGGCTTCACGAA-----661
Db      399 gGluGlyIleValAlaArgLeuThrGlnSerLeuPheLeuAspLeuGluGluGluAs 419
QY      660 -GGTGTGTACTGCTCGTCAAGAT-----CTGCTCAGGCTCCCTCC--622
Db      419 nGlyGlyPheCysGlnGlnAspMetGlyGluSerCySLeuLeu-----ProProSerG 437
QY      621 -----TCGGCCACGCTCCG-----607
Db      437 ySerThrSerAlaHisMetProTrpAspGluPheProSerAlaGlyProLysGluAlaPr 457
QY      607 -----607
Db      457 oProTrpGlyLysGluGlnProLeuHisLeuGluProSerProProAlaSerProThrGl 477
QY      607 -----607
Db      477 nSerProAspAsnLeuThrCysThrGluThrProLeuValIleAlaGlyAsnProAlaTy 497
QY      606 -----GAAACTCTTCGAGACAGCTGACGTCGAGTGGTGTCCAGAGAGGC 557
Db      497 rArgSerPheSerAsnSerLeuSerGln-----SerProCysProArg--511
QY      556 GCAGGTGGAACATGTCCCGGATCTCCGTGCTGAGAACACAAAGATCCCTCAACAGAA 497
Db      512 -----GluLeuGlyProAspProLeuLeuAlaArgHisLeuGln-----GluValGlu 527
QY      496 CCAAGT-----CCGACGGGTAGACA 476
Db      528 ProGluMetProCysValProGlnLeuSerGluProThrThrValProGlnProGluPro 547
QY      475 CCGTGTCTCTGTAACTTGAAGTGTGTACAAATATATATGTCGACCTCCACCGTTT 416
Db      548 Glu--ThrTrp-----GluGlnIleLeuArgArgAsn-----ValL 559
QY      415 TGCCCTCAGAGATTTCTCAGAGTCCCTGCTGCAATATCATTAAGATGAT 356
Db      559 euGln--HisGlyAlaAlaAlaAlaProValSer-----AlaProThrSerGlyT 575
QY      355 GGTCAAAATTG-----345
Db      575 YrGlnGluPheValHisAlaValGluGlnGlyGlyThrGlnAlaSerAlaValValGlyL 595
QY      345 -----345
Db      595 euGlyProProGlyGluAlaGlyTyrLysAlaPheSerSerLeuLeuAlaSerSerAlav 615
QY      344 -----TACTGTCTTCA 332
Db      615 AlSerProGluLysCysGlyPheGlyAlaSerSerGlyGluGluGlyTyrLysProPheG 635
QY      331 AGGCGTGGCTTCTGTGCTGCGTCAAGACTTGTAGAACCTGTGCTGCTCAGATGA 272
Db      635 lAspLeu-----IlePro--Gly-----CysProGly-----As 644
QY      271 CCACTTTCGCTGCGCTGTTCa-----CCTGTTCTGTCCAGCA 230
Db      644 pProAlaProValPro--ValProLeuPheThrPheGlyLeuAspArgGluProProArg 663
QY      229 ACTTCATGATCTTCTCACAACAGGTGACCTTCCCGCTGGGAGTGC-----186
Db      664 SerProGlnSerSerHis-----LeuProSerSerSerProGlnHisLeuGlyLe 680

```

```

QY 185 -----CCGCGCTGACCCCTATCAGAGG 160
Db 680 uGIuProGlyGluValGluAspMetProlySProProLeu--ProGlnGluGlnAla 639
QY 159 -----CCGCTGTCGGACGCGTCGCGCTCCGCG- 132
Db 700 ThrAspProLeuValAspSerLeuGly--SerGlyIleValIySerAlaLeuThrCysH 719
QY 132 ----- 132
Db 719 sLeuCySGlyHisLeuLysGlnCysHsGlyGlnGluAspGlyGlyGlnThrProValMe 739
QY 131 -----GCGGGCTCTCGACAGTCTTCGCTCCGCCAGAGC 97
Db 739 tAlaserProCySsCyGlyCyAcScySgly--AspArgSerSerProProthr----- 756
QY 96 CATCTCGGCTCCGCTCCGCGCATGGGTCGCCGCGCGCTTCGCCGGGCGCGGC 37
Db 757 -----ThrProLeu-----Arg-----AlaProAspProSerProGly--Gly 768
QY 36 GCGGCC----- 31
Db 769 ValProLeuGluAlaSerLeuCySProAlaSerLeuAlaProSerGlyIleSerGlyLys 788
QY 30 -----GCCAGCGCGCGAGGTCGAGG 10
Db 789 SerIySerSerSerSerPheHisProAlaProGlyAspAlaGln-----SerSerSerG 807
QY 9 CGACCCCA 2
Db 807 InThrPro 809

RESULT 40
US-09-488-725A-3367
Sequence 3367, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: HySeq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/539,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pt_fl_genes_b Versions 1.0
SEQ ID NO 3367
LENGTH: 1455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-3367

Alignment Scores:
Pred. No.: 32.3 Length: 1454
Score: 438.90 Matches: 213
Percent Similarity: 20.054 Conservative: 44
Best Local Similarity: 16.618 Mismatches: 154
Query Match: 14.468 Indels: 871
DB: 1 Gaps: 24

```

```

us-09-896-522-1 (1-1624) x US-09-488-725A-3367 (1-1454)
QY 4 GAGTCGCTCCGACCTCGGCGCTGGCGCGCGCGCGCGCGGAGAGGCGCGCGC- 62
Db 431 GlyGlyProGlyGlyThrAsp--GlyAlaGlnAlaSerPro--AlaArgGlyGlyArgL 449
QY 63 -----GGGACCGCAT- 74
Db 449 yAsProSerProProGluAlaAlaSerProArgLysAlaValGlyThrProMetAlaAla 469
QY 75 -----CGCGGAGCGGAGCGCGAGTCGCTTC- 101
Db 469 erThrProArgGlySerSerGlyProAspThrHisGlnGlyThrProGluProCyLysA 489
QY 101 ----- 101
Db 489 lAtLeValTrpGlyAspGlnArgGluAspSerSerAlaTrpProGluLeuLeuValProG 509
QY 102 -----GGCGGAGGCGGAGACTGCGAGAGCGCGCGCGC- 135
Db 509 LuLyAlaAlaValAspGlyGlyArgArgProLeu--ProSerProAlaProProPro 528
QY 136 -----GAGCGCGACCGTCGCGACCGCGCGCTTCGATAGGCGGTGAGCGCGGC 186
Db 529 GlnLeuLeuGluAlaCysArgAlaProGluGluPro-----Gly-GlyGlyGly 544
QY 187 ACT----- 189
Db 545 ThrAspGlyValAlaArgThrProProValGlyMetSerGlyGlnValAlaGlySerPro 564
QY 190 -----GCCAGCGGAGATCGACCGTGT----- 213
Db 565 MetLeuProGlyAlaThrCySerProArgLeuAla-AlaGlySerArg-----CySProGlu 582
QY 214 -----GAGAAGATCATGAGTTCGTGAGACAGAAC 243
Db 583 ArgGlyLeuLeuThrThrThrValThrLeuGlnArgProValGluLeuSnglyGluAsp 602
QY 244 GAGGTG----- 249
Db 603 GluLeuValPheThrValValGluGluLeuSerLeuGlyAlaLeuAlaGlyArg 622
QY 249 ----- 249
Db 623 ProThrSerLeuAlaSerPheAspSerAspCySerLeuArgAlaLeuAlaSerGlySer 642
QY 250 -----GAACAGCGG 258
Db 643 ArgProValSerIleIleSerSerIleAsnAspGluPheAspAlaTrThrSerGln--A 662
QY 259 CAGCGGAGGTGTCAT----- 275
Db 662 laProGluGlyGlyProLeuGluGlyAlaAlaTrpAlaGlySerSerHisGlySerSer 682
QY 276 -----CCGG 279
Db 682 leSerSerTrpLeuSerGluValSerValCyThrAlaAspSerArgAspProThrPro 702
QY 280 AGCCAGACAGAGTTCTACAGGCTCTGACGCGAGACAGAGCCAGAGCCTTGAAAGGA 339
Db 702 InPro--ArgPhe--SerProAspSerLeuAla-----GlyLeuAspPro- 715
QY 340 CAGTACAAATTGACCATCCAGATCCCTTGATTAATGATTGATGCACAGACTCT- 395
Db 716 -----GlyGlyProProAlaLeuAspGlySerLeu-----GlyAspGlySers 730
QY 395 ----- 395
Db 730 erGlyPheLeuGlyProAspArgProAspSerProGlyProThrTrpGlyProCySProG 750
QY 396 -----GAGAACATCGTGGAGGCAAA 417
Db 750 LyGluValAlaAlaValAlaProSerArgProGlyArgGluProGlnAlaGly--ProSe 769

```

```

QY 418 ACGGTGAGGTCCGACCTATGATTTGTGACACACTCAAGTTACGAG----- 468
   |||||
Db 769 rArgTrpAlaSerAlaAlaGlnThrIle-----HisSerLeuProArgLysProArg 787
   |||||
QY 469 -----ACCAGGTGTCTACCTCCGCGACGT----- 494
   |||||
Db 788 ThrAlaSerAlaThrThrArgVal--glyCysAlaAlaGlnGlnSerProProGlyA 807
   |||||
QY 495 -----GGTTCTGTTGAGGCGATCTTGTTTCTACAGCCAGAGATCCGGACATGTTTC 549
   |||||
Db 807 rGlyGlyLysLeuPheGlnAsp-ProTyr-LeuLeu-----ArgValGlyGlnCysAs 823
   |||||
QY 550 CACC----- 553
   |||||
Db 823 pThrGlnAlaAlaSerAlaGlyArgAlaProSerProThrLeuGlySerProArgLeuPr 843
   |||||
QY 554 -----TCGCGCTCT----- 562
   |||||
Db 843 oGluAlaGlnValMetLeuAlaCysAlaGlnArgValAlaAspLysCysGluValAlaAl 863
   |||||
QY 562 ----- 562
   |||||
Db 863 aArgAlaAlaArgArgProGluAlaValAlaArgLysProProLeuArgArgGlyAlaThr 883
   |||||
QY 563 -----TCGTGACACCCGACCTCCGAG----- 583
   |||||
Db 883 rThrLeuGlyValThrThrProAlaValaSerTrpGlyAspAlaProThrGluValAlaAl 903
   |||||
QY 584 -----TCAGGTGTCTCGAAGAGTTCTCCG-----GAGCGTCCGCGGAGGAGG 627
   |||||
Db 903 aCysSerGlySerLeu-LysAlaSerProThrSerLysGlyLeuAlaProLysAlaG 923
   |||||
QY 628 GA-----CTGAGCGAATTCTTGACGACGATACACACCACTTCGTGAAGCG 672
   |||||
Db 923 LysPheLeuProArgProSerGlyAla-----AlaProProAla-----Pro 936
   |||||
QY 673 GCCTTCAGAGAGTTCTGCGTCCGACCAAGAGATGCGGATGATCATCCCA----- 726
   |||||
Db 937 -ProThrArgLysSerSerLeuGlnArgSerSerPro--AlaSerAlaProProHis 955
   |||||
QY 727 -----CGAGAGTGGACATATGATT 747
   |||||
Db 956 AlaValaLeuProAlaArgValaGlyAlaAlaValaValaLeuArgGlyGlnGlnPro-Arg 975
   |||||
QY 748 GCCATCAACTGATCTGTGACGACAT----- 773
   |||||
Db 975 gProSerSer--ArgAlaAspHisSerValProArgAlaThrSerSerLeuLysAlaA 994
   |||||
QY 774 -----CCAGGACATTCGAAATGATGACATCGC 801
   |||||
Db 994 rGlaSerLysValaGlnAlaAlaHisArgLeuAlaGlyHisAlaSer-----LeuG 1011
   |||||
QY 802 AAATGCGACCGAGGA-----GGTCCAAATGGCGGAGCTACACAGCGACCTTT 849
   |||||
Db 1011 LysArg-LysGlnGlyLeuAlaHisSerSerSerLysGlyArg-----GlnAla----- 1026
   |||||
QY 850 TCTGAGCCAGGAGACCACTCGGATGCTGACCTTCGCAAAAGGTGACATTTGAGTTC 909
   |||||
Db 1027 -----ProGly--ArgPro-----ProArgAlaValaProLysLeuGlyValaPr 1040
   |||||
QY 910 AGCAGCAGACCCCACTGAGGGGTCCGAGGCTCAGGCGCAGGTCTCCCGCGGACATGTG 969
   |||||
Db 1040 oProSerSerProThrHisGly--ProAla-----ProAlaCys- 1052
   |||||
QY 970 TGTTCAGGAGACTGAGCTGGGGAGCGCCACCAACCACTGCTTCCTCGGGCGACCC 1029
   |||||
Db 1053 ArgSerGlyAlaAlaValaValaGlyAlaProLysPro-----ProValaGlyGly 1070
   |||||
QY 1030 CAGGGAGAGTGTAGCAGCGAGCGCTT----- 1055
   |||||
Db 1071 LysGly-----ArgGlyLeuValaAlaGlyLysArgAlaLeuGlyProSerV 1087
   |||||

```

```

QY 1055 ----- 1055
Db 1087 aLysLeuSerThrAlaSerValThrGlyArgSerProGlyGlyProValaAlaGlyProA 1107
   |||||
QY 1056 -----CCTCACTCAGAGGTGAAACTCAGATGTGTCACTCAGACTCAACTGCTGG 1107
   |||||
Db 1107 rGlaAlaPro-----ArgAlaGlyProSer--ValGlyAlaLysAlaGly--ArgGly 1123
   |||||
QY 1108 ACACTGACAGCGCTTCTCTGAGGTTTTCAGCCACTTAGGCTCGTGGGTTTAAAGATCC 1167
   |||||
Db 1124 ThrValMetGlyThrLys-----GlnAlaLeuArg----- 1133
   |||||
QY 1168 TCTAGTCACTGAGAAATGCCACAGATGTGACGAG-----CTGGAGGCTTCTGT 1221
   |||||
Db 1134 -AlaAlaHis-SerArgValHisGlnLeuSerAlaSerGlyAlaProGlyArg----- 1150
   |||||
QY 1222 GAGGAATGTGAGGCGACATTAATTGGGAAATTGAGAGACAGCTTACACTGGCTGGCCT 1281
   |||||
Db 1151 --Gly-----GlySer-SerTrpGlySer--AlaAspSer--AspSerGlyHis-- 1164
   |||||
QY 1282 GATGTTTGTGTGACAGTGAACCAACAGTGGAGAGAGTTTTCAGTCTGATCGATCTTC 1341
   |||||
Db 1165 -----AspSerGlyValaAsnValaGlyGlnLys--ArgProPro--ThrGlyPr 1179
   |||||
QY 1342 TTACACATCACACACATTAACCAAAAGTTTGTGAAACAAGTACTTCTCTTTTTCATG 1401
   |||||
Db 1179 oAla-----LeuProSer-----ProLysSerLysV 1188
   |||||
QY 1402 TTACATGTCTCTCAT----- 1415
   |||||
Db 1188 aThrAlaProArgArgProGlnArgTyrSerSerGlyHisGlySerAspAsnSerSerV 1208
   |||||
QY 1416 -----GTTTCGTGTTTCTGTTTCATA 1437
   |||||
Db 1208 aLeuSerGlyGlnLeuProProAlaMetGlyArgThrAla-----LeuPheHis- 1224
   |||||
QY 1438 ACACAAAGCTGT----- 1450
   |||||
Db 1225 -HisSerGlyGlySerSerGlyTyrGlnSerLeuArgArgAspSerGlyAlaThrGlySe 1244
   |||||
QY 1450 ----- 1450
   |||||
Db 1244 rAlaSerSerAlaProAspSerMetSerGlnSerGlyAlaAlaSerProGlyAlaArgTh 1264
   |||||
QY 1450 ----- 1450
   |||||
Db 1264 rArgSerLeuLysSerProLysAlaArgAlaThrGlyLeuGlnArgArgLeuLePr 1284
   |||||
QY 1451 -----TGTGCTTACAAACCTAATTTTCATGACCCAGTGT 1485
   |||||
Db 1284 oAlaProLeuProAspThrThrAlaLeuGly-ArgLysProSerLeuProGlyGlnTrp- 1303
   |||||
QY 1486 TTGCAGTCCAGCGTGCCTTACAGATATGGAGGCCACTGAGAGATGTTTCCCCCTT 1545
   |||||
Db 1304 -----ValaAspLeu--Pro-----ProProLeu 1310
   |||||
QY 1546 GCTTGGCTTAAAG-----GCAGAGAG 1569
   |||||
Db 1311 AlaGlySerLeuLysGlnProPheGlnLysValaLysValaLysGlnLeuAspValaGlnArg 1330
   |||||
QY 1570 CGAGGCGGATGCTCTGAGACACCCAGCATCACCCAGG 1609
   |||||
Db 1331 -----LeuGlnArgProArgProThrProArg 1339
   |||||

```

```

RESULT 41
US-09-488-725A-2639
; Sequence 2639, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22

```





SOFTWARE: pc\_fl\_genes\_b Versions 1.0  
 SEQ ID NO 3157  
 LENGTH: 1079  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-488-725A-3157

## Alignment Scores:

Pred. No.:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
Score:	16.4	1078	196	40	141	884
Percent Similarity:	18.72%					
Best Local Similarity:	15.54%					
Query Match:	1					

us-09-488-522-1 (1-1624) x US-09-488-725A-3157 (1-1078)

```

QY 1622 GGGCCCGCACAAG-----CCTGGGTGTGATGC 1596
DB 100 GlyPro---LysGlyAspValGlyAlaArgGlyValSerGlyPheProGlyAlaAsp-- 117
QY 1595 TGGGTGCTTCCAGGATCCGCTCGCTTCTGCTTAAAGCACAAGAGGGGGAA 1536
DB 118 --Gly-IleProGlyIlePro---Gly---GlnGlyGly-- 127
QY 1535 AACATCCCTCAGTGGCTCCCATATCCGTGTAGGCCACGCTGGACTGCAAA----- 1485
DB 128 -----ProArg-GlyArgPro-----GlyIlyAspGly-CysAsnGlyThrGln 141
QY 1484 -----CCACTGGGTGATGAAATTAGTTTGTAGGCCACAACAG 1446
DB 142 GlyAspSerGlyProGlnGlyProProGlySerGly---GlyPheThrGlyProProGly 160
QY 1445 CCTGTGTTATGAAACAGAAACAGAAACATAGACATGTAACATGTAATAAAGGAA 1386
DB 161 Pro---GlnGlyProlys---Gly---GlnGlySerGly 170
QY 1385 G---TACTTGTTCACAAACTTTTGAATTATGTGTGAGTGTGTGAAGACCAAGAT--- 1333
DB 170 uProGlyAlaLeuProlys-----Gln-----GluArgAspArgT 182
QY 1333 ----- 1333
DB 182 yfArgGlyGluProGlyGluProGlyLeuValGlyPheGlnGlyProProGlyArgProG 202
QY 1333 ----- 1333
DB 202 yHfValGlyGlnMetGlyProValGlyAlaProGlyArgProGlyProGlyProG 222
QY 1332 -----CAGACTGGAAAAAATCTCTCCCACTGGGTTTC 1299
DB 222 roGlyProlysGlyGlnGlnGlyAsnArgGlyLeu---GlyPheIlyGlyValIly 239
QY 1298 -----ACTGTCAACAAACATCAGGCGCAGCAGTGTCTAGGCTGTCTCTCAA 1251
DB 240 GAllyLylLysGlyAspVal-----GlyGlnPro-----Gly----- 249
QY 1250 TTTCCTCATATGTCCTTCACATTC----- 1224
DB 250 -----ProAsnGlyIlePro-----SerAspThrLeuHisProIleLeuAlaProThrGly 266
QY 1224 ----- 1224
DB 267 ValThrPheHisProAspGlnIlyLysGlyGlyLysGlySerGlnGlyGluProGlyIle 286
QY 1224 ----- 1224
DB 287 ArgGlyIleSerLeuLysGlyGlnGlnGlyIleMetGlyPheProGlyLeuArgGlyTyr 306
QY 1223 -----TCACAGAG----- 1215
DB 307 ProGlyLeuSerGlyGlnLysGlySerProGlyGlnLysGlySerArgGlyLeuAspGly 326

```

```

QY 1214 -----CCTCC 1209
DB 327 TyrGlnGlyProAspGlyProArgGlyProLysGlyLysAlaIleAspProGlyProPro 346
QY 1208 AGGCTTCCTGACATTCCTGTGTCATTTCTCAGTACCTAGAGGATCTTAAACCGCAC 1149
DB 347 GlyLeuProAlaIlySerPro-HisProSerLeuAla--LysGlyAla-----ArgGly 363
QY 1148 GAGCTTAAGTGGCTGAAAACTCAGAGACGCTGTCACTGTCCAGCAAGTTAGTCTGA 1089
DB 364 AspProGlyPheProGlyAlaGlnGlyGlnProGlySer-----GlnGly 379
QY 1088 GTACACATCTAGTTTCCACTCCTCAGTAGAGAGAGGCGCTGCTAACATCCTCCCTGG 1029
DB 379 u-----Pro-GlyAspProGlyLeu-----ProG 387
QY 1028 GGTGCCCGAGAGAGACAGTGGGTGTGGGTGGCGCTCCCAAGCTCAGTCCCTGAACAC 969
DB 387 y---ProProGlyLeuSer-----IleGlyAspGlyAspGlnArgArgGlyLeu----- 402
QY 968 ACATGCCGGGC-----GGAGACTGCTGCTGA 942
DB 403 -----ProGlyLysMetGlyProLysGlyPheIleGlyAspProGlyIleProAlaLeuT 421
QY 941 GGCTCGCAGCCCTCAGTGGGGTGTGCTGTGACTCCAAATGTACCGTTTGCCAGAG 882
DB 421 yrelGlyProPro-----GlyPro-----AspGlyLys-----ArgG 432
QY 881 GTACAGATCCAGAGGTGTGCTCCCTGCTCAGAAAGTCCGCTTGTAGTCCGCCATTG 822
DB 432 lProPro-----ProGly---ProProGly-----LeuProGlyProPro---G 444
QY 821 GACCTCTCTCGGTGCTTGTGATGATGATCAATTCAGATGCTCGATGCTGCACG 762
DB 444 lProAspGlyPheLeuPheGly-----LeuLysGlyAlaIleAspGlyTyr 458
QY 761 ATCAGTTGATGAGCAACATATTGTCCACTCCTCGTGGAGATATCATCAGGATCTTC 702
DB 458 GAlaGly-----PheProGlyLeuProGly----- 466
QY 701 TTTTTCGAGCAGAGAACTCTCGAAGCGCGCTTCAGCAAGATGG----- 656
DB 467 -----SerProGlyAlaProGlyProLysGlyTyrLysGlyAspAlaG 481
QY 655 -----TGTACTGCTCAGAACTGCT----- 635
DB 481 yGlnCysArgCysThrGlnGlyAspGlnAlaIleLysGlyLeuProGlyLeuProGlyPr 501
QY 635 ----- 635
DB 501 oLysGlyPheAlaGlyIleAsnGlyGluProGlyArgLysGlyAspLysGlyAspProG 521
QY 634 -----CC 633
DB 521 yGlnHisGlyLeuProGlyPheProGlyLeuLysGlyValProGlyAsnIleGlyAlaArg 541
QY 632 AGCTCCCTCCTCGGCGCAGTCCCGAGAACTTTCAGACAGCCTGACGTGGAGTGG 573
DB 541 oGlyProLys---GlyAlaLys---GlyAsp---SerArg-ThrIleThrThrLys--G 557
QY 572 GTGTCCAGAGAGAGCGCAGGTGGAACATGTCCTCGATCTCTGCTGAGAG----- 521
DB 557 lY-----GluArgGlyGlnProGlyVal---ProGlyValProGlyMetLysGlyAspAs 574
QY 521 ----- 521
DB 574 pGlySerProGlyArgAspGlyLeuAspGlyPheProGlyLeuProGlyProProGlyAs 594
QY 520 -----ACACCAAGATGCTCTCAACAGAA----- 497
DB 594 pGlyIleLysGlyProProGlyAspProGlyTyrProGlyIleProGlyThrLysGlyTh 614
QY 497 ----- 497

```







```

; SOFTWARE: pc_fla_gene_b Versions 1.0
; SEQ ID NO 5944
; LENGTH: 1088
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-5944

```

## Alignment Scores:

```

Pred. No.: 17 Length: 1086
Score: 435.30 Matches: 184
Percent Similarity: 23.04% Conservative: 72
Best Local Similarity: 16.56% Mismatches: 128
Query Match: 14.54% Indels: 727
DB: 1 Gaps: 17

```

```

us-09-488-522-1 (1-1624) x US-09-488-725A-5944 (1-1086)

```

```

QY 1619 CCGCAGACAGCC--TGGGTGTGATGCTGGTGTCTCCAGGGCATCCGCTTCTCT 1563
DB 402 ProhlaGlnSerThrTrp-----GlyProPhe-----ProValArg----- 413
QY 1562 GCCCTTTAAGCAGACGAGGGGAGAAACATCCCTCAGTGGCTCCCATATCCGCTAG 1503
DB 414 -ProLeu--SerProAlaArgAlaThrAsnSerProLys-----ProHisMetValProA 431
QY 1502 GCCAGCGT----- 1495
DB 431 rghIsSerAsnGlnAsnSerSerGlySerGlnValAsnSerAlaGlySerLeuThrSers 451
QY 1494 ----- 1476
DB 451 erProThrThrThrSerSerSerAlaSerThrValProGlyThrSerThrAsnGlyS 471
QY 1475 CATGAATTTAGGTTTGTAGGCCACACACGCTTGTGTATGAACAG----- 1428
DB 471 er-----Pro-SerSerProSerValArgArgGlnLeuPheValThr 484
QY 1427 -----AAAACAGAAACATGAGGACATGTAACATGTAAGAAAGAAAGTACTTGTTCAC 1374
DB 485 ValValLysThrSerAsnAlaThrThrThrVal-----ThrThrThrAlaSerA 502
QY 1373 AAAACTTTGAGTATGTGTGTGTGTGTGAAGAACGATCAGACTGGAAGAAACTCTC 1314
DB 502 AsnAsn-----AsnThrA 506
QY 1313 TCCCACTGTGGCTTCACTGTCAACAAACATCAGGCCAGCGAGTGTCTAGGCTTCTCT 1254
DB 506 Iapro-----ThrAsnAlaThrTyRProMetProThrAlaLys-----Glu 519
QY 1253 CAATTTCCCAATATATGTCCTCATCTCAGAGAGGCTCCAGGCTTCTCT----- 1200
DB 520 HisTyRPro-----ValSerSerProSerSerProSerProAlaGlnProGlyGly 537
QY 1200 ----- 1200
DB 538 ValSerArgAsnSerProLeuAspCysGlySerAlaSerProAsnLysValAlaSerSer 557
QY 1200 ----- 1200
DB 558 SerGlnGlnAlaGlySerProProValAlaGlnThrThrAsnThrArgProProAsn 577
QY 1199 -----GCACATTTCTGGCATTTCTCAAGTCAAGCTTAGAG 1167
DB 578 SerSerSerSerSerGlySerSerSerAlaHisSer--AsnGlnGlnGlnProPro--- 595
QY 1166 GGATCTTTAAACCGCAGACGAGCTTAAG----- 1140
DB 596 GlySerValSerGln--GluProArgProProLeuGlnGlnSerGlnValAlaProProPro 614
QY 1139 -----TGGCTGAAGAACTTACAGAAAGCCTGTGACAGTGTCCAGCA 1101
DB 615 GluValArgMetThrValProProLeuAlaThrThrSerSerAlaProValAlaValProSer 634

```

```

QY 1100 AGTTGAGTCTAGAGTACACACATCTGAGTTTCCACTCTCTAGTGAAGAGCCCTGCTCTA 1041
DB 635 Thr--AlaProValThr-----TyrProMet-----ProGln----- 644
QY 1040 ACATCCCCCTGGGGGTGGCCGAGAGAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 981
DB 645 --ThrProMetGlyCys-ProGlnProThr-----ProLysMetG 657
QY 980 GTCCCTGAACACACATCCGCGGGGAGAGACTGCGCTGAGAGGCTCGGAGCCCTCAGTGG 921
DB 657 Lu-----ThrProAlaLeuGly-----ProProProHisG 667
QY 920 GGTCTGTCTGTGATCCAAAT----- 899
DB 667 LyrThrThrAla-----ProHisLysAsnSerAlaSerValGlnAsnSerSerValAlaVa 685
QY 899 ----- 899
DB 685 IleuSerValAsnHisAlaLysArgProHisSerValProSerSerValGlnLeuProSe 705
QY 898 -----GTACCGTTTGGCCAGAGTACAGATCCAGAGGTGTCCCTGAGCTCA 852
DB 705 rThrLeuSerThrGlnSerAlaCysGlnAsnSer-----ValHisPro--AlaAla 721
QY 851 GAAAGGTCCGCTTGTAGTCTCG-----CCCATTTGAACCTCTCTCGG 810
DB 721 nLys--Pro-----IleAlaProAsnPheSerAlaProLeuProPheGlyProPheSer 739
QY 809 TGCATTTGACATGTGATCCATTCAGATGCTCTGATGCTGACAGATCAGTTGATG 750
DB 739 hrlLeuPhe--GluAsnSerPro-----ThrSerAlaHisAlaPhe--Tr 752
QY 749 G-----CAACCATATTGTCACCTCGTGAGATGATCA-- 714
DB 752 pGlyGlySerValValSerSerGln-----SerThrProGlnSerMetLeuSerGly 769
QY 713 --TGGCATATCTTCTTGTGTGCGAGGACAGACTCTCGAAGCGGCTTACAGAAAGTG 657
DB 770 LysSerSerTyLeu-----ProAsnSerSer--Pro-LeuHisGln-- 782
QY 656 GTGACTGCGTCAAGATCTGCTCAGGT----- 629
DB 783 --SerAspThrSerLysAlaProGlyPheArgProProLeuGlnArgProAlaProSe 801
QY 628 -----CCCTCCCTCGGCGC 615
DB 801 rProSerGlyTLeuValAsnMetAspSerProTyGlySerValThrProSer--SerThr 821
QY 614 ACGTCCCGAGAACTCTTGCAGACAGCCTGACGTGCGAGTGCACAGAAAGGCGC 555
DB 821 IAsnLeu--Gly--Asn--Phe-----AlaSerAsnHisSer----- 830
QY 554 AGGTGAACATGT-----CCCGATCTCTT----- 530
DB 831 -GlyGlyGlnMetTyGlyProGlyAlaProLeuGlyGlyAlaProAlaAlaAsnPh 850
QY 530 ----- 530
DB 850 eAsnArgGlnHisPheSerProLeuSerLeuLeuThrProCysSerSerAlaSerAsnAs 870
QY 529 -----GGCTGTAGAACCAAGATGCCCTTCAACAGAAC 495
DB 870 pSerSerAlaGlnSerValSerSerGlyValAlaGlnAlaPro-----SerP 885
QY 494 ACGTCCGAGAGGTAGACACCGGTGTCTGTGTAACCTTGAAGTGTCAAAAATCATAG 435
DB 885 oAlaProSerSerValProLeuGlySerGlyLysProSerAsnValSerGlnAspArgly 905
QY 434 G-----TCGGC 429
DB 905 sValProValProLleGlyThrGluArgSerAlaArgTlAlaArgGlnThrGlyThrSerAl 925
QY 428 ACTTCACCGTTTTCCTCCACAGATGTCTTCAAGTCTGTGATCAATCAATCATATATCA 369

```



[illegible][illegible]

Db 1282 a1ProGlyProlys-----GlyAspPro 1289

Search completed: December 12, 2003, 10:42:29  
Job time : 150.5 secs

**This Page Blank (uspto)**

**This Pa**



```

Db      364 ATGATTTGATGACAGGACTGTAAGAAACATGTGTGAGGGGCAAAACGGTGGAGTGCAG 423
Qy      434 CTTATGATTTGTGACACACTCAAGGTTTACCAAGAGACCAAGGTGTCTACCTTCGGAGC 493
Db      424 CTTATGATTTGTGACACACTCAAGGTTTACCAAGAGACCAAGGTGTCTACCTTCGGAGC 483
Qy      494 TGGTTCGTGTTGAGGGGACTTGGTGTCTACAGCCAGAGAGATCCGGGACATGTTTCCACC 553
Db      484 TGGTTCGTGTTGAGGGGACTTGGTGTCTACAGCCAGAGATCCGGGACATGTTTCCACC 543
Qy      554 TGCCTCTCTTCGTGAGACACGACTCCGACGTCAAGGCTGTCTGAAGATTCTCCGGAGC 613
Db      544 TGCCTCTCTTCGTGAGACACGACTCCGACGTCAAGGCTGTCTGAAGATTCTCCGGAGC 603
Qy      614 TGGCCCGAGGGAGGAGCCTTGAGAGAGATTCTGAGCGAGTACACCACTTCTGTAAGCCG 673
Db      604 TGGCCCGAGGGAGGAGCCTTGAGAGAGATTCTGAGCGAGTACACCACTTCTGTAAGCCG 663
Qy      674 CTTTCGAGGAGTTCTGCTGCGCGACAAAGAGTA-TGGCGAGTGTGATGTCGACGAGGA 732
Db      664 CTTTCGAGGAGTTCTGCTGCGCGACAAAGAGTATGGCGAGTGTGATGTCGACGAGGA 723
Qy      733 GTGACATATGTTGTCATCACTGATCGTGCAGACATCCAGACATTCGTAATGCT 792
Db      724 GTGACATATGTTGTCATCACTGATCGTGCAGACATCCAGACATTCGTAATGCT 783
Qy      793 GACATCTGCAATGCGACCCGAGAGGTTCCATATGGGCGGAGCTACAGCGGACCTTTTCT 852
Db      784 GACATCTGCAATGCGACCCGAGAGGTTCCATATGGGCGGAGCTACAGCGGACCTTTTCT 843
Qy      853 GAGCGAGGGGACCACTCGGAGTGTGACTCTGCGCAACGCTACATTTGAGTCCAGC 912
Db      844 GAGCGAGGGGACCACTCGGAGTGTGACTCTGCGCAACGCTACATTTGAGTCCAGC 903
Qy      913 AGCAGACCCCACTGAGGGGCTGCGAGGCTTCAAGGACAGTCTCCGCGCCGACATGTGT 972
Db      904 AGCAGACCCCACTGAGGGGCTGCGAGGCTTCAAGGACAGTCTCCGCGCCGACATGTGT 963
Qy      973 TCAGGAGATTGAGCTTGGGGAGGCCCAACCACTGCTTCTCTGGGGGACCCGAG 1032
Db      964 TCAGGAGATTGAGCTTGGGGAGGCCCAACCACTGCTTCTCTGGGGGACCCGAG 1023
Qy      1033 GGGAGTGTAGAGGAGGAGGCTTCTCTCACTCAGAGGTGAAATCAGATGTGCACTCAG 1092
Db      1024 GGGAGTGTAGAGGAGGAGGCTTCTCTCACTCAGAGGTGAAATCAGATGTGCACTCAG 1083
Qy      1093 ACTCAACTTGTGGGACACTGACAGGCGTTCCTGAGGTTTTCAGGCACTTGAAGCTGTG 1152
Db      1084 ACTCAACTTGTGGGACACTGACAGGCGTTCCTGAGGTTTTCAGGCACTTGAAGCTGTG 1143
Qy      1153 CGGTTTAAAGATCCCTTAAGTCACTGAGAAATGCGACAGATGTGCAAGAGCTGGGA 1212
Db      1144 CGGTTTAAAGATCCCTTAAGTCACTGAGAAATGCGACAGATGTGCAAGAGCTGGGA 1203
Qy      1213 GGGCTTGTGAGGAATGAGGACATTAATGGGGAAATTAAGAGAGAGGCTGAGACT 1272
Db      1204 GGGCTTGTGAGGAATGAGGACATTAATGGGGAAATTAAGAGAGAGGCTGAGACT 1263
Qy      1273 GGGCTGAGCTGATGTTTGTGACAGTGAACCAAGTGGGAGAGATTTTTCAGTGTG 1332
Db      1264 GGGCTGAGCTGATGTTTGTGACAGTGAACCAAGTGGGAGAGATTTTTCAGTGTG 1323
Qy      1333 ATCTGTTTCTTACACACTGACACACATTAACCTCAAAAGTTTGTGAACAAGTACTTCTT 1392
Db      1324 ATCTGTTTCTTACACACTGACACACATTAACCTCAAAAGTTTGTGAACAAGTACTTCTT 1383
Qy      1393 TTTTACATGTTACATGCTCTGATGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 1452
Db      1384 TTTTACATGTTACATGCTCTGATGTTTCTGTTTCTGTTTCTGTTTCTGTTTCTGTTTCT 1443
Qy      1453 TGGCTTACAAACCTTAATTTATGATGACCAAGTGTGAGTCCAGGCTGCTTACAGGAT 1512
Db      1444 TGGCTTACAAACCTTAATTTATGATGACCAAGTGTGAGTCCAGGCTGCTTACAGGAT 1503

```

```

Qy      1513 ATGGGGAGCCACTGAGGGATGTTTCCCTTGTGCTTGTGCTTAAAGGACAGAAAGCGA 1572
Db      1504 ATGGGGAGCCACTGAGGGATGTTTCCCTTGTGCTTGTGCTTAAAGGACAGAAAGCGA 1563
Qy      1573 GGGGATGCTCTGGAAGACCCAGCATCACACAGGCTTGTGCGGGGCGAG 1624
Db      1564 GGGGATGCTCTGGAAGACCCAGCATCACACAGGCTTGTGCGGGGCGAG 1615

RESULT 2
US-09-488-725B-7130
; Sequence 7130, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; APPLICANT: Radolje T. Drmanac
; TITLE OF INVENTION: Novel Configs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT FILING DATE: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PAM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 7130
; LENGTH: 2152
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(2153)
; OTHER INFORMATION: n = a,t,c or g
; NAME/KEY: misc_feature
; LOCATION: (110)...(891)
; OTHER INFORMATION: similar to g1471981 in the genepept database release 114,
; US-09-488-725B-7130

Query Match      97.6%; Score 1585.8; DB 1; Length 2152;
Best Local Similarity 99.9%; Pred. No. 8.9e-309;
Matches 1587; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```



```

QY 156 GCGGCCCTTCCTGATAGGGGTGAGCGGCGGCACTGCCAGCGGGAAGTCACCCGTTGTGA 215
DB 121 GCGGCCCTTCCTGATAGGGGTGAGCGGCGGCACTGCCAGCGGGAAGTCACCCGTTGTGA 180
QY 216 GAAGATCATGAGATTCTGGGACAGAACGAGTGAACAGCGGCAAGCGGAGGTGTCTAT 275
DB 181 GAAGATCATGAGATTCTGGGACAGAACGAGTGAACAGCGGCAAGCGGAGGTGTCTAT 240
QY 276 CCTGAGCCAGGACAGAGTTCTTCAAGGTCCTGACGGCAGACAGAAAGGCCATTGAA 335
DB 241 CCTGAGCCAGGACAGAGTTCTTCAAGGTCCTGACGGCAGACAGAAAGGCCATTGAA 300
QY 336 AGGACGATCAATTTTGAACATCCAGATGCTTGAATTAATTTGATGACAGAACTCT 395
DB 301 AGGACGATCAATTTTGAACATCCAGATGCTTGAATTAATTTGATGACAGAACTCT 360
QY 396 GAAAGACATCTGTGAGAGGCAAAAAGGTGAGGTGCGGACCTATGATTTGTGACACATC 455
DB 361 GAAAGACATCTGTGAGAGGCAAAAAGGTGAGGTGCGGACCTATGATTTGTGACACATC 420
QY 456 AAGGTTACAGAGAACCAAGGTGTCTACCTGCGGACGTGTCTGTGTTGAGGCACTT 515
DB 421 AAGGTTACAGAGAACCAAGGTGTCTACCTGCGGACGTGTCTGTGTTGAGGCACTT 480
QY 516 GGTGTTCTACAGCGCAGGAGATCCGGGACATGTTCACTGCGGCTCTGTGAGACACGA 575
DB 481 GGTGTTCTACAGCGCAGGAGATCCGGGACATGTTCACTGCGGCTCTGTGAGACACGA 540
QY 576 CTCGCAAGTCAGGCTGTCTGAAAGTTCTCCGGGACGTGCGGCGAGAGGAGCACTGGA 635
DB 541 CTCGCAAGTCAGGCTGTCTGAAAGTTCTCCGGGACGTGCGGCGAGAGGAGCACTGGA 600
QY 636 GCGAGATTCGACGCAAGTACCACTTCTGTGAAGCGGCTTGGAGAGTTCTGCTGCC 695
DB 601 GCGAGATTCGACGCAAGTACCACTTCTGTGAAGCGGCTTGGAGAGTTCTGCTGCC 660
QY 696 GACAAAGAGTATGCGGATGTCATCCCAAGAGGTGAACAATATGTTGCCATCA 755
DB 661 GACAAAGAGTATGCGGATGTCATCCCAAGAGGTGAACAATATGTTGCCATCA 720
QY 756 CCTGATCTGTCAGACATCCAGGACATTTGAAATGTTGATCTGCAATATGACACGAG 815
DB 721 CCTGATCTGTCAGACATCCAGGACATTTGAAATGTTGATCTGCAATATGACACGAG 780
QY 816 AAGGTCATATGCGGAGCTTCAAGCGGACCTTTTCTGAGCCAGAGGACCACTTGAGAT 875
DB 781 AAGGTCATATGCGGAGCTTCAAGCGGACCTTTTCTGAGCCAGAGGACCACTTGAGAT 840
QY 876 GCTGACCTCTGGGAAACGGTCATATTGAGTCCAGACAGAACCCCACTGAGAGGCTGC 935
DB 841 GCTGACCTCTGGGAAACGGTCATATTGAGTCCAGACAGAACCCCACTGAGAGGCTGC 900
QY 936 CGAGCTTCAGAGGAGTCTCCCGCGGACATGTGTGTTGAGGACATGAGCCTGAGACGC 995
DB 901 CGAGCTTCAGAGGAGTCTCCCGCGGACATGTGTGTTGAGGACATGAGCCTGAGACGC 960
QY 996 CCAACCAACCACTGCTTCTCTCGGCGGACCCAGGGAGTGTGACAGCAGGCTTT 1055
DB 961 CCAACCAACCACTGCTTCTCTCGGCGGACCCAGGGAGTGTGACAGCAGGCTTT 1020
QY 1056 CCTCACTCAGAGATGAAACTGAGATGTCTCACTCACTCACTCACTGCTGAGCACTGAC 1115
DB 1021 CCTCACTCAGAGATGAAACTGAGATGTCTCACTCACTCACTCACTGCTGAGCACTGAC 1080
QY 1116 AAGCGTTCTGAGGTTTCTGAGCACTTGAAGCTGTGCGGTTTAAAGATCCCTAGGTC 1175
DB 1081 AAGCGTTCTGAGGTTTCTGAGCACTTGAAGCTGTGCGGTTTAAAGATCCCTAGGTC 1140
QY 1176 ACTGAGAAATGCAAGATGTGACAGAGACCTTGGAGAGCTTGTGAGAAATGTAGGC 1235
DB 1141 ACTGAGAAATGCAAGATGTGACAGAGAGCTTGGAGAGCTTGTGAGAAATGTAGGC 1200

```

```

QY 1236 ACATATTTGGGGAAATTTGAGAGACAGACCTTAGACATGCGCTGGCTGATGTTTGTGAC 1295
DB 1201 ACATATTTGGGGAAATTTGAGAGACAGACCTTAGACATGCGCTGGCTGATGTTTGTGAC 1260
QY 1296 AGTGAACCAAGTGGGAGAGAGTTTTCAGTCTGATCTGATCTTTACACTGACAC 1355
DB 1261 AGTGAACCAAGTGGGAGAGAGTTTTCAGTCTGATCTGATCTTTACACTGACAC 1320
QY 1356 ACATTACTGAAGTTTGTGAAACAGTACTTCCCTTTTACATGTTACATGCTCCAT 1415
DB 1321 ACATTACTGAAGTTTGTGAAACAGTACTTCCCTTTTACATGTTACATGCTCCAT 1380
QY 1416 GTTTCGTTTCTGTTTCAATACACAGGCTGTGTGAGCTTAACTTAATTTGATG 1475
DB 1381 GTTTCGTTTCTGTTTCAATACACAGGCTGTGTGAGCTTAACTTAATTTGATG 1440
QY 1476 ACCAGTGTGTTGACGTCCAGCGTGGCTTACACGATATGAGGAGCCACTGAGGATGTT 1535
DB 1441 ACCAGTGTGTTGACGTCCAGCGTGGCTTACACGATATGAGGAGCCACTGAGGATGTT 1500
QY 1536 TTCCCTCCCTTCTGTTGCTTAAAGGACAGAGAGCGAGTGGCTTGGAGACACCA 1595
DB 1501 TTCCCTCCCTTCTGTTGCTTAAAGGACAGAGAGCGAGTGGCTTGGAGACACCA 1560
QY 1596 GCATCAACCCAGGCTTGTGCGGAGCCAG 1624
DB 1561 GCATCAACCCAGGCTTGTGCGGAGCCAG 1589

```

```

RESULT 3
US-09-536-647-1
; Sequence 1, Application US/09536647
; Patent No. 6579708
; GENERAL INFORMATION:
; APPLICANT: Ho, Yen Sen
; APPLICANT: Johnson, Randall
; TITLE OF INVENTION: No. 6579708e1 Human Uridine Kinase
; FILE REFERENCE: GP50020
; CURRENT APPLICATION NUMBER: US/09/536,647
; CURRENT FILING DATE: 2000-03-27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(780)
US-09-536-647-1

```

```

Query Match 51.3%; Score 832.4; DB 2; Length 834;
Best Local Similarity 99.9%; Pred. No. 2e-158;
Matches 833; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 94 ATGGCTTCGCGGAGGCGAAGACTGCCAGACCCCGCGGAGCCGACCGTCCGAC 153
DB 1 ATGGCTTCGCGGAGGCGAAGACTGCCAGACCCCGCGGAGCCGACCGTCCGAC 60
QY 154 CAGCGGCCCTTCTGATAGAGGTTGAGCGGCACTGCGAGCGGAAAGTCAGCCGTGTG 213
DB 61 CAGCGGCCCTTCTGATAGAGGTTGAGCGGCACTGCGAGCGGAAAGTCAGCCGTGTG 120
QY 214 GAAAGATCATGAGATTGCTGGGACAGAACGAGTGAACAGCGGACGCGAAGGTGTC 273
DB 121 GAAAGATCATGAGATTGCTGGGACAGAACGAGTGAACAGCGGACGCGAAGGTGTC 180
QY 274 ATCTGAGGCAAGAGTTCTTCAAGGTCCTGACGGCAGACGAAAGGCCAAAGCTTGG 333
DB 181 ATCTGAGGCAAGAGTTCTTCAAGGTCCTGACGGCAGACGAAAGGCCAAAGCTTGG 240
QY 334 AAAGGACATCAATTTTGAACATCCAGATGCTTGAATTAATTTGATGACAGAGACT 393
DB 1141 AAAGGACATCAATTTTGAACATCCAGATGCTTGAATTAATTTGATGACAGAGACT 1200

```

```

Db      241 AAAGACAGTACATTTTGAACATCCAGATGCTTTTGAACATGATTTGATGACAGAGACT 300
Qy      394 CTGAAGAACATCGTGAAGGGGAAACCGTGAAGGTGCCGACCTTATGATTTGTGAACAC 453
Db      301 CTGAAGAACATCGTGAAGGGGAAACCGTGAAGGTGCCGACCTTATGATTTGTGAACAC 360
Qy      454 TCAAGTTTACAGAGACCAAGGTGATCTACCTCGAGAGTGGTCTTCTGTTTGAAGGGACTC 513
Db      361 TCAAGTTTACAGAGACCAAGGTGATCTACCTCGAGAGTGGTCTTCTGTTTGAAGGGACTC 420
Qy      514 TTGATGTTTACAGACCAAGAGATCCGGACATGTTTCCACTGCGCTTCTTGTGGAACACC 573
Db      421 TTGATGTTTACAGACCAAGAGATCCGGACATGTTTCCACTGCGCTTCTTGTGGAACACC 480
Qy      574 GACTCCGACGTCAGAGCTCTCTGAAGAGTTCTCCGGACGTCGCGCCGAGAGGAGGAGACTG 633
Db      481 GACTCCGACGTCAGAGCTCTCTGAAGAGTTCTCCGGACGTCGCGCCGAGAGGAGGAGACTG 540
Qy      634 GAGCAGATTTGACGACAGTACACCACTTGTGTAAGCCGCGCTTCAAGAGATTCTGACTG 693
Db      541 GAGCAGATTTGACGACAGTACACCACTTGTGTAAGCCGCGCTTCAAGAGATTCTGACTG 600
Qy      694 CCGACAAAGAGATATGCCGATGTATCATCCACAGAGAGTGAACAATATGTTGCCATC 753
Db      601 CCGACAAAGAGATATGCCGATGTATCATCCACAGAGAGTGAACAATATGTTGCCATC 660
Qy      754 AACCTGATCTGACGACATCCAGACATTTGTAATGTGACATCTGTAATGTGACACCGA 813
Db      661 AACCTGATCTGACGACATCCAGACATTTGTAATGTGACATCTGTAATGTGACACCGA 720
Qy      814 GGAGGGTCCATGAGCGGAGCTACCAAGCGACCTTTTGTAGCCAGGGGACCACTCTGGG 873
Db      721 GGAGGGTCCATGAGCGGAGCTACCAAGCGACCTTTTGTAGCCAGGGGACCACTCTGGG 780
Qy      874 ATGTGACCTTGTGCAACCGTCACTTTGTGAGTCCAGACAGACCCCACTGA 927
Db      781 ATGTGACCTTGTGCAACCGTCACTTTGTGAGTCCAGACAGACCCCACTGA 834

```

```

RESULT 4
US-09-235-076-30379
; Sequence 30379, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: PaSeq for Windows Version 3.0
; SEQ ID NO 30379
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-30379

```

```

Query Match      26.7%; Score 432.8; DB 4; Length 472;
Best Local Similarity 98.2%; Pred. No. 1,1e-78;
Matches 437; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

```

```

Qy      177 GAGCGCGCGCACTGCGCAGCGGGAAGTCCAGCGTGTGTGAGAAGATCATGAGTTGCTGGG 236
Db      28 GTGCGTGAANCGCAGCGGGAAGTCCAGCGTGTGTGAGAAGATCATGAGTTGCTGGG 87
Qy      237 ACAGAGCAGAGGTGAACAGCGGCGAGCGGAAGGTGTCATCTTGAAGCCAGGAGTTCTA 296
Db      88 ACAGAGCAGAGGTGAACAGCGGCGAGCGGAAGGTGTCATCTTGAAGCCAGGAGTTCTA 147

```

```

Qy      297 CAAGTCTTGAACGCGACAGAGAGGCAAGGCTTTGAAGAAGACAGTACATTTTGAACA 356
Db      148 CAAGTCTTGAACGCGACAGAGAGGCAAGGCTTTGAAGAAGACAGTACATTTTGAACA 207
Qy      357 TCCAGATGCTTTGATATGATTTGATGACAGAGACTTGAAGAATCTGTGAAGGCA 416
Db      208 TCCAGATGCTTTGATATGATTTGATGACAGAGACTTGAAGAATCTGTGAAGGCA 267
Qy      417 AACGGTGAAGTCCGACCTATGATTTTGAACAACCTGAAGTTTACAGAGCAACGGT 476
Db      268 AACGGTGAAGTCCGACCTATGATTTTGAACAACCTGAAGTTTACAGAGCAACGGT 327
Qy      477 GGTCTACCTTCCGACAGTGTCTTGTGAGGCACTTGTGATCTTCAACAGAGAGAT 536
Db      328 GGTCTACCTTCCGACAGTGTCTTGTGAGGCACTTGTGATCTTCAACAGAGAGAT 387
Qy      537 CCGGACATGTTCCACTGCGCTTCTTGTGACACCGACTCCGAGTCAAGCTGTCTG 596
Db      388 CCGGACATGTTCCACTGCGCTTCTTGTGACACCGACTCCGAGTCAAGCTGTATCG 447
Qy      597 AAGAGTTCTCCGAGAGTGGCCGA 621
Db      448 AAGAGTTCTCCGAGAGTGGCCGA 472

```

```

RESULT 5
PCT-US00-05988-220
; Sequence 220, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: P0101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 1310
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US00-05988-220

```

```

Query Match      22.8%; Score 370.699; DB 5; Length 1310;
Best Local Similarity 68.6%; Pred. No. 2.8e-66;
Matches 550; Conservative 1; Mismatches 244; Indels 7; Gaps 3;

```

```

Qy      14 CGACCTGCGCTGAGCGGCGCGCGCGCGCGGAGAGGCGCGCGGACCCGAT 73
Db      140 CGGCTGCGGAAGCGAGAGGAGTCCAGCGCGCGCGCGGAGCGTCCCTTCC 199
Qy      74 GCGCGGAGCGGAGCGGAGATGCTTCCGCGGAGCGGAAGCTGAGAGCCCGCGC 133
Db      200 CACAGCGAGCGGAGGAGGCGCGCGGACATGCGCGGAGCAGGAGCAACCTTGC 259
Qy      134 CGAGGCGGACGTCGCGACAGG--GCCCTTCTGATAGGGGTAGCGCGGCACTG 190
Db      260 AGAACCAACAGCAGCCCAAGCGGCGCGCGCGCTTCTTATAGCGTCA-CGGGGAAACAG 318
Qy      191 CCGCGGGAAGTGAACGCTGTGTGAGAAGATCATGAGTTGCTGGGACAGAACGAGGTG 250
Db      319 CTACCGGCAAGTCTTCCGTGTGTCTAAGATCTGACGCTCTGCGGACAGATGAGGTG 378
Qy      251 AACGCGGACGCGAGAGGTGTCATCTTGAAGCAGAGACAGTTCTACAGGTCTGACG 310
Db      379 ACTATGCCAAGAGCAGTGTGATCTTGAAGCAGAGATAGTCTTACGATCTTACT 438
Qy      311 CAGAGCAAGGCGCAAGGCTTGAAGAAGACATTTTGAACATTCAGATGCTTTTG 370
Db      439 CGAGCAGAAAGGCCAAGGCCCTGTAAGSCCAGTTCACTTGAACACCGGATGCTTTG 498

```

QY	371	ATAATGATTTGATGCAAGGACTCTGGAAGAAACATGCTGAGGGCAAAACGGTGGAGATGC	430
Db	499	ACAATGAATCTATTCTCAAAACACTTCAAAGAAATTCCTGAAGGAAACAGTCCAGATCC	558
QY	431	CGACCTATGATTTTGTGACACACTGAAGTTACAGAGACCACGGTGTCTACCTCCGCG	490
Db	559	CCGTGTATGACTTTGTCTCCCATTCCTCCGGAAGAGAGACAGTTACTGTCTATCCGCAg	618
QY	491	AACGTGTTCTGTTTGAAGGCATCTTGTTGTTTCTTACAGCCAGAGATCCGGACATGTTCC	550
Db	619	AAGTGTCTCTTTTGAAGGGAATCTCGGCCCTTCTACTCCAGAGAGTACAGACACTGTCC	678
QY	551	ACCTGCGCTCTTCGTGACACCGACTCCGAGTCAAGCTGTCTCGAAGTGTCTCCGG	610
Db	679	AGATGAACCTTTTGTGTGATACAGATGCGGACACCCGGCTCTCACCCAGAGATTTAAGG	738
QY	611	ACGTGCGC--CGAGGAGGGGACCTGAGACAATTCTGACGACGTAACCAACCTTGTA	667
Db	739	ACATCAGGAGAGAGGACGAGGATCTTGACACATTTTATCTCAGTACATTACCTTGCTCA	798
QY	668	AGCCGCGCTTGAGAGAGTTCTGCTCGCCGACAAAGAAGTATGCCGATGTGATATCCAC	727
Db	799	AGCTTCCTTTGAGGAATTTCTGCTTGCCCAACAAAGAAGTATGCTGATATATCCCTTA	858
QY	728	GAGGAGTGAACATATGTTGCTCCATCAACTGTATCTGTGAGACATATCCAGACATTTCTGA	787
Db	859	GAGGTGCAGATATATCTGTGTGCGCCATCAACTCATCTGTGAGACATATCCAGACATCTGA	918
QY	788	ATGTGACATCTGCAATGCGCA	809
Db	919	ATGAGGGCCCTCCAAACGCA	940

```

US-09-488-725B-6367/c
RESULT 6
; Sequence 6367, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinphast
; APPLICANT: Ankura Sinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
;
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_CT_genes Version 1.01
; SEQ ID NO 6367
; LENGTH: 1316
; TYPE: DNA

```

```
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/key: misc feature
; LOCATION: (1030)..(289)
; OTHER INFORMATION: similar to gi471961 in the genepept database release 114
; OTHER INFORMATION: Run with FASTyX 3.3t00, default parameters
US-09-488-125B-6367
```

Query Match	17.6%	Score 285.899;	DB 1;	Length 1316;
Best Local Similarity	-65.3%;	Pred. No. 2.4e-49;		
Matches 520;	Conservative 0;	Mismatches 261;	Indels 15;	Gaps 7;

Qy	22	GCCTGTGGCCGACGCGCCGGGACCCGAGGAAAGGGGCGGCGCGGGACCCCATGTGCGGGAA	81
Db	1163	GCGGAGGGAATCCGACGCGGGCGCGGGGAGCGTGCCTCCGTTGCAACAGCAGCGG	1104
Qy	82	GCGGAGGCCGAGATGCTTCGCGCGGAGGCGAAGACTGCAGAGCCCCGCGCGGAGGCC	141
Db	1103	GAGGAGGGGCGGCGGAACATGCGCGGGGACAGCGAGCAAGCCTGTGAGAACCAACGACGA	1044
Qy	142	GACGCTCCGACCAAGCGGCCCCCTTCTGTATGAGGGGTGAGCGCGGCACTGGCATGCGGAA	201
Db	1043	GCCCCAAGGGGCGGCG--GAGCCCTTCTTTATGCGGTCAAGCGGAGAAACAGCTTACGGGAA	986
Qy	202	TGCACGCTGTGTGAGAAAGATCATGAGATCTCTGGGACAGAAAGAGGTGAAACAGCGCAG	261
Db	985	TCTTCCCTGTGTGTGAAGATCTGTGACGCTCTGTGGGCGAATAGGTGACATACCGCAG	926
Qy	262	CGAAGGTGTATCTTGAGCCAGGACAGGTTCTAAGGTCTTGACGAGGAGCAGAA	321
Db	925	AAGCAGGTGTATCTTGAGCCAGGATAGCTTCTACCGTGTCTTACTCTGAGGACGAAG	866
Qy	322	GCCAAAGCCTTGAAGAAGCAGTACAAATTTTGACATCTCABAATGCTTTGATATGATTTG	381
Db	865	GCCAAAGCCTTGAAGGCGCAGTTCACTTGACACCGGATGCTTTGCAATGAATCTC	806
Qy	382	ATGCACAGGACTCTGAGAAACATCTGTGAGGGGCAAAACGCTGAGGTTCCGACCTATGAT	441
Db	805	ATTCTCAAAACATCTCAAAAGAAATCATCTGAAGGGAACAGTCCAGATCCCCGTATGAC	746
Qy	442	TTTGTGACACATCTAGGTTTACAGAGACCAAGGTGTCTACCTCTGGAGCGTGTCTG	501
Db	745	TTTGTCTCCCATTCCTCCGGAAGAGGAGACAGTTACTGTCTATCCCGAGACGTGTGCTC	686
Qy	502	TTTGAAGGCACTTGTGTTCTACAGCAGG--AGATCCGGGACATGTTCACTGCGCC	559
Db	685	TTTGAAGGATCTGTGCTTCTACTCCAGAGAAAGTACGAGACCTGTTCAGATGAGC	626
Qy	560	TCTTCGTGACAACCGAATCCGAGGTGACGCTGTCTGAAAGTTCTCGGAGCGTGC	618
Db	625	TTTTTGTGATACAGATGCGGACACCGCGTCTCAGCAGAGTATTAAGACATCAGCG	566
Qy	619	--CGAGGAGGACCTGAGACGAATCTGACGCAATAC---CACCTTCGTAAGCCG	672
Db	565	AGAGAGGCAAGGATCTTGAACCAATTTTATCTCAAGTACATTACGTTTGTCAAGCTG	506
Qy	673	GCCCTGAGAGATTCGCTCGCGGACAAA--GAGTATGCGGATGTATCATGCC--ACGA	729
Db	505	CCCTTTGAGGAATTCGTCTTGCCACCAAGAAAGTATGCTGATGTATCATCTCTAGAGA	446
Qy	730	GGAATGACAATATGTTGCTCATCAACTGTATGTGACAGCATATCA--GGACATTCTGAA	788
Db	445	GTGCAAGTATATCCGGGTGCGCATCAACTCATGTGACAGCATATCAGGACATCTGAA	386
Qy	789	TGTGTACATCTGCAA 804	
Db	385	TGAGAGGCTCTTCAA 370	

RESULT 7  
US-09-235-076-24042  
; Sequence 24042, Application US/09235076  
; GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/235, 076  
 CURRENT FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 24042  
 LENGTH: 472  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(472)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-235-076-24042

Query Match 13.6%; Score 221; DB 4; Length 472;  
 Best Local Similarity 73.0%; Pred. No. 2,1e-36;  
 Matches 284; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

Qy 159 GCCCTTCTGATAGGAGGTGAGCGGCACTGCCAGCGGGAAGTCAGCCGTGTGAGAA 218  
 Db 84 GCCCTTCTTATAGCGCTGACGGGGAAAGCTAGCGGCAAGCTTCCGTGTGCTAA 143  
 Qy 219 GATTATGAGTGTCTGGGACAGAACGAGTGGAAACAGCGGCAAGGAGGTGTCTCT 278  
 Db 144 GATGTGACAGTCTGGGGGAGATGAGTGAATGCTATGCGCAAGAGAGGTGTCTCT 203  
 Qy 279 GAGCCAGAGACAGTCTTCAACAAGTCTGACGCGCAGAGCAGAGAGGCAAGGCTTGAAG 338  
 Db 204 GAGCCAGAGATAGCTTCAACGCTGTCTTACCTCGAGAGAGGCAAGGCTTGAAG 263  
 Qy 339 ACAGTCAATTGACCACTCCAGATGCTTGAATGATTTGATGACAGGACTCTGAA 398  
 Db 264 CCACTTCAACTTGAACCAACCGAGTGCCTTGAACAATGATCTTCAAAACACTCAA 323  
 Qy 399 GAATCGTGGAGGCAAAAGGTGAGGTGCGGACCATGATTTGACACACTCAAG 458  
 Db 324 AGAATCACTGAAGGAAACAGTCCAGATCCCGTGTATACCTTCTCCCAATCCG 383  
 Qy 459 GTTACCAAGACACAGGTGTCTTACCTCGGACGAGGTGTCTGTTGAGGCACTTGT 518  
 Db 384 GAAAGAGAGACAGTACTGTCTATCCGACAGACTGTGTCTTTGAAGGATCTGCG 443  
 Qy 519 GTTCTACAGCCAGAGATCCGGGACATGT 547  
 Db 444 CTTCTACTCCAGAGGTACGAGACTGT 472

RESULT 8  
 US-09-235-076-23923

Sequence 23923, Application US/09235076  
 GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/235, 076  
 CURRENT FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 23923  
 LENGTH: 455  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(455)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-235-076-23923

Query Match 13.0%; Score 210.4; DB 4; Length 455;  
 Best Local Similarity 72.8%; Pred. No. 2.8e-34;  
 Matches 271; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

Qy 159 GCCCTTCTGATAGGAGGTGAGCGGCACTGCCAGCGGGAAGTCAGCCGTGTGAGAA 218  
 Db 84 GCCCTTCTTATAGCGCTGACGGGGAAACAGTACCGGCAAGCTTCCGTGTGCTAA 143  
 Qy 219 GATTATGAGTGTCTGGGACAGAACGAGTGGAAACAGCGGCAAGGAGGTGTCTCT 278  
 Db 144 GATGTGACAGTCTGGGGGAGATGAGTGAATGCTATGCGCAAGAGAGGTGTCTCT 203  
 Qy 279 GAGCCAGAGACAGTCTTCAACAAGTCTGACGCGCAGAGCAGAGAGGCAAGGCTTGAAG 338  
 Db 204 GAGCCAGAGATAGCTTCAACGCTGTCTTACCTCGAGAGAGGCAAGGCTTGAAG 263  
 Qy 339 ACAGTCAATTGACCACTCCAGATGCTTGAATGATTTGATGACAGGACTCTGAA 398  
 Db 264 CCACTTCAACTTGAACCAACCGAGTGCCTTGAACAATGATCTTCAAAACACTCAA 323  
 Qy 399 GAATCGTGGAGGCAAAAGGTGAGGTGCGGACCATGATTTGACACACTCAAG 458  
 Db 324 AGAATCACTGAAGGAAACAGTCCAGATCCCGTGTATACCTTCTCCCAATCCG 383  
 Qy 459 GTTACCAAGACACAGGTGTCTTACCTCGGACGAGGTGTCTGTTGAGGCACTTGT 518  
 Db 384 GAAAGAGAGACAGTACTGTCTATCCGACAGGTGTGTCTTTGAAGGATCTGCG 443  
 Qy 519 GTTCTACAGCCA 530  
 Db 444 CTTCTACTCCCA 455

RESULT 9

US-09-235-076-9667/C  
 Sequence 9667, Application US/09235076  
 GENERAL INFORMATION:

APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/235, 076  
 CURRENT FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 9667  
 LENGTH: 470  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(470)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-235-076-9667

Query Match 7.8%; Score 126.5; DB 4; Length 470;  
 Best Local Similarity 57.3%; Pred. No. 1.5e-17;  
 Matches 246; Conservative 0; Mismatches 180; Indels 3; Gaps 1;

Qy 360 AGATGCTTGTATGATGATTTGATGACAGGACTGTGAAGAACATCTGTGAGGCAAAAC 419  
 Db 470 AGATGCTTGTGACTGTGACCTCATCATTTCCACCTTCMAAGACTGAAGGAGAAAG 411  
 Qy 420 GGTGAGAGTCCCACTATATTTTGTGACACACTCAAGGTTACAGAGACACAGGTGT 479  
 Db 410 TGTCAAGTCCCACTTATATCTTCAACAGCAGAGCGGAAAGAGACTGAAAAACT 351  
 Qy 480 CTACCTCGGAGAGTGTCTGTTGAGGCACTTGTGTCTTACAGCAGAGATCCG 539  
 Db 350 GTATGTGCAAAAGTATATCTTTGAGGCACTATAGCCCTTGTCTGAACAAGACTGT 291  
 Qy 540 GGAATGTTCACCTGCGCTCTTGTGTGACACCGAATCCGAGCTCAGGCTGTCTGAG 599

```

Db      290 GGAAGCTCTGGACATGATGATCTTTGTGACACAGACTCCGACATCCGCTGTGATCGCG 231
Qy      600 AGTTCTCCGGAGAGCTGCG---CCAGGGAGAGGACCTTGAGCAATCTGACGAGTACAC 656
Db      230 GCTGCGCCGGGAGATAGTACGAGCGCGCGCGGAGCATGAGGGTGTATCAAGAGTACAA 171
Qy      657 CACCTTGTAAGACCGCGCTTTCAGAGAGTTCGTGCTGCGCAGCAAGAAATGATGCCATGT 716
Db      170 CAAGTTGTCAAGCCCTCTTTCAGCAGTACATTCAGCCACCAACCATGCGCTGGAGACAT 111
Qy      717 GATCATCCCAAGAGAGTGAACATATGTTGCTCATTAACCTGATCTGTGACATCCCA 776
Db      110 CGTGTCTCCCAAGAGAGCGGCAACAGGTGCGCATCGACCTGCTGTGACGCTGTGCA 51
Qy      777 GGACATTTCT 785
Db      50 CGAATTCCT 42

```

# RESULT 10

US-09-516-448-307/c

Sequence 307, Application US/09516448

GENERAL INFORMATION:

APPLICANT: Robison, Keith E.

TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs

FILE REFERENCE: 5800-119

CURRENT APPLICATION NUMBER: US/09/516,448

CURRENT FILING DATE: 2000-02-29

NUMBER OF SEQ ID NOS: 2050

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 307

LENGTH: 5771

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc\_feature

LOCATION: (1)...(5771)

OTHER INFORMATION: n = A,T,C or G

US-09-516-448-307

## Query Match

Best Local Similarity 2.8%; Score 45.4; DB 3; Length 5771;  
Best Local Similarity 52.2%; Pred. No. 0.23;  
Matches 94; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

```

Qy      17 CCTCGGCGCTGGGCGGGCGCGCGCGCGGGAAGGGCGGGCGGGGAGCCCATGCG 76
Db      5694 CCGGGTTGCGGGGCTGCGCGCGCGCGGAGGCGGGGAGCGGGAGCGGTGACG 5635
Qy      77 CGGAGCGGAGGCGGAGATGCTTCCGCGGAGGCGGAAGCTGCGAGAGCCCGCGCGCG 136
Db      5634 CNGGGAAGGGGGGAGCGCAGAGGAGGCGCGCGCGGAGAGGCGGAGCCCGCCCT 5575
Qy      137 AGCCGCAACGTCGCGCAGCGGCGCTTCTGATAGGGGTGAGCGGCGGCACTGCCAGCG 196
Db      5574 AGACGAGAGTGGCGCGCGAGCGGAGCGGAGCGGCGGGGGCGGACTCTGAGCGAGCG 5515

```

## RESULT 11

US-09-488-725B-769

Sequence 769, Application US/09488725B

GENERAL INFORMATION:

APPLICANT: Yuanhua T. Tang

APPLICANT: John Tillinghast

APPLICANT: Ankura Sanku

APPLICANT: Chenghua Liu

TITLE OF INVENTION: Novel Configs Obtained

FILE REFERENCE: 784

CURRENT APPLICATION NUMBER: US/09/488,725B

CURRENT FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 09/004,182

PRIOR FILING DATE: 1998-01-07

```

; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_CT_genes Version 1.01
; SEQ ID NO 769
; LENGTH: 4975
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2)...(4975)
; OTHER INFORMATION: similar to g15689519 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTXY 3.3c00, default parameters
US-09-488-725B-769

```

Query Match 2.8%; Score 45.2001; DB 1; Length 4975;  
Best Local Similarity 55.8%; Pred. No. 0.25;  
Matches 86; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

```

Qy      1 GTGGGATGCTCCGACCTCGGCGCTGGGCGGGCGCGCGCGGAGAGGGCGGGC 60
Db      33 GTGCCCCCGCCCGCCGTACCGGACGCGCGCGCGCGGAGCGGAGCGGAGCGGCGG 92
Qy      61 GCGGGAGCCCGATGCGCGGAGCGGAGCGCGGATGCTTCCGCGGAGCGGAGACTGC 120
Db      93 GCGGGCGCGCGGAGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 152
Qy      121 GAGAGCCCGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 154
Db      153 GGGCGCGCGGTTGCGGGGCTCGGTGCGGCTCC 186

```

## RESULT 12

US-09-488-725B-966

Sequence 966, Application US/09488725B

GENERAL INFORMATION:

APPLICANT: Yuanhua T. Tang

APPLICANT: John Tillinghast

APPLICANT: Ankura Sanku

APPLICANT: Chenghua Liu

TITLE OF INVENTION: Novel Configs Obtained

FILE REFERENCE: 784

CURRENT APPLICATION NUMBER: US/09/488,725B

CURRENT FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US 09/004,182

PRIOR FILING DATE: 1998-01-07

PRIOR APPLICATION NUMBER: US 09/034,341

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 09/045,400

PRIOR FILING DATE: 1998-03-20

PRIOR APPLICATION NUMBER: US 09/321,214

PRIOR FILING DATE: 1999-05-26

PRIOR APPLICATION NUMBER: US 09/131,598

PRIOR FILING DATE: 1998-08-10











Qy 68 CCCGATCGCGGAGCGGAGCCCGAGATGCTTCGGCGGAGCGGAG 115  
 Db 800 TAGCAGACGCGGTAGCAGTGGCGGCGGTGCGGTAGCGGTAGCGGAG 847

RESULT 20  
 US-09-488-725B-292/c  
 ; Sequence 292, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghaast  
 ; APPLICANT: Ankura Sinku  
 ; APPLICANT: Chenghua Liu  
 ; APPLICANT: Radoje T. Drmanac  
 ; TITLE OF INVENTION: Novel Configs Obtained  
 ; FILE REFERENCE: 784  
 ; CURRENT APPLICATION NUMBER: US/09/488,725B  
 ; CURRENT FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/034,341  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 09/045,400  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/321,214  
 ; PRIOR FILING DATE: 1999-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/131,598  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: US 09/170,294  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: US 09/179,473  
 ; PRIOR FILING DATE: 1998-10-27  
 ; PRIOR APPLICATION NUMBER: US 09/181,430  
 ; PRIOR FILING DATE: 1998-10-28  
 ; PRIOR APPLICATION NUMBER: US 09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; PRIOR APPLICATION NUMBER: US 09/234,611  
 ; PRIOR FILING DATE: 1999-01-22  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10289  
 ; SOFTWARE: pt\_ct\_genes Version 1.01  
 ; SEQ ID NO 292  
 ; LENGTH: 825  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (72)....(825)  
 ; OTHER INFORMATION: similar to g15174770 in the genepept database release 114,  
 ; US-09-488-725B-292

Query Match 2.3%; Score 37.8; DB 1; Length 825;  
 Best Local Similarity 50.9%; Pred. No. 7.7;  
 Matches 112; Conservative 0; Mismatches 102; Indels 6; Gaps 1;  
 Qy 17 CCTCGGCGTGGCGGCGCGCGCGCGGGAAGGCGGCGCGCGGAGCCCGATGCG 76  
 Db 565 CCCAGAGACTGGGGGAGACTCCAGCCCGGGAACCTGCTGGGAGGCGAGTGG 506  
 Qy 77 GGGGAGCGGAGCGGAGATGCTTCGGCGGAGGAGGAGACTGCGAGAGCCCGCGCGCG 136  
 Db 505 CTGGTGCAGCCCCCGGTTGCTCTGGGTGCATCGGAGGCTTCAGAGCTGCCCCAGAGG 446  
 Qy 137 AGGCCGACCGTCCGACGACGCGGCGCTT-----CCTGATAGGGGTGAGCGCGGCACTG 190  
 Db 445 GGGAGAGCTTCACTTCCCGGAGAGCATGCGAGGCGCTTGAGAGAGGCTTTGGCAGTCC 386  
 Qy 191 CCAAGGGAAGTGCACCGTGTGTGAGAGATCATGAGAGTT 230  
 Db 385 CTCTGGGGAATCCCTCTGAGTGGGAGTGGAGGAGATT 346

RESULT 21  
 US-09-488-725B-891  
 ; Sequence 891, Application US/09488725B

; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghaast  
 ; APPLICANT: Ankura Sinku  
 ; APPLICANT: Chenghua Liu  
 ; APPLICANT: Radoje T. Drmanac  
 ; TITLE OF INVENTION: Novel Configs Obtained  
 ; FILE REFERENCE: 784  
 ; CURRENT APPLICATION NUMBER: US/09/488,725B  
 ; CURRENT FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/034,341  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 09/045,400  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/321,214  
 ; PRIOR FILING DATE: 1999-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/131,598  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: US 09/170,294  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: US 09/179,473  
 ; PRIOR FILING DATE: 1998-10-27  
 ; PRIOR APPLICATION NUMBER: US 09/181,430  
 ; PRIOR FILING DATE: 1998-10-28  
 ; PRIOR APPLICATION NUMBER: US 09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; PRIOR APPLICATION NUMBER: US 09/234,611  
 ; PRIOR FILING DATE: 1999-01-22  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10289  
 ; SOFTWARE: pt\_ct\_genes Version 1.01  
 ; SEQ ID NO 891  
 ; LENGTH: 1041  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (208)....(1011)  
 ; OTHER INFORMATION: similar to g13858883 in the genepept database release 114,  
 ; US-09-488-725B-891

Query Match 2.3%; Score 37.8; DB 1; Length 1041;  
 Best Local Similarity 54.7%; Pred. No. 7.7;  
 Matches 75; Conservative 0; Mismatches 62; Indels 0; Gaps 0;  
 Qy 4 GGGTGGCTCGACTCGCGCTGGCGGCGCGCGCGCGGGAAGGCGGCGCGCG 63  
 Db 435 GCGGGCGCTGCTCTTAACCGGGGCGGGGTCCGAGCGCGCGCGGAGCGGCGG 494  
 Qy 64 GGGACCCATGCGCGGAGCGGAGCGCGAGTGGCTTCGGCGGAGGCGGAGACTGCGAG 123  
 Db 495 GGGAGACACTGGGCTGTAGAGGCGCGGAGGCTCAAGCGGCGGAGCGAGCGGAGG 554  
 Qy 124 AGCCCGCGCGGAGGCG 140  
 Db 555 AGCTGCGCTGCAGGCGC 571

RESULT 22  
 US-09-488-725B-3303  
 ; Sequence 3303, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghaast  
 ; APPLICANT: Ankura Sinku

```

APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Contigs Obtained
TITLE OF INVENTION: From Various Libraries
FILE REFERENCE: 784
CURRENT APPLICATION NUMBER: US/09/488,725B
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE: pc_ct_genes Version 1.01
SEO ID NO 3819
LENGTH: 4134
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (4136)...(639)
OTHER INFORMATION: similar to g11504026 in the genepept database release 114
OTHER INFORMATION: Run with FASTXY 3.3ct00, default parameters
US-09-488-725B-3819

```

Query Match	2.3%	Score 37.2;	DB 1;	Length 4134;
Best Local Similarity	47.1%	Pred. No. 10;		
Matches 114;	Conservative	0;	Mismatches 128;	Indels 0;
			Gaps	0
QY	395	TGAAGAACATCGTGGAGGGCAAAACGGTGGAGGTCCGACCTATGATTTTGTGACACT	454	
DB	1050	TGCGGTACCTGGAGGCGGGCGGAGGGGTGTCTACCCGCTGCAGAGCGCGCGGAGCG	991	
QY	455	CAAGGTTACAGAGACACACGGTGTCTACCTGCGGACGTGGTTCTGTTTGAAGGCAATCT	514	
DB	990	GGTCAGAGAAATCCCGAGTTGTGTCCACGATTCGAACTCGGACCTAAGAGAGGCGCTCCG	931	
QY	515	TGTGTCTTACAGCCAGAGAGATCCGGGACATTTTCCACTGGCGCTTTCGAGGACACCG	574	
DB	930	AGCTGCTCTCTCATCGAGGCGCAATGCGCTGGGCACTCACTTCTCTGGACGACGACG	871	
QY	575	ACTCCGAGCTCAGGCTGTCTCGAAGATTCTCCGGACGTGGCGCCGAGGAGAGGACCTGG	634	
DB	870	AGAGCGAGCGCACTTAAGGTGGCTTCTGGACGCCACAGCGCGCAGTAGAGGACAGCTGG	811	
QY	635	AG 636		
DB	810	AG 809		

RESULT24  
US-09-488-725B-7170/C  
; Sequence 7170, Application US/09488725B  
; GENERAL INFORMATION:  
; APPLICANT: Yvanhua T. Tang  
; APPLICANT: John Tillinghaast  
; APPLICANT: Ankura Sinks

```

? APPLICANT: Chenhua Liu
? APPLICANT: Radoje T. Drmanac
? TITLE OF INVENTION: Novel Contigs Obtained
? TITLE OF INVENTION: From Various Libraries
? FILE REFERENCE: 784
? CURRENT APPLICATION NUMBER: US/09/488,725B
? CURRENT FILING DATE: 2000-01-21
? PRIOR APPLICATION NUMBER: US 09/004,182
? PRIOR FILING DATE: 1998-01-07
? PRIOR APPLICATION NUMBER: US 09/034,341
? PRIOR FILING DATE: 1998-02-13
? PRIOR APPLICATION NUMBER: US 09/045,400
? PRIOR FILING DATE: 1998-03-20
? PRIOR APPLICATION NUMBER: US 09/321,214
? PRIOR FILING DATE: 1999-05-26
? PRIOR APPLICATION NUMBER: US 09/131,598
? PRIOR FILING DATE: 1998-08-10
? PRIOR APPLICATION NUMBER: US 09/170,294
? PRIOR FILING DATE: 1998-10-13
? PRIOR APPLICATION NUMBER: US 09/179,473
? PRIOR FILING DATE: 1998-10-27
? PRIOR APPLICATION NUMBER: US 09/181,430
? PRIOR FILING DATE: 1998-10-28
? PRIOR APPLICATION NUMBER: US 09/235,076
? PRIOR FILING DATE: 1999-01-20
? PRIOR APPLICATION NUMBER: US 09/234,611
? PRIOR FILING DATE: 1999-01-22
? Remaining Prior Application data removed - See File Wrapper or PALM.
? NUMBER OF SEQ ID NOS: 10289
? SOFTWARE: pc CT_genes Version 1.01
? SEQ ID NO 7170
? LENGTH: 2303
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1270)...(794)
? OTHER INFORMATION: similar to gi37481 in the genepept database release 114,
? OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
? US-09-488-725B-7170

```

```

Query Match      2.2% ; Score 36.5 ; DB 1, Length 2303;
Best Local Similarity 52.0% ; Pred. No. 14;
Matches 104; Conservative 0; Mismatches 95; Indels 1; Gaps 1,

QY      11 CTCCGACCTCGGCCCTTGCGCGGGCGCGCCCGGGACC CGGGGAAGGGCGGGCGCGGGACCC 70
Db       1625 CTTGTGCCTTCGCGCGGCGAAGGGCGCGCCCGCAACCCGGGGCCGGAAAGGTGCGAGGGGCTC 1566

QY       71 GATCGCGCGGAGCGGAGGCGGAGTGGCTTTCGCGGGAGGCGGAAGA CTGCGAGAGCCCCG 130
Db       1565 CGGGCGGCGGGCGGGCGCACACCATCCCGCGGGCGGCGGAGCCGCGACAG -CGCG 1507

QY      131 CGCCGAGAGCCGGAACCTCCGCAACAACGCGGCCCTTCTCATATGGGGTGAAGCGCGGACTG 190
Db       1506 CGAGAGGAGACCGGGCGGTGTGCGGGCGGCGGACCGGATGAAAGGAGCGCGGTGACTGTCTC 1447

QY      191 CCAGCGGGAATGCAACCGTG 210
Db       1446 CTTGAGCGCGGAGGGGCGAG 1427

RESULT 25
US-09-488-725B-6720/c
; Sequence 6720, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinhuast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries

```

```

1 FILE REFERENCE: 784
2 CURRENT APPLICATION NUMBER: US/09/488,725B
3 CURRENT FILING DATE: 2000-01-21
4 PRIOR APPLICATION NUMBER: US 09/004,182
5 PRIOR FILING DATE: 1998-01-07
6 PRIOR APPLICATION NUMBER: US 09/034,341
7 PRIOR FILING DATE: 1998-02-13
8 PRIOR APPLICATION NUMBER: US 09/045,400
9 PRIOR FILING DATE: 1998-03-20
10 PRIOR APPLICATION NUMBER: US 09/331,214
11 PRIOR FILING DATE: 1999-05-26
12 PRIOR APPLICATION NUMBER: US 09/131,598
13 PRIOR FILING DATE: 1998-08-10
14 PRIOR APPLICATION NUMBER: US 09/170,294
15 PRIOR FILING DATE: 1998-10-13
16 PRIOR APPLICATION NUMBER: US 09/179,473
17 PRIOR FILING DATE: 1998-10-27
18 PRIOR APPLICATION NUMBER: US 09/181,430
19 PRIOR FILING DATE: 1998-10-28
20 PRIOR APPLICATION NUMBER: US 09/235,076
21 PRIOR FILING DATE: 1999-01-20
22 PRIOR APPLICATION NUMBER: US 09/234,611
23 PRIOR FILING DATE: 1999-01-22
24 Remaining Prior Application data removed - See File Wrapper or PALM.
25 NUMBER OF SEQ ID NOS: 10289
26 SOFTWARE: pt CT_genes Version 1.01
27 SEQ ID NO 6720
28 LENGTH: 2864
29 TYPE: DNA
30 ORGANISM: Homo sapiens
31 FEATURE:
32 NAME/KEY: misc_feature
33 LOCATION: (44)..(2252)
34 OTHER INFORMATION: similar to gi805095 in the genepept database release 114
35 OTHER INFORMATION: Run with FASTXY 3.3c00, default parameters
36 US-09-488-725B-6720

```

```

Query Match      2.2%; Score 36.4; DB 1; Length 2864;
Best Local Similarity 54.5%; Pred. No. 15;
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY      9  GCCTCCGACCTCGGCGCTGGGCGGCGCGCGCGCGCGGAGAGGCGCGCGCGGAGC 68
Db      145 GCTGCTCTCGCGCGCGCGCGCTCCCTTACTGTGCGGCGCGCGCGCGGAGGCGGAGAC 86

QY      69  CCGATGCGCGGAGCGGAGGCGCGAGATGGCTTTCGCGGAGCGGAAGACTGCGAGAGCCC 128
Db      85  CCGGCGCGCGCGCGCGAGTGGGGCGAGGCGCGCGCTGAGCGGAGCGAGCGAGGAGGCG 26

QY      129 CGGCGCGGAGGCGCG 142
Db      25  GCGCGCGCGGAGCGCG 12

RESULT 26
US-09-488-725B-7063/C
; Sequence 7063, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dymnac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400

```

```

RESULT 27
US-09-516-448-1266/C
; Sequence 1266: Application US/09516448
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/516.448
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: PasteSeq for Windows Version 3.0
; SEQ ID NO 1266
; LENGTH: 320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1) .. (320)
; OTHER INFORMATION: n = A,T,C or G
US-09-516-448-1266

Query Match      2.2%   Score 35.9, DB 3, Length 320
Best Local Similarity 57.6%   Pred. NO. 19,

```

Query Match	2.2%	Score 35.8	DB 3	Length 1176
Best Local Similarity	56.3%	Pred. No. 19		
Matches	67	Conservative	0	Indels 52
				Gaps 0
QY	22	GCGCTGGGCGGGCGCGCCGGGCGCGGGAAGCTGCGCGCGGGA	81	
DB	347	GGGCCCGGGGCAAGGCGCGCGGGAGGAACTCAAGTAAAGCGCGCGGAGCCCGGGA	288	
QY	82	GCGAGGCGCGAAGATGCTTCGCGCGGAGCGCAAGCTCGAAGCGCCCGCGGAGCGC	140	
DB	287	GCGGAGGCTGGAACGCTGAGCGGGCGCTGCGCCACCGAAGCGCGCCCGGAGCGGGAGC	229	

RESULT 29  
US-09-488-725B-8488  
Sequence 8488, Application US/09488725B  
GENERAL INFORMATION:  
APPLICANT: Yuanhua T. Tang  
APPLICANT: John Tillinghast  
APPLICANT: Ankura Sanku  
APPLICANT: Changhua Liu  
APPLICANT: Radolje T. Dmanac  
TITLE OF INVENTION: Novel Contigs Obtained  
TITLE OF INVENTION: From Various Libraries  
FILE REFERENCE: 784  
CURRENT APPLICATION NUMBER: US/09/488, 725B  
CURRENT FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 09/004, 182  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 09/034, 341  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 09/045, 400  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: US 09/321, 214  
PRIOR FILING DATE: 1999-05-26  
PRIOR APPLICATION NUMBER: US 09/131, 598  
PRIOR FILING DATE: 1998-08-10



```

; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 6268
; LENGTH: 8872
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(8873)
; OTHER INFORMATION: n = a,t,c or g
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (170)...(5244)
; OTHER INFORMATION: similar to g1212917 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-6268

```

```

Query Match          2.2%; Score 35.8; DB 1; Length 8872;
Best Local Similarity 54.1%; Pred. No. 19;
Matches 73; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

```

```

QY 151 CACGAGCGGCGCTTCTGATAGGGGTGAGCGCGGCACTGCGCAAGGAGTCCAGCCGTG 210
Db 1427 CTCACAGAGCGCATCTTTGTTCGCCCGGCGAGCGAGGACCATTTGAAAGCTGAAGAA 1486
QY 211 TGTGAGAAATCATGAGTTGCTGGAGACAGACAGGTGGAACAGCGGACGGAAGCTG 270
Db 1487 ACAGAGAAATCATGAGTCTGAGCTCAATGAGACTGTGGAGAGAAAGTGGCGGACAGAA 1546
QY 271 GTGATCTGAGCCG 285
Db 1547 GCCATCCGATGGAG 1561

```

```

RESULT 32
US-09-488-725B-2990/c
; Sequence 2990, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289

```

```

; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 2990
; LENGTH: 2432
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)...(2320)
; OTHER INFORMATION: similar to g14589628 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-2990

```

```

Query Match          2.2%; Score 35.6999; DB 1; Length 2432;
Best Local Similarity 48.7%; Pred. No. 20;
Matches 150; Conservative 0; Mismatches 153; Indels 5; Gaps 2;

```

```

QY 28 GCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 87
Db 638 GGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 579
QY 88 GCGGAGATGCTTCTGCGCGGAGCGGAGACTGCGGAGGCGCC-----GCGCGGAGGCGGA 143
Db 578 ACCGGGGGTGGCGGGGGCGGGGCGGCGGAGAGAGAGCCCGAGGGGCTGGGCTCA 519
QY 144 CCGTCCGACACAGCGGCGCTTCTGATAGGGGTGAGCGCGGCGGCACTGCGGAGAAATC 203
Db 518 GCGCGGAGAGGCTGCGCGGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 459
QY 204 GACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 263
Db 458 GA-CATGGGGGAGGAGGAGGCTGACAGAGCTGGGGCTGAGAGCCGGCGGTGCGGCCCA 400
QY 264 GAAGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 323
Db 399 CCGGGGCGCGGAGGTTCTGCGCGGCGGCGGAGTGAATCTGTGGGCGGCGGCGGCGG 340
QY 324 CAAGGCGCT 331
Db 339 GAGAGACT 332

```

```

RESULT 33
US-09-488-725B-3659/c
; Sequence 3659, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289

```









```

; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/119,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc CT_genes Version 1.01
; SEQ ID NO 3800
; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4305)..(2761)
; OTHER INFORMATION: similar to gi1054874 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-3800
```

```

Query Match          2.1%; Score 34.9; DB 1; Length 4308;
Best Local Similarity 50.2%; Pred. No. 29;
Matches 110; Conservative 0; Mismatches 106; Indels 3; Gaps 1;
```

```

QY 53 GGGCGGGCGCGGAGACCCGATGCGCGGAGCGGAGCGCGGAGATGCTTCGCGGAGAGCGG 112
DB 4007 GTGTGACCTTGAGAACCGCTGCCAGAGCCCTGACAGAGAGCTGACTTCGCGAAGAG-- 3950

QY 113 AAGACTGCGAGAGCCCGCGCGCGGAGCGGAGCGCGGAGATGCTTCGCGGAGAG 172
DB 3949 -TGTTCTGAGAGAGAGAGTGTGCGAGAGCGCGCGCGGAGCGCGCTGTGTGAGG 3891

QY 173 GGGTGAAGCGGCGGCACTGCCAGCGGAGAGTGCAGCCGTGTGTGAGAGATCATGAGATTGC 232
DB 3890 TGGACACAGAGCGGAGAGAGAGTACGACTTCAGAGATGCGACAGCGCTGAGAGAGCTGC 3831

QY 233 TGGACACAGAGCGGAGAGTGCAGCGGAGCGGAGAGGTTG 271
DB 3830 GAGCCAGACGACGAGAGAGAGTGCAGCGCTCTCAAGCTGG 3792
```

```

RESULT 42
US-09-488-725B-6580/c
; Sequence 6580, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sinks
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: From Various Libraries
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
```

```

; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc CT_genes Version 1.01
; SEQ ID NO 6580
; LENGTH: 2585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (220)..(1654)
; OTHER INFORMATION: similar to gi516381 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-6580
```

```

Query Match          2.1%; Score 34.8; DB 1; Length 2585;
Best Local Similarity 53.7%; Pred. No. 30;
Matches 72; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
```

```

QY 28 GGGCGGGCGCGCGGAGAGGAGCGCGGAGACCCGATGCGCGGAGCGGAG 87
DB 188 GCGCGGAGCGGAGACAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 129

QY 88 GCGGAGATGCTTCGCGGAGAGCGGAGAGTGCAGAGCGCGCGGAGCGCGGAGCGCGGAGCGG 147
DB 128 CGCGGGGGGGCGCGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 69

QY 148 CCGCAGCAGCGGCGC 161
DB 68 CCGCAGGCTCGGCG 55
```

```

RESULT 43
US-09-488-725B-2608
; Sequence 2608, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sinks
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: From Various Libraries
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
```

```

RESULT 44
US-09-488-725B-6750/c
Sequence 6750, Application US/09488725B
GENERAL INFORMATION:
APPLICANT: Yuanhua T. Tang
APPLICANT: John Tillinghast
APPLICANT: Ankura Sinks
APPLICANT: Chenguha Liu
APPLICANT: Radote T. Drmanac
TITLE OF INVENTION: Novel Configs Obtained
FILE REFERENCE: From Various Libraries
CURRENT APPLICATION NUMBER: US/09/488,725B
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remaining Prior Application data removed - See File Wrapper or PALM.
SOFTWARE OF SEQ ID NOS: 10289
SEQ ID NO 6750
LENGTH: 2026
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (16)...(1867)

```

Db 941 GGGACACCGGGTCCGAGGC 922

US-09-488-725B-5404

```

Matches      71; Conservative      0; Mismatches      61; Indels      0; Gaps      0;

```

QY	28	GGGGGGGGCGCCCGGGCCCGGGGAAGGGGCGGGCGCGGGGACCCGATGCGGGAGCGGAG	87
Db	371	GGCGACCGAAGCGGAGCTGGGGCCGGGGACGGCGGGCGGGCGGACGGCG	430
QY	88	GCCGAGATGGCTTCGGCGGGAGGCGAAGACTGCGAGAGCCCGCGCCGAGGCCGACCGT	147
Db	431	GGGGCGCGGGGTGGGATGGGTGCGACAGCGTGCAGATCTCCGACAGGGGGGTGTGGGC	490
QY	148	CCGCACCAAGCGG	159
Db	491	CGCGCTCAGCGG	502

Search completed: December 11, 2003, 23:48:24  
 Job time : 28715 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: December 12, 2003, 10:34:41 ; Search time 16 Seconds

(Without alignments)  
1199.346 Million cell updates/sec

Title: us-09-896-522-2

Perfect score: 1450  
Sequence: 1 MASAGDESPAPADRP.....HPGMLTSGKSHLESSRPH 277

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.1  
Ygapop 10.0 , Ygapext 0.1  
Fgapop 6.0 , Fgapext 0.1  
Delop 6.0 , Delext 0.1

Searched: 51343 seqs, 34638147 residues

Total number of hits satisfying chosen parameters: 102686

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=xlh -Q=us-09-896-522-2 -DB=\*seq -SUFFIX=p2n  
-OUT=align2\_nuc -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1  
-END=1 -MATRIX=DIOSUM62 -TRANS=human40.cdi -LIST=45 -DOCALLION=200  
-THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=45 -MODE=LOCAL -OUTFMT=pco  
-NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -ICPU=3 -NO\_XLPHY  
-NRG\_SCORES=0 -DSPBLOCK=100 -LONGLOG -DRV TIMEOUT=120 -WARN TIMEOUT=30  
-THREADS=1 -KAPOP=10 -XGAPEXT=0.1 -FGAPOP=6 -FGAPEXT=0.1 -YGAPOP=10  
-YGAPEXT=0.1 -DELOP=6 -DELXT=0.1

Database :

\*seq:\*  
1: /home/sdavid/sdavid-tmp/dectemp/swope522/US09488725B.seq:\*  
2: /home/sdavid/sdavid-tmp/dectemp/swope522/6579708.seq:\*  
3: /home/sdavid/sdavid-tmp/dectemp/swope522/US09516448.seq:\*  
4: /home/sdavid/sdavid-tmp/dectemp/swope522/US09235076.seq:\*  
5: /home/sdavid/sdavid-tmp/dectemp/swope522/PCUUS0005988.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1450	100.0	834	2	US-09-536-647-1
2	1450	100.0	2152	1	US-09-488-725B-7130
3	1443.9	99.6	1648	3	US-09-516-448-2048
4	951.4	65.6	1310	5	PCT-US00-05988-220
5	904.3	62.4	1316	1	US-09-488-725B-6367
6	727.9	50.2	472	4	US-09-235-076-30379
7	559.6	38.6	452	4	US-09-235-076-24042
8	527.9	36.4	455	4	US-09-235-076-23923
9	384.9	26.5	470	4	US-09-235-076-9667
10	315.7	21.8	2659	1	US-09-488-725B-6890
11	304.3	21.0	5773	1	US-09-488-725B-6460
12	302.3	20.8	5276	1	US-09-488-725B-5593
13	300	20.7	2349	1	US-09-488-725B-7018
14	298.1	20.6	6050	1	US-09-488-725B-4307
15	298.1	20.6	6057	1	US-09-488-725B-8411

16	297.9	20.5	2124	1	US-09-488-725B-7320	Sequence 7320, Ap
17	297.6	20.5	4558	1	US-09-488-725B-8009	Sequence 8009, Ap
18	295.7	20.4	2932	1	US-09-488-725B-5757	Sequence 5757, Ap
19	294.1	20.3	6506	1	US-09-488-725B-4967	Sequence 4967, Ap
20	293.7	20.3	6506	1	US-09-488-725B-4967	Sequence 4967, Ap
21	293.6	20.2	2996	1	US-09-488-725B-5251	Sequence 5251, Ap
22	291.8	20.1	2782	1	US-09-488-725B-8306	Sequence 8306, Ap
23	291.8	20.1	4254	1	US-09-488-725B-6550	Sequence 6550, Ap
24	291.6	20.1	5059	1	US-09-488-725B-3853	Sequence 3853, Ap
25	291.2	20.1	8435	1	US-09-488-725B-6204	Sequence 6204, Ap
26	291.1	20.1	4182	1	US-09-488-725B-6655	Sequence 6655, Ap
27	290	20.0	3629	1	US-09-488-725B-8160	Sequence 8160, Ap
28	289.4	20.0	4453	1	US-09-488-725B-8644	Sequence 8644, Ap
29	289.1	19.9	3073	1	US-09-488-725B-7478	Sequence 7478, Ap
30	288.3	19.9	3918	1	US-09-488-725B-5709	Sequence 5709, Ap
31	287.4	19.8	4593	1	US-09-488-725B-5625	Sequence 5625, Ap
32	287.3	19.8	3022	1	US-09-488-725B-5785	Sequence 5785, Ap
33	286.9	19.8	4188	1	US-09-488-725B-4150	Sequence 4150, Ap
34	286.5	19.8	2915	1	US-09-488-725B-3474	Sequence 3474, Ap
35	286.3	19.7	4461	1	US-09-488-725B-3363	Sequence 3363, Ap
36	286.3	19.7	7502	1	US-09-488-725B-3360	Sequence 3360, Ap
37	285.9	19.7	4975	1	US-09-488-725B-769	Sequence 769, App
38	285.9	19.7	4975	1	US-09-488-725B-966	Sequence 966, App
39	285.9	19.7	4975	1	US-09-488-725B-1107	Sequence 1107, Ap
40	285.8	19.7	3925	1	US-09-488-725B-5599	Sequence 5599, Ap
41	285	19.7	5195	1	US-09-488-725B-3427	Sequence 3427, Ap
42	285	19.7	6941	1	US-09-488-725B-6263	Sequence 6263, Ap
43	284.9	19.6	4927	1	US-09-488-725B-6173	Sequence 6173, Ap
44	284.6	19.6	2340	1	US-09-488-725B-6286	Sequence 6286, Ap
45	284.6	19.6	7431	1	US-09-488-725B-6100	Sequence 6100, Ap

#### ALIGNMENTS

```

RESULT 1
US-09-536-647-1
; Sequence 1, Application US/09536647
; Patent No. 6579708
; GENERAL INFORMATION:
; APPLICANT: Ho, Yen Sen
; TITLE OF INVENTION: No. 6579708el Human Uridine Kinase
; FILE REFERENCE: GP50020
; CURRENT FILING DATE: 2000-03-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 834
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(780)
US-09-536-647-1

Alignment Scores:
Pred. No.: 1.2e-35
Score: 1450.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 2
Gaps: 0

us-09-896-522-2 (1-277) x US-09-536-647-1 (1-834)
QY 1 MetAlaSerAlGlglyGluaspCygsGluSerProAlaProGluAlaaspArgProHis 20
Db 1 ATGGCTTCGAGCGGAGCGAAGCTGCGAGAGCCCGCGAGGCCACGTCGCGAC 60
QY 21 GlnArgProPheLeuIleGlyValSerGlyThrAlaSerGlyLysSerThrValCys 40
Db 61 CAGCGCCCTTCTCTATAGGGGTGAGCGGCGGACGTCGACAGCGGAGAAAGTCGACCGTGTGT 120

```

```

QY 41 GtulyseillemetGtuleuLeuglyGlnbengluValGluGlnatrgGlnatrglyValVal 60
Db 121 GAGAAAGTACATGAGGTTGCTGGACAGAACAGGTTGAAACGGCGACGGAGAGTGGTC 180
QY 61 lIleuSerGlnaSPaRgPheTyTlyValValLeuThraIagluGlnlyValAlaValAla 80
Db 181 ATCTGACCCAGACAGGTTCTTCAAGGTCCTTGACCGAGACAGAACAGGCGCCCTTG 240
QY 81 LysGlyGlnTyraenPheAspPheProAspAlaPheAspAsnAspLeuMetHisArgThr 100
Db 241 AAAGACAGTACAAATTTGACCATTCAGATGCTTTGACAAATGATTTGATGACACAGACT 300
QY 101 LeuLysAsnIleValGluGlyLysThrValGluValProThyTyraAspPheValThHis 120
Db 301 CTGAAGAACATCGTGAGAGGCGAAACGGTGAAGGTGGCGACCTGATGATTTTGACACAC 360
QY 121 SerArgLeuProGluThrThrValValTyraProAlaAspValValLeuPheGluGlyIle 140
Db 361 TCAAGGTTACCAAGAACACCGGTGGTCTACCTCGGACGTTGCTTTGAGGAGCATC 420
QY 141 LeuValPheTyraenGlnGluIleArgAspMetPheHisLeuArgLeuPheValAspThr 160
Db 421 TTGGTGTCTACAGCCAGAGAGATCCGGGACATGTTCCACTGGCGCTCTTGAGACACC 480
QY 161 AspSerAspValArgLeuSerArgArgValLeuArgAspValArgArgGlyArgAspLeu 180
Db 481 GACTCCGACGTGAGCGGTCTCTGAGAGAGTTCTCCGGACGTCGGCGGAGGAGGACTCG 540
QY 181 GluGlnIleLeuThraGlnTyraThrPheValLysProAlaPheGluGluPheCysLeu 200
Db 541 GAGCAGATTCAGACCGCATACACACTTCTGTAAGCGCGCTTGAGAGATTCCTGCTG 600
QY 201 ProThyLysTyraIleAspValIleIleProArgGlyValAspAsnMetValAlaIle 220
Db 601 CCGACAAAGAGTATGCGATGTGATCCACAGAGAGTGACAAATATGTTGCCATC 660
QY 221 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysLysTyraHisArg 240
Db 661 AACCTGATCGTGACAGCATCAGACACATCTGAAATGTGACATCTGAAATGTGACACGA 720
QY 241 GlyLysSerAsnGlyArgSerTyraArgThraPheSerGluProGluAspHisProGly 260
Db 721 GGAAGGTCATATGGCGGAGCTACAGCGGACCTTTTCTGAGCCAGGAGACACCTTGG 780
QY 261 MetLeuThraSerGlyLysArgSerHisLeuGlnSerSerSerArgProHis 277
Db 781 ATGCTGACCTCTGGCAACGGTCACTTTGAGAGTCCAGACAGACCCAC 831

```

```

PRIORITY APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remaining prior application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pc_ct_genes Version 1.01
SEQ ID NO 7130
LENGTH: 2152
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(2153)
OTHER INFORMATION: n = a,t,c or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (110)...(891)
OTHER INFORMATION: similar to g1471981 in the genepept database release 114,
OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-7130

Alignment Scores:
Pred. No.: 1,78e-33 Length: 2152
Score: 1450.00 Matches: 277
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

us-09-896-522-2 (1-277) x US-09-488-725B-7130 (1-2152)
QY 1 MetAlaSerAlaGlyGlyGluAspCysGluSerProAlaProGluAlaAspArgProHis 20
Db 59 ATGGCTTCGGCGGAGGAGCGAAGACTGCGAGAGCCCGCGGAGCGGACCTGCGCAC 118
QY 21 GlnArgProPheLeuIleGlyValSerGlyTyraIleAsnSerGlyLysSerThraValCys 40
Db 119 CAGCGCCCTTCTCTGATAGGAGGTGAGCGCGCATCTCCAGCGGAAAGTGCACCTGTGT 178
QY 41 GtulyseillemetGtuleuLeuglyGlnbengluValGluGlnatrgGlnatrglyValVal 60
Db 179 GAGAAAGTACATGAGGTTGCTGGACAGAACAGGTTGAAACGGCGACGGAGAGTGGTC 238
QY 61 lIleuSerGlnaSPaRgPheTyTlyValValLeuThraIagluGlnlyValAlaValAla 80
Db 239 ATCTGACCCAGACAGGTTCTTCAAGGTCCTTGACCGACAGAACAGGCGCCCTTG 298
QY 81 LysGlyGlnTyraenPheAspPheProAspAlaPheAspAsnAspLeuMetHisArgThr 100
Db 299 AAAGACAGTACAAATTTGACCATTCAGATGCTTTGACAAATGATTTGATGACACAGACT 358
QY 101 LeuLysAsnIleValGluGlyLysThrValGluValProThyTyraAspPheValThHis 120
Db 359 CTGAAGAACATCGTGAGAGGCGAAACGGTGAAGGTGGCGACTATGATTTTGACACACAC 418
QY 121 SerArgLeuProGluThrThrValValTyraProAlaAspValValLeuPheGluGlyIle 140
Db 419 TCAAGGTTACCAAGAACACCGGTGGTCTACCTCGGACGTTGCTTGTGAGGAGCATC 478
QY 141 LeuValPheTyraenGlnGluIleArgAspMetPheHisLeuArgLeuPheValAspThr 160
Db 479 TTGGTGTCTACAGCCAGAGATCCGGACATGTTCCACTTGCGCTTCTTGAGACACC 538
QY 161 AspSerAspValArgLeuSerArgArgValLeuArgAspValArgArgGlyArgAspLeu 180
Db 539 GACTCCGACGTGAGCGGTCTCGAAGAGTTCTCCGGACGTCGGCGGAGGAGGAGACTCG 598

```

```

QY 181 GluGlnIleuThrGlnTyrThrPheValIysProAlaPheGluGluPheCysLeu 200
Db 599 GAGCAATTCGTGACGACGACACCACTTGTGAAGCCGCTTCGAGAGGTTCTGCTG 658
QY 201 ProThrIlySerArgIlyAlaAspValIleIleProArgIlyValAlaAspMetValAlaIle 220
Db 659 CCGACAAAGAGATGATGCCGATGATCATCCCGAGAGAGTGAACAATATGTTGCCATC 718
QY 221 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysIlySTPHISArg 240
Db 719 AACCTGATCGTGAGACATCCAGACATTCGAAATGTCACATCTGCAAAATGCGACCGA 778
QY 241 GlyIlySerAsnGlyArgSerIlyIlyArgIlyThrPheSerGluProGlyAspHisIlyProGly 260
Db 779 GAGGAGTCCATGAGCGGAGCTACAGCGGACCTTTTCTAGCCAGGAGGACCACTTGGG 838
QY 261 MetLeuThrSerGlyIlyArgSerHisIleuGluSerSerArgProHis 277
Db 839 ATCGTACCTCTGCAAGCGTCACATTTGAGTCCAGACGACGACCCAC 889

RESULT 3
US-09-516-448-2048
; Sequence 2048, Application US/09516448
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: Novel Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/516,448
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2048
; LENGTH: 1648
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1648)
; OTHER INFORMATION: n = A,T,C or G
US-09-516-448-2048

Alignment Scores:
Pred. No.: 6 69e-34 Length: 1648
Score: 1443.90 Matches: 277
Percent Similarity: 99.64% Conservative: 0
Best Local Similarity: 99.64% Mismatches: 0
Query Match: 99.58% Indels: 1
DB: 3 Gaps: 0

us-09-896-522-2 (1-277) x US-09-516-448-2048 (1-1648)
QY 1 MetAlaSerAlaGlyIlyGluAspCysGluSerProAlaProGluAlaAspArgProHis 20
Db 84 ATGGCTTCGCGCGGAGGCGAAGACGACGAGCCCGCGCGGAGCGGACCGCTCCGCGAC 143
QY 21 GlnArgProPheLeuIleGlyValIlySerGlyIlyThrAlaSerGlyIlySerThrValCys 40
Db 144 CAGCGGCGCTTCCTGATAGGCGTGAGCGGCGGCGACCTCCAGCGGGAAGTGCACCGTGTG 203
QY 41 GlnValIleMetGluLeuGluGlyIlyAsnGluValGlnGlnArgGlnArgIlyValVal 60
Db 204 GAGAAATCATGTGAGTTCGCGAGACAGAACGAGTGAAGGCGGACCGGAAAGGTGCTC 263
QY 11leuSerGlnAspArgPheIlyIlyValIleuThrAlaGluGlnIlyIlyValIleu 80
Db 264 ATCTTACGCGAGACAGGTTCTTCAAGTCTCTGACGCGACAGACAGGCGGAGCGCTTG 323
QY 81 IySGIlyGlnTyrAsnIleAspHisIlyProAspAlaPheAspAsnAspIleuMetHisIlyArg 100
Db 324 AAAGGACAGTACAAATTTGACATCCAGATGCTTGTGATATGATTTGATGACAGAGACT 383
QY 101 LeuIlyAsnIleValIlyGlyIlyThrValGluValProThrIlyAspPheValThrHis 120

```

```

Db 384 CTGAAGAAATCGTGAAGGGCAAAACGCTGAGAGTCCGACCTATGATTTTGGACACAC 443
QY 121 SerArgLeuProGluThrThrValValIlyThrProAlaAspValIleuPheGluGlyIle 140
Db 444 TCAAGGTACCAAGACCAAGCGGTGTCTACCCCTCGGACCTGTGTTCTGTTGAGGGCATC 503
QY 141 LeuValPheTyrSerGlnGluIleArgAspMetPheHisIleuArgLeuPheValAspThr 160
Db 504 TTGGTGTTCACGACGAGATCCGGACATTTCCACTGCGCTTCTTCTGTGACACC 563
QY 161 AspSerAspValArgLeuSerArgValIleuArgAspValArgArgIlyArgAspLeu 180
Db 564 GACTCCAGAGTACAGGCTGTCTCGAAGATTCCTCGGAGCGTGGCGGAGGAGGACCTG 623
QY 181 GluGlnIleuThrGlnTyrThrPheValIysProAlaPheGluGluPheCysLeu 200
Db 624 GACGACATTCGTGACGACGACACCACTTCTGTAACCGGCTTCAGAGAGTCTGCTG 683
QY 201 ProThrIlySerIlyrAlaAspValIleIleProArgIlyValAlaAspMetValAlaIle 220
Db 684 CCGACAAAGAGATTTGCGATGTGATCATCCACGAGAGTGAACATATGTTGCCAT 743
QY 220 eAsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysIlySTPHISArg 240
Db 744 CAACCTGATCGTACACATCCAGACATTCGAAATGTCACATCTGCAAAATGCGACCG 803
QY 240 gGlyIlySerAsnGlyArgSerIlyIlyArgIlyThrPheSerGluProGlyAspHisIlyProGly 260
Db 804 AGGAGGTCAATAGGCGGAGCTACAGCGGACCTTTCTGAGCCAGGGGACCACTTGG 863
QY 260 yMetLeuThrSerGlyIlyArgSerHisIleuGluSerSerArgProHis 277
Db 864 GATGCTACCTCTGCAAGCGTCACATTTGAGTCCAGACGACGACCCAC 915

RESULT 4
PCT-US00-05988-220
; Sequence 220, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: PA101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; EARLIER FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 220
; LENGTH: 1310
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US00-05988-220

Alignment Scores:
Pred. No.: 1.76e-19 Length: 1310
Score: 951.40 Matches: 198
Percent Similarity: 62.89% Conservative: 24
Best Local Similarity: 56.09% Mismatches: 35
Query Match: 65.61% Indels: 98
DB: 5 Gaps: 2

us-09-896-522-2 (1-277) x PCT-US00-05988-220 (1-1310)
QY 2 AlaSerAlaGlyIlyGluAspCys-----Glu 10
Db 168 GCGGCGCGCGGCGGAGCG-TGCGTCCGTTGCGACAGCGAGCGGAGAGGCGGCGCG 226
QY 11 SerProAlaPro-----GluIlyAspArgPro-----HisGlnArg----- 22
Db 227 GAACCATGCGCGGAGGACAGGACGACGACCTTCAGAACACGACGACGCCAAGCGCGGCG 286

```

```

Qy 23 --ProPheLeuIleGlyValSerGlyThrAlaSerGlyLysSerThrValCysGlu 42
Db 287 AGCCCTCTCTTATAGGCTCAC-GGGGAGACAGCTAGCGGAACTCTTCGTGTGCTA 345
Qy 42 YsIleMetGluLeuLeuGlyGlnAangluValGluGlnArgGlnArgValValIle 62
Db 346 AGATCGTGACGCTCTCGGGGAGATGAGGTGACTATCCGACAGAGAGAGGTGTCTATCC 405
Qy 62 eusSerGlnAspArgPheTyrLysValleuThrAlaGluGlnLysAlaLysLeuLysG 82
Db 406 TGAACCCAGGATAGCTTCTTACCGTGTCTTACCTCGAGGACAAAGCCCAACCTGAGG 465
Qy 82 YglnTyrAsnPheAspHisProAspAlaPheAspAsnAspLeuMetHisArgThrLeu 102
Db 466 SCCGTTCACTTGACCAACCCGATGCTTGTGACATGASTACTTCTCAAAACACTCA 525
Qy 102 YsAenIleValGluGlyLysThrValGluValProThrTyrAspPheValThrHisSer 122
Db 526 AAGAAATCACTGAAGGGAACAGCTCCAGATCCCGGTATGACTTGTCTCCACTTCCC 585
Qy 122 rgleuProGluThrThrValValTyrProAlaAspValValLeuPheGluGlyIleLeu 142
Db 586 GGAAGAGAGACAGTACTGTCTATCCCGACAGCTGTGCTCTTGAAGGAGATCCTGG 645
Qy 142 aPheTyrSerGlnGluIleArgAspMetPheHisLeuArgLeuPheValAspThrAsp 162
Db 646 CTTTCTACTCCAGAGAGTACGAAACCTGTTCCAGATCAACCTTTGTGTGATACAGATG 705
Qy 162 eArAspValArgLeuSerArgArgValleuArgAspVal--ArgArgLysArgAspLeu 181
Db 706 CGGACACCCGGCTCTCAGCAGAGATTAAGGACATCAGCAGAGAGAGGAGGATCTTG 765
Qy 181 YglnIleLeuThrGlnTyrThrThrPheValLysProAlaPheGluGluPheCysLeu 201
Db 766 AGCAGATTTTATCTCAGTACATTCGTTCCGCAAGCCGCTTGAAGAAATTCGTGCTGC 825
Qy 201 rOThrLysLysTyrAlaAspValIleIleProArgGlyValAspAspMetValAlaIle 221
Db 826 CAACAAAGAGTATGCTGATGTATCATCTTAAGAGTGCGAGATATATGTGTGCTCATCA 885
Qy 221 sIleuIleValGlnHisIleGlnAspIleLeuAangluAspIleCysLysTrpHisArg 241
Db 886 ACCATCATGTCACACATCCAGACGACATCTGAATGA-----G 924
Qy 241 YglnYser-AangLysArgSerTyrLysArgThrPheSerGluProGlyAspHisPro 259
Db 925 GGCCCTCCAAACGGCAGAG-----CCATG 948
Qy 260 -----GlyMetLeuThrSerGlyLysArgSerHisLeuGluSerSerSerArgP 276
Db 949 GCTGTCTCAGCGCTACACCCCTTCAACGAAAGAGCAGGATCGAGTCCAGACAGAGC 1008
Qy 276 rOHis 277
Db 1009 CGCAT 1013

```

```

RESULT 5
US-09-488-725B-6367/c
; Sequence 6367, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinhuast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341

```

```

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 6367
; LENGTH: 1316
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1030)...(289)
; OTHER INFORMATION: similar to g1471981 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3f00, default parameters
US-09-488-725B-6367

Alignment Scores:
Pred. No.: 4,85e-18 Length: 1316
Score: 904.30 Matches: 194
Percent Similarity: 61.28% Conservative: 26
Best Local Similarity: 54.04% Mismatches: 39
Query Match: 62.37% Indels: 102
DB: 1 Gaps: 1

us-09-896-522-2 (1-277) x US-09-488-725B-6367 (1-1316)
Qy 2 AlaserIaGlyGluAspCys-----GluS 11
Db 1147 GCGGGCGCGGGGCGGAGCG-TGGTCCGTTCCGACAGCGAGGCGGAGGGCGCG 1089
Qy 11 erProAlaPro---GluAlaAspArgPro-----HisGlnArg----- 22
Db 1088 AACCATGGCGGGGACAGCAGACGACCTTGCAAGACACACAGAGCCCAACGGCGCGCA 1029
Qy 23 -ProPheLeuIleGlyValSerGlyThrAlaSerGlyLysSerThrValCysGlu 42
Db 1028 GCCCTTCTTATAGGCTCAGCGGGGAGACAGCTAGCGGAGAGCTTCCGTTGTGCTTA 969
Qy 42 sIleMetGluLeuLeuGlyGlnAangluValGluGlnArgGlnArgValValIleLe 62
Db 968 GATCGTCACTCTCTGCGGAGATGAGTGTGACTATCCGACAGAGAGGTGTCTCATCT 909
Qy 62 uSerGlnAspArgPheTyrLysValleuThrAlaGluGlnLysAlaLysLeuLysG 82
Db 908 GAGCAGAGATGACTTACCGGTGCTTACCTCGAGCAAGAGCCCAAGCCCTGAAAGG 849
Qy 82 YglnTyrAsnPheAspHisProAspAlaPheAspAsnAspLeuMetHisArgThrLeu 102
Db 848 CAGTTCACTTGACCAACCCGATGCTTGAACATGAATCAATCTTCAAAACACTCA 789
Qy 102 sAenIleValGluGlyLysThrValGluValProThrTyrAspPheValThrHisSer 122
Db 788 AAGAAATCACTGAAGGGAACAGCTCCAGATCCCGGTATGACTTGTCTCCACTTCCG 729
Qy 122 rgleuProGluThrThrValValTyrProAlaAspValValLeuPheGluGlyIleLeu 142
Db 728 GAAGAGAGACAGTACTGTCTATCCGACAGCTGTGTCTCTTGAAGAGATCTGCG 669

```



```

Qy 142 lphetyrserglinglu--lleargaspmecpnehisleuargleuphevalaspthr 161
Db 668 CTCTTACTCCAGGAAGATGACGACGCTGTTCAGATGAAGCTTTTGTGGATACGAT 609
Qy 162 Seraspvalargleuserargvalleuargaspval---Argargglyargasp 180
Db 608 GCCGACACCCGGCTCTCAGCAGAGATTAAGACATCAGCAGAGAGAGGAGGATCTT 549
Qy 181 GluglnlleuThr--GlnTyrThrThr-PheValysProAla-PheglugluPneCy 199
Db 548 GAGCAGATTTTATTCCTCAACATTAACGTTTCCTCAAGCCTTCCTTGAAGATTCG 489
Qy 199 sleuprothrlye-lystyralaaspvalilleleproarg-glyValaaspasn-MetVa 218
Db 488 CTGGCCACCAAGGAAGATATGCTGATGTGATCTCTTACAGAGTGCAGATATCCGGGT 429
Qy 218 lalalleasnleuilevalginhisilegin-AspilleuasngllyaspilleCylyst 238
Db 428 GCCCATCAACCTCATCGTGACGACATCCAGGACATCTGAATGAGGGGCC----- 376
Qy 238 rphisargglyserasparglysergtyrlysaargthrpheserGluProGlyaspH 258
Db 375 -----TCCAAACCCGCGACACC 360
Qy 258 isProglymetleuThr-----serglyysargserhisleuGlyserSers 274
Db 359 AAT--GGCTGTCTCAACGGCTACACCCCTTCAAGCAGAGGACGAGGATCGGATCCAGCA 302
Qy 274 earGProhis 277
Db 301 GCAGCCGCGCAT 291

RESULT 6
US-09-235-076-30379
; Sequence 30379, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30379
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-30379

Alignment Scores:
Pred. No.: 4,9e-15 Length: 472
Score: 727.90 Matches: 145
Percent Similarity: 97.32% Conservative: 0
Best Local Similarity: 97.32% Mismatches: 4
Query Match: 50.20% Indels: 1
DB: 4 Gaps: 0

us-09-896-522-2 (1-277) x US-09-235-076-30379 (1-472)
Qy 28 valserglylythrllaserglylyserthrvalcyserglunylleuGluLeu 47
Db 28 GTCGCGGAA--ANCGCAGCGGGAAGTGCACCGTGTGCGAAGATCAATGAGGTTGCTG 85
Qy 48 glylnasngllyvalgluglnargglinaarglyvalilleuSerGlnaspargpne 67
Db 86 GGCACAAAGAGAGGTGAAACGCGCAGCGGAGAGGTGTCTCTGAGCCAGGACAGGTTTC 145
Qy 68 TyrLysValleuThrllagluGlnlysaValleuLysgllyGlnTyrAsnphneap 87

```

```

Db 146 TACAGGTCTCTGACGGAGAGGAGAGGCCAAGCCCTTGAAGAAGCATTTTGGAC 205
Qy 88 HisProaspAlaPheaspasnaPleuMetHisargThrleuylsannilleValgluGly 107
Db 206 CATCCAGATCCCTTGTGATATGATTGATGATGACAGGACCTCTGAAGAATCATGTGAGGGC 265
Qy 108 lyeThrValGluValProthrlyrAsnphneValThrHisserArgleuPProGluThrThr 127
Db 266 AAAACGGTGAAGGTGCGACCTATGATTTGTACACATCAAGGTTTACAGAGACACG 325
Qy 128 ValValTyrProAlaaspValValleuPhegluglylleuValPheTyrserGlnGlu 147
Db 326 GTGGTCACTCCCTCGAGCGGTCTCTGTGGAGGCATCTTGATCTTCAAGCCAGAG 385
Qy 148 lleargaspmecpnehisleuargleuphevalaspthrAspseraspValaTyrleuSer 167
Db 386 ATCCGGAGACATGTTCACCTCGCGCTTCTGTGACACCGACATCCGACGTCAAGCTGTAT 445
Qy 168 ArgArgValleuArgaspValaArgArg 176
Db 446 CGAAGATTCTCCGAGACGTGCGCGA 472

RESULT 7
US-09-235-076-24042
; Sequence 24042, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24042
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(472)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-24042

Alignment Scores:
Pred. No.: 6,28e-10 Length: 472
Score: 559.60 Matches: 109
Percent Similarity: 71.75% Conservative: 18
Best Local Similarity: 61.58% Mismatches: 16
Query Match: 38.59% Indels: 34
DB: 4 Gaps: 0

us-09-896-522-2 (1-277) x US-09-235-076-24042 (1-472)
Qy 9 CyGlu--SerProAlaPro-----GluAlaaspArgPro-----HisGlnAr 22
Db 9 TGTACTGATCGCTGACGATGCGCGGAGACGAGCGAGACCTTCAGAACCAACAGCA 68
Qy 22 g-----ProPheleuilleGlyValserglylyThrllaserglylyys 37
Db 69 GCCCAAGCGCGGAGACCTTCTTATAGCGCTGACGGGAGGAACGCTAGCGGCAAGTC 128
Qy 37 rThrValCyGluTylleuMetGluLeuLeuGlylnasnGluValGluGlnArgGlnAr 57
Db 129 TTCCGTTGTGTGATGATGTCGACGCTCTGGGGAGAGATGAGTGAATTCGCCAGAA 188
Qy 57 glyValValilleuSerGlnaspArgPheTyrlysaValleuThrllagluGlnlysa 77
Db 189 GCGAGTGTCACTCGAGCGAGAGATAGCTTACCGCTGCTTACCTCGAGCAGAAAGGC 248
Qy 77 alysaValleuLysgllyGlnTyrAsnphneaspHisProaspAlaPheaspasnaPleu 97

```

```

Db      249 CAAAGCCCTGAAGGCGCATCTTGAACACCCGAGTCCTTGAACATGAATCAT 308
Qy      97 CHSARGThrLeuYsaAnlleValGluGlyValThrValGluValProThrTyraSp 117
Db      309 TCTCAAAACACTCAAAAGAACTACTGAAGGAGAAAGGAGATCCCGGTATGACTT 368
Qy      117 evalThHisSerArgLeuProGluThrThrValValTyreProAlaAspValValLeuPh 137
Db      369 TGCTCCCATTCCTCCGGAAGGAGAGACAGTACGTCTATCCGACAGCGGTGCTCTT 428
Qy      137 eGluGlyTlleuValPheTyreSerGluGluIleArgAspMet 151
Db      429 TGAAGGATCCTGGCCTTCTACTCCAGAGAGTACGAGACTG 471

RESULT 8
US-09-235-076-23923
; Sequence 23923, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23923
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (455)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-23923

Alignment Scores:
Pred. No.: 4,74e-09 Length: 455
Score: 527.90 Matches: 104
Percent Similarity: 67.60% Conservative: 17
Best Local Similarity: 58.10% Mismatches: 17
Query Match: 36.41% Indels: 41
Gaps: 1

us-09-896-522-2 (1-277) x US-09-235-076-23923 (1-455)
Qy      5 GlyGly-----GluAspCysGluSerProAlaProGluAlaAspArgPro 19
Db      2 GGTGGCTTGCTCGATCACTGTGAGAAATGCNCGCG-----ACAGCCAGACAGACC 52
Qy      20 -----HlaGlnArg-----ProPheLeuIleGlyValSerGlyGlyT 32
Db      53 TGCAGAACACACAGACGAGCCGAGCGGAGCCCTTCTTATAGCGCTCAGCGGGGGA 112
Qy      32 hralaSerGlyLysSerThrValCysGlyValIleMetGluLeuGluGlyGlnaangluv 52
Db      113 CAGCTAGGCGGAGACTTCGCTGTGTCTAGATGATGTCAGACTCTGGCGGAGATGAG 172
Qy      52 alGluGlnArgGlnArgLysValValIleLeuSerGlnAspArgPheTyrlsValLeuT 72
Db      173 TGGACTTTCGCAAGAGGAGGTGTGATCTGAGCGCAGATAGCTTTCACGCTGCTT 232
Qy      72 hralaGluGlnLysAlaLysAlaLeuLysGlyGlnTyraSpPheAspHisProAspAlaP 92
Db      233 CCTGGAGCAGAGAGCCCAAGCCCTGAAGGCGCAGTTTAACCTTGAACACCGGATGCT 292
Qy      92 heaAspAspLeuMetHisArgThrLeuLysAsnIleValGluGlyLysThrValGluV 112
Db      293 TTGACATGAACCTATCTCAAAACACTCAAAAGAAATCAGTGAAGGAGAAACAGTCCGA 352
Qy      112 alProThrTyraSpPheValThrHisSerArgLeuProGluThrThrValValTyraPro 132
Db      353 TCCCGGTATGATGACTTGTCTCCATTCCTCCGGAAGAGAGAGACAGTACTGTATCCCG 412

```

```

Qy      132 laaSpValIleuPheGluGlyIleuValPheTyreSer 145
Db      413 CAGACGTGTGTCTCTTGAAGGAGATCTGGCCTTCACTCC 453

RESULT 9
US-09-235-076-9667/C
; Sequence 9667, Application US/09235076
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/235,076
; CURRENT FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9667
; LENGTH: 470
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (470)
; OTHER INFORMATION: n = A,T,C or G
US-09-235-076-9667

Alignment Scores:
Pred. No.: 0.000123 Length: 470
Score: 384.90 Matches: 74
Percent Similarity: 64.33% Conservative: 36
Best Local Similarity: 43.27% Mismatches: 40
Query Match: 26.54% Indels: 21
Gaps: 1

us-09-896-522-2 (1-277) x US-09-235-076-9667 (1-470)
Qy      90 AspAlaPheAspAsnAspLeuMetHisArgThrLeuYsaAnlleValGluGlyLysThr 109
Db      469 GATGCCCTTACCTTGCAGCCCTCATCATTTCCACCCTCAAGAAAGCTGAAGGAGAGT 410
Qy      110 ValGluValProThrTyraSpPheValThrHisSerArgLeuProGluThrThrValVal 129
Db      409 GTCAGGTGCCCATTTATGACTTCACACGACGCGGAAAGAGACTGGAACAACATG 350
Qy      130 TyrProAlaAspValIleuPheGluGlyIleuValPheTyreSerGlnIleArg 149
Db      349 TATGTCGAACGTCATCATCTTTGAAGGCATCATGCTTGTGTCACAAAGACTGTG 290
Qy      150 AspMetPheHisLeuArgLeuPheValAspThrAspSerAspValArgLeuSerArgArg 169
Db      289 GAGCTCCTGACATGAAGAAATCTTTGTGACACAGACTCCGACATCCGCTGTACGGCG 230
Qy      170 ValLeuArgAspVal---ArgArgGlyArgAspLeuGluIleLeuThrGlnTyThr 188
Db      229 CTGGCCGCGGACATCACTGATGAGCGCGCGGAGATCAGAGGTGTCTCAAGCACTAC 170
Qy      189 ThrPheValLysProAlaPheGluGluPheCysLeuProThrLysLysTyraAlaAspVal 208
Db      169 AAGTTGTCAAGCCCTCTTCAACATATCCAGCCACCAATGCGCTGGCAGACATC 110
Qy      209 IleIleProArgGlyValAspAsnMetValAlaIleAsnLeuIleValGlnHisIleGln 228
Db      109 GTGCTCCCAAGAGGAGCGGCAACAGCGTGCATGACCTGCGTGTGAC----- 59
Qy      229 AspIleLeuAnGlyAspIleCysLysTyr-----His-Arg---GlyGlySer 243
Db      58 ---GTGCTGACGAATCTCTACTACTGACTAGTATCATATGATAGGGGGGATG 3

RESULT 10
US-09-488-725B-6890
; Sequence 6890, Application US/09488725B
; GENERAL INFORMATION:

```

```

APPLICANT: Yuanhua T. Tang
APPLICANT: John Tillinghast
APPLICANT: Ankura Sanku
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Dzmanac
TITLE OF INVENTION: Novel Contigs Obtained
FILE OF INVENTION: From Various Libraries
FILE REFERENCE: 784
CURRENT APPLICATION NUMBER: US/09/488,725B
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remainder Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pc_ct_genes Version 1.01
SEQ ID NO 6890
LENGTH: 2659
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (219)...(320)
OTHER INFORMATION: similar to g14589612 in the genepept database release 114,
US-09-488-725B-6890
Alignment Scores:
Pred. No.: 144 Length: 2659
Score: 315.70 Matches: 164
Percent Similarity: 13.80% Conservative: 49
Best Local Similarity: 10.62% Mismatches: 62
Query Match: 21.77% Indels: 1273
Gaps: 3
us-09-896-522-2 (1-277) x us-09-488-725B-6890 (1-2659)
QY 2 AlaSer-----AlaGlyGlyGlu---Asp-----CysGluSerPro----- 12
Db 55 GCGAGTGGGTACCGGGGACCGAGCGAGCGTAGCCGTCCAGAGCCCGGGCGCTCTC 114
QY 13 -----AlaProGluAlaAspArg----- 18
Db 115 GATGGGGGACGACAGCTGACCGGCTCTCTGAGGCGCGGGGAGATGCTGAAGCGC 174
QY 19 -----ProHisGln----- 21
Db 175 AGGCGCGCGCTGGGACCATCTCTGACATGTGCTCAAGAGCGACGCTGATTTCC 234
QY 22 -----ArgProPheLeuLeu-----GlyVal----- 28
Db 235 GACCGCGCGCCCGG-CTGCTGTGACCCCTTGAAGCCGGAGTTGATACCAAGTTGAATTC 293
QY 29 -----SerGlyGlyThr-----AlaSerGlyL 36
Db 294 ACTCTTGAGCCATCTTTAGGTCAAAATGCTTTTCAGCAGAGTGATGATGCTCTCAAGCA 353

```

```

QY 36 ys-----SerThr-----ValCysGlyLys-----IleMetGluLeu- 46
Db 354 GTTGCAGGCTATTCACAGGAATACCAAGAAATGAGAGAAAGTTGTTGACCTTG 413
QY 47 -----LeuGlyGlnAnglu----- 51
Db 414 GCAGATCATTTTGGACAGTATAGCATTCGAGTGGAGAAACCATGGCCTTCACTTC 473
QY 52 -----ValGluGlnArgGln 56
Db 474 AATGAAAGAGTATCTGTATGATGATCTCCATGGGAATTGATGATGACGACCTTAC 533
QY 57 Arg-LysValValIleLeuSer-----GlnAspArg-----PheTyr 68
Db 534 CGCAGCGCTGTGCTTATCTGTGGCCAGAGGCTGAGCAGCAGGCTGTGTTGAAG 593
QY 69 LysValLeuThrAla-----GluGln-----LysAla----- 77
Db 594 CGGCTGTGTGCTGCTATGCGGATGGAACAAACTGTGGTACTGCCAAGCTTTAAC 653
QY 78 -----LysAlaLeuLysGlyGln-----TyrAsp 86
Db 654 ATCTGGCTGCTACTAATTCGAGAGTGAAGAGGCAATGAGGAGTCCCTGAAATTT 713
QY 86 LeuAsp-----HisProAspAla--PheAspLeuAspLeu----- 96
Db 714 ATGATTTTACCTTATGATGAAGTACTTCCGAAAGCTATTTCTCATTAATTCCTCGGCA 773
QY 97 -----MetHisArgThrLeuLysAsnIleValGluGly----- 107
Db 774 TTGCTGTGATATGCTGCTGCTTCAAGACCTTTTAAGATGAAGCTCCGCAATATCT 833
QY 108 -----LysThrValGluVal-----P 113
Db 834 CAGCACCCTGATACTCTTCAGAGACTGCAACAAAGAAAGTGAAGTATGAGCC 893
QY 113 roThrTyr-----Asp-----PheValThr-----HisSerArgLeuP 124
Db 894 CCACTTACAAATGCTTCAAGATGAGTGGTCTTCACTCTTCCACATGC-CTCC 951
QY 124 roGluThrThrValValTyrProAlaAspValValLeuPheGluGly-----IleLeuV 142
Db 952 CTATATGACCGCTTTAAAGATCTGGGATTCAGTCTTTTGAAGTTCCAGAAATCATCC 1011
QY 142 a1----- 142
Db 1012 TAAGGTGTGCTGCTATCTGGCAAAATTAGAGAGCAGATGATGTTGAAACAG 1071
QY 143 -----PheTyrSer-----GlnGluLeu--ArgAsp----- 150
Db 1072 CAGATGAATTTTACACACACATGGGCGCTTACCAGAGAGATGAGAAATGATCTTC 1131
QY 151 -----MetPheHis--LeuArg----- 155
Db 1132 TGCAAAGCATGACATGACAGACTGTTTATTCAGGCTCCGTTCCCTTTCCACAAT 1191
QY 155----- 155
Db 1192 TGGCAGATTTGAGGAAATAACACTTACACATTAACCGTTCCAGCCACAGTTAAAC 1251
QY 156 -----LeuPheValAsp--Thr-----AspSerAsp--ValArgLeuSer--Ar 168
Db 1252 CCACTCAAGTTCTTGACACATATGTAAGCCAGACAGATGATGAAGAAATGACCCAG 1311
QY 168 GARG-----ValLeu----- 171
Db 1312 ACATATGATGCTGTGCTTATGATGAGTGGGCTGCTTGAACCTTTTAACTGCTCTG 1371
QY 172 -----ArgAspValArg-----ArgGlyArg----- 178
Db 1372 CTCCTGAAGTGAAGATACCAAAATTAAGACCAATATGAGGAGAGAGTCTGA 1431

```

```

Qy 179 Aspleu-----Glu-----181
Db 1432 GATCTAATACATTCAGAGCTGAGTCCAGAGCAATCAATCTCTGCAAGTAATACC 1491
Qy 182 -GlnlleuThr-----185
Db 1492 ATGAGCTTTTAAAGATATGATGAAACGATGACACAGATATCAATGACTGAAGC 1551
Qy 186 -GlnTYrThrPheValIysProAlaPheGluPhe-----Cys-----199
Db 1552 GCGAGTACTCTGCAATTAAGAAAGCAAGCAGAGGTTTCATCAGGTGATCAGG 1611
Qy 200 -----LeuProThr-----LysIysTyraIaIaPVal11 209
Db 1612 CAGACAAAGGCGCAGTACCGCATTCCTCCCTCTCAGTAAAGTTTCCA--GTTAT 1669
Qy 209 eilePro-----ArgIyValAsp-----AsnMetValAlaIleAsnLeu1 223
Db 1670 AAA-CCACCTTCTTTTGAAGAAAGATGAAATGACTAACAAGAGCTGCCAAGATCTG 1728
Qy 223 leValGlnHleIle-----GlnAsp1 230
Db 1729 TCATC--CACATCTCGTGTCACAGAGGAGAAATATCTCTGCTCCCTAGCAAGACC 1785
Qy 230 le-----LeuAsn-----GlyAspIle-----Cys 236
Db 1786 TTAAGACGAAGCTCAATCTCCCGTGGCAACTCATCCAGTCACAAAAGAAATGTC 1845
Qy 237 Lys-----Trp-----HisArg-----240
Db 1846 CAAGACCAAGAGTCAATCCGGGCTGTGGGACACCGTAGGCGTATAGATGACAGAACG 1905
Qy 241 -----GlyIysSerAsnGly-----245
Db 1906 AGGCCAGCAAGACCAATGAGGCTG3GGGACAGAGGATCCCTCGTGTGTAACAGCA 1965
Qy 246 -----ArgSerTyr-LysArgThrPhe-----252
Db 1966 CAGCTGGAGAGAAAGCAGCAGCCCTGAAGGCACTACAGAGACATGACAGGGCAGT 2025
Qy 253 -----SerGlu-----254
Db 2026 CTCGGAGCGGCTGTGGAGATGCTGATGTGTCTGCAATTCAAGCGAAGTTGG 2085
Qy 255 -ProGlyAspIlePro-GlyMet-----LeuThrSerGly-----265
Db 2086 GAGCCTGGAATGAAACCAAGGAGATGCTGCACTGAAGCTCAGGGTGCACCCAC 2145
Qy 266 -----LysArgSerHisLeuG1 271
Db 2146 CTGCGCAGCGCACTGCCCAAGCGCCGAGTGCACCCGAAAGAAACCAAGCCACAGCA 2205
Qy 271 userSerSerArg-----ProHis 277
Db 2206 AAGCTCCCAAGCAGCAACTCAAAAACCCCAT 2239

RESULT 11
US-09-488-725B-6460
; Sequence 6460, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinhuast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drihanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341

```

```

; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 6460
; LENGTH: 5773
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1318)..(4281)
; OTHER INFORMATION: similar to g1388237 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-6460

Alignment Scores:
Pred. No.: 1,74e+04 Length: 5773
Score: 304.30 Matches: 146
Percent Similarity: 14.51% Conservative: 65
Best Local Similarity: 10.04% Mismatches: 62
Query Match: 20.99% Indels: 1183
DB: 1 Gaps: 6

us-09-896-522-2 (1-277) x US-09-488-725B-6460 (1-5773)

Qy 4 AlaGlyGly-----Glu 7
Db 14 GCTGGGGAAGCTGAGGCTGAGGCGGTGCGCAATCTGCTGAAGCAAGGAAATGAG 73
Qy 8 AspCys-----GluSerProAlaPro-GluAla--AspArg 18
Db 74 TCTTGCTTGCTTCTCTCTCACTGGCGCTGAGAGCCCTGCGCAGAGGCCAGACAAA 133
Qy 19 -ProHisGlnArgProPhe-----LeuIleGlyVal-----SerGly-----30
Db 134 TGGCCCCATAGTGAAGAACTGGGAAGCTTTTAGGCATCTGATCAGAGCGGAGCCAGCA 193
Qy 31 GlyThr--AlaSerGly-----L 36
Db 194 GGGACCAACAGTGTGAGCAGGCAACCACTGAACCTTGAAGATGAAATCCCAAGA 253
Qy 36 ySerThrValCys-----GluIysIle-----MetG1 45
Db 254 GAACCACTTGTGCTTCATGTTATGTGATTTATCTTCCAAGCTGACCTGAAGTGA 313
Qy 45 uLeu-----LeuGlyGlnAsnGluVal--GluGln-54
Db 314 ATTACAGTCTACTATTCATTCCTTTGAGTCTTATGAACATGAACACAGCTGTGTAAG 373
Qy 55 -ArgGlnArgIysValVal-----60
Db 374 CACTGAGCAAAAAGCAGCGCTTGCCCAAAAAGTCTACGAGCTGAAGATACTGTTA 433
Qy 60 -----60
Db 434 ATATTGATCAGTTTGAAGAAATGATCTCTCTGATCTTATCAAGCCTACTTGACA 493

```

```

QY 61 -----IleLeuSer----- 63
Db 494 GCCTCAGTTTTCATTCATGGAAATPAACCTGACCAATTAATGACATTA 553
QY 64 -----GlnAspArg-- 66
Db 554 ATGTGACAAACAGTCGTGACAGCTGTGAAATGAATGTGTCTCTCTGTGACAGGT 613
QY 67 -----PheTyrLeuValLeuThrAlaGlu 74
Db 614 ATGGGTGCTCGGGAAAGGTGTCTTCAACATCTCATTTGTCAAGAGCGTGTCTCC 673
QY 75 GlnLys-----AlaLysAlaLeuLys-----GlyGlnTyrAspPhe----- 86
Db 674 TCCAGAGGACCATTTGACGTGCTTAAAGAACTGCTCCCAATGACCTTTTGTGCTGC 733
QY 87 -----Asp--HisProAsp-----AlaPheAspAsnAspL 96
Db 734 TTCAGGAAGATGTACCTGTCAATGAGAGTCAAGTCACTAATGTAGGCTTTCAGAAAGACC 793
QY 96 eumet-----HisArgThrLeuLysAsnIleValGlu----- 106
Db 794 TCATGGAACATCTCCCTCCGCTCTATAGTCTTACAAAGACCACTTGGAAGACGCTTCC 853
QY 107 GlyLysThrValGlu--ValProThrTyrAspPheValThr----- 119
Db 854 GGAAGGTTACGGAATTTTACAGGCTTCAAGGCGTGTGACAGGTTCAAGTCTG 913
QY 120 -----His--SerArgLeu-----ProGlnThrValValTyrP 131
Db 914 GAAGTGTGTGTGATATGAGTCAAGCTACACCAACCATCATTTGATTAATCATTA 973
QY 131 xalaAsp-----ValVal----- 135
Db 974 AAGCAATGACAAAGTTGTACAGAGCTCAATCAGACTCAAAATGAGTCAACTCCT 1033
QY 136 -----LeuPheGluG 139
Db 1034 TTCACAGCTTACTATCATGAAAGCAATTTCTTGTACACAGCAATCATCTTTGAG 1093
QY 139 IY-----IleLeuValPb 143
Db 1094 GGGACACAGTCACTGTGTGTGAAAGAGTTTGTCTCCCAATGTGTCTTGCGGC 1152
QY 143 eTyr-----SerGlnGluIleArgAsp-----Met 151
Db 1153 -TATGAAGAACAGACAGTGGAAATCCAGAACAGACAGAGATCTCGATTTACACCCCACT 1211
QY 151 tPhe-----His--LeuArg-----LeuPheValAspThrAspSer----- 162
Db 1212 TTTCAACAACATGACTTCGTGTCCAAAGTCCACCATCC--ACAACATCACTCCAGGTAT 1269
QY 163 -----AspValArg-----LeuSerArgArg----- 169
Db 1270 GCGAGTGAATATGTTCACAACTGATATTAACATTTTGAATATAGTGCAGAAAGAAA 1329
QY 170 -----ValLeu-----Arg-----AspValArgArg- 176
Db 1330 ATAGATGTATATGCCATCCAAATTTTGGCAATGAAGAAATGAAGGTATGTGCAACAAC 1389
QY 176 ----- 176
Db 1390 AATCTCTATCTTTGAACTGTGCACTCAAGGTATGTTAATGTAGCAAAAGTAGAATGG 1449
QY 177 -----GlyArg-----AspLeuGlnIleLeu 184
Db 1450 AAGCAGGAAGAAATAATATATTCAGAGAACCCCTGAGACAGACATAGATTTCTACTGTC 1509
QY 185 ThrGlnTyrThr----- 188
Db 1510 ACGACATACACCTCAAGGCTATGTGAACCCAGCGGTCGTCTGAGACACAGA 1569
QY 188 ----- 188

```

```

Db 1570 GTGATCTACACTTGTGAGTTTCATCAGTGCCTATGAGCCAGAGGCAAGTGCACATATAA 1629
QY 189 ---ThrPheValLys-----ProAlaPhe----- 195
Db 1630 GTGACATTCATCTCTGTGGCCATCTTAACATPAACCCGGAGCCCAATTTCTGTTCGAG 1689
QY 196 -----G 196
Db 1690 GGAACAAACTTTTCTATTAATATGATCAGTATGTGATGACTATGATGAGTTTATGG 1749
QY 196 IuGluPheCys-----LeuPro-----ThrLysLysTyrAlaAsp 207
Db 1750 AACACTTGTGCTGATTAATAATATACAAAGATTTTATACCGAGAGGTATCTTGAT 1809
QY 208 -----ValIleIle-----ProArg--GlyValAsp--AsnMet--- 217
Db 1810 GGAGCAGAAATCAGTACTGACAGTCAAGACCTCGACAGAGGAGTGAATGGAACCTATCAC 1869
QY 218 -----ValAlaIleAsnLeuIleValGln-----His-IleGlnAsp 229
Db 1870 TGCATATTTAGATATAGAAATTCATACAGTATTTGCAACCAAGACGTATTTGACCCG 1929
QY 230 Ile-----LeuAsn-----GlyAspIleCys-----LysTyrP- 238
Db 1930 CTCCTCTAAAGCTGAACATCATGTGTGATCCTTTGGAAGCTACTGTTTCATGACAGTGT 1989
QY 239 -----HisArgGly----- 241
Db 1990 TCCCATCATCATCAAGTGTGATGAGAGAGATGAGACTACAAAGTTACTTTCCATATG 2049
QY 242 GlySerAsnGly-----ArgSer-----TyrLysArg 250
Db 2050 GGTTCCTCATCCCTTCTGTCTGTGCAAAAGATTAAACAAAAAACAAGTGTCTACAAACAC 2109
QY 251 ThrPheSer----- 253
Db 2110 AATTTCATGCAAGCTCACTTCTGTGTTCAAAAAAGTGTGATGTGTGTCACTTT 2169
QY 253 ----- 253
Db 2170 ACCAATGCTGTATTAATTCAGTTTGAAGCCCATCTATGAGCTGAATCTGTGCTGG 2229
QY 254 -----GluProGly--AspHisPro- 259
Db 2230 GAAACATCATCATGCCAGATCCCTTAATAGTGTGCGAGACCCGGGAAAGTCATCCAG 2289
QY 260 -----GlyMetL 262
Db 2290 AAGCTATGCCGTTCTCAAGCTTCCAGACAGCCCTGAGAGATCCCATTTAGCGGGAGCA 2349
QY 262 euThr-----SerGly-----LysArgSer-----HisLeu----- 270
Db 2350 TCACATTCAAAATGTAGGCTCCCAAGTGGGGGTAGAAAGAAATACATCATCTCTGCC 2409
QY 271 --GluSerSerSerArgPro 276
Db 2410 CCAATPAACAGTCTGTCTCA 2429

```

RESULT 12  
 US-09-488-725B-5593  
 / Sequence 5593, Application US/09488725B  
 / GENERAL INFORMATION:  
 / APPLICANT: Yuanhua T. Tang  
 / APPLICANT: John Tillinghast  
 / APPLICANT: Ankura Sinks  
 / APPLICANT: Chenghua Liu  
 / APPLICANT: Radoje T. Drmanac  
 / TITLE OF INVENTION: Novel Contigs Obtained  
 / FILE REFERENCE: From Various Libraries  
 / CURRENT APPLICATION NUMBER: US/09/488,725B  
 / CURRENT FILING DATE: 2000-01-21





```

Db      743 ATATTGTCACAGAGCTGATATGCGCATGCTGTGTGACACACCCCAAGGCAATTGG 802
Qy      79  laLeuLysGly-----GlnTrpAsnPro-----AspHisPro-----A 90
Db      803 TGCTGATAGGGGATGTAGAGAAAGGCTTCAACCCGAGCTGAAAGTATCATCTTATATGG 862
Qy      90  spAlaPheAspAsnLeuMetHisArgThrLeuLysAsnIleValGlu----- 106
Db      863 ACCCTTGATGATGACCTGAAAGAGAGGAGAGAGTGAATGGAATGATCTTATCCC 922
Qy      107 -----GlyLys-----ThrValGlu-----ValPro----- 113
Db      923 TATATGATGCTGAGAACCTAGGCAAGACACTTCAGAAAACTGTGCTCTAGCCAG 982
Qy      114 -----ThrTrpAsp-----PheVal 118
Db      983 AAGACCTGAGCGTCATGCTGCTTCCAGTGGACCAAGGTCAGCCCAAGAGCCATGA 1042
Qy      118  alThrHisSerArg-----LeuProGlnThrThrVal-----ValTr 130
Db      1043 TAACCCATCAAAATATGTTTCAAAATGCTGCTGCTTTCCAATGTGTGAGCATGCTT 1102
Qy      130  yr-----ProAlaAspValVal-----LeuPheGluG 139
Db      1103 ATGAGCCCACTCCTGATGATGTGGCCATATCTACTCTCCCTGTGCTCATATGTTTGA 1162
Qy      139  lyIleLeu-----ValPheTrpSerGlnGluIleArg-----AspMetPheHis----- 153
Db      1163 GGATGTGTACAGGCTGTGTGTGTACAGCTGTGAGGCCAGTTGATTC-TTCCAAAGGGAT 1221
Qy      154  LeuArgLeuPheValAsp-----ThrAspSerAspValArgLeu-----SerArg----- 168
Db      1222 ATTGCTGTTCTGCGCTGAGCAGATGAAGACTTTGAAGCCCACTGTTCCGCGGTGCT 1281
Qy      169  ArgValLeu-ArgAspValArg-Arg-----GlyArgAsp-----LeuGluGlnI 183
Db      1282 CGATCTCTTAACAGAGATCTACGATAGAGTACAAATAGAGGCCAAGACCTTGAAGAAG 1341
Qy      183  leLeuThrGln-----Tyr----- 187
Db      1342 TTCTGTGTGAGAGCTGCTGTTTCCAGTAATTCAAAGAGCTTCAAAAGGATATCATGAG 1401
Qy      188 -----ThrThr-----PheValLys-Pro-----AlaPheGluGln- 197
Db      1402 CATATATGTTCTTGGGACACAGCTCATCTTTCCAAAGATCCAGACAGCTTGGGGGGAAG 1461
Qy      198  Phe-----Cys-----LeuPro----- 201
Db      1462 GTTCGTGTAATGTCACTGAGAGCTGCCCCCATGTCACCTTCAGTCATGACATCTTCGCG 1521
Qy      202 -----ThrLysLysTrpAlaAspValIleI 210
Db      1522 GCAGCAATGAGATGTCAGGTGTATGAAAGCTTATGCTCAACAGATGACAGGTGGCTGT 1581
Qy      210  e-----ProArgGlyValAsp-----AsnMetValAlaIleAsnIleValG 225
Db      1582 ACATTATACATTAACCTGG-GGACTGGACATCAGCTCAGCTTGGGGTGGCCCTGCGCTGCA 1640
Qy      225  nHisIle-----GlnAspIle-----LeuAsn-----GlyAs 234
Db      1641 TTACGTGAAGCTGGAAGAGTGGCTGACATGACATTAACAAGTAATATGAAGAGGA 1700
Qy      234  pIleCys--Lys----- 237
Db      1701 GGTGTGATCAAGAGGTACAAAGTGTTCAAAGATACCTGAAGAGACCTTGAGAAAGACA 1760
Qy      238 -----Trp-----HisArg-----GlyGlySer--As 244
Db      1761 GGAAAGCCCTGAGACAGTATGGCTGCTTCAACAGAGACATTTGTCGCTGCTCCGAA 1820
Qy      244  nGly-----ArgSer-----TyrLysArgThrPhe----- 252
Db      1821 TGGAACTGTGAAGATCATGACCCGTAAGAAAGACATTTTCAAGCTGCGCCAAAGAGATA 1880

```

```

Qy      253 -----SerGluPro----- 255
Db      1881 CATTGCACAGAGAAATAGAAATATCTACAAAGAGATCAACAGCTTTACAAATTTT 1940
Qy      256 -----GlyAsp-----HisPro----- 259
Db      1941 TGTAACAGGGGAGAGCTTACGGTCATCTTAGTAGAGATGTGTGTTCTGACACAGATGT 2000
Qy      260 -----GlyMetLeu----- 262
Db      2001 ACTTCCCTCATTTGACGCCAGAGCTGGGGTGAAGGAGCTCTTTAGAGAACTGTGCCAAA 2060
Qy      263  ThrSerGlyLysArgSerHis-LeuGlu----- 271
Db      2061 CCAAGTTGTAAAGGAAGCCATTTTAAAGACTTCAGAAATTTGGAAAGAAAGTGAGCCT 2120
Qy      272 -----SerSerSerArg-Pro-----His 277
Db      2121 TAAACTTTTGAACAGGTCAAGCCATTTTCTTCATCCAGGCCATTTTCCAT 2174

RESULT 14
US-09-488-725B-4307
; Sequence 4307, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; APPLICANT: Radojko T. Dimanac
; TITLE OF INVENTION: Novel Configs Obtained
; FILE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt CT_genes Version 1.01
; SEQ ID NO 4307
; LENGTH: 6050
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc_feature
; LOCATION: (3)..(531)
; OTHER INFORMATION: similar to g11504002 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTYX 3.3f00, default parameters
US-09-488-725B-4307

Alignment Scores:
Pred. No.: 3.16e+04 Length: 6050
Score: 298.10 Matches: 152
Percent Similarity: 15.06% Conservative: 48

```



Best Local Similarity: 11.45% Mismatches: 75  
 Query Match: 20.56% Indels: 1055  
 DB: 1 Gaps: 1  
 us-09-896-522-2 (1-277) x US-09-488-725B-4307 (1-6050)

QY 3 SerAlaGlyGly-----GlnAsp-----CysGluSer----- 11  
 DB 1514 AGTCAGAGTGGCTGTCCCTATTGAAGACATGCAGAGATCATCTGCGATTTCG 1573  
 QY 12 -----ProAlaPro----- 14  
 DB 1574 ACATCGCATCTCTGGATCTTAAGATAAGAGAAAGAACTTGGCCATGCTTATGT 1633  
 QY 15 GlnAlaAspArg-----Pro 19  
 DB 1634 GAAGCTGATGAAGAAGAGAGGAGCTACTACAGATGATTCATGACTTAAGTTGCTT 1693  
 QY 20 His-----GlnArg-----ProPheLeuIle----- 26  
 DB 1694 CAAGGGGACAGCAAGATGAGAGATGCCAGCGCATCTACCTGCTTCTTATCG 1753  
 QY 27 -----GlyValSerGlyGly----- 31  
 DB 1754 ACACCATGTGGAACCAAGGGGGCCACGCTGAGAGAGAGCTCCAGAGTGTGGGGGCT 1813  
 QY 32 -----ThrAlaSerGlyLys-----SerThr-----ValCysGlu-----LysIleLeu 44  
 DB 1814 TTCTGTGAGTCCCGGAGATGTCTTCATTTCCACCTGCTGTGTCCCAAAAGCTCAC 1873  
 QY 44 Leu-----LeuLeuGly-----Glu 49  
 DB 1874 TCGAATGTGGGCTTGTCTGAGTTTGTCTGAAGTGGCGTATGAAGCTTCACTGCTCAAGCA 1933  
 QY 49 nAsn-----GluValGluGln-----ArgGlnArgLys-----ValValIleLeuSer----- 63  
 DB 1934 GAATTTAGAAAGAGTTGAAGTGTGTGATGAGAGAAAGTGTTGAAGTTTCCAGGATAC 1993  
 QY 63 ----- 63  
 DB 1994 TCTGATGCCCTTTCACATCATCATGATGAGCATTTCTCAAGATGATATGATCATCTT 2053  
 QY 63 ----- 63  
 DB 2054 CGCTTTGATGCTTGAATTTACATAATAGAGCTCATTTGACAGCCGGAATTTACGATTT 2113  
 QY 64 -----GlnAspArgPhe-----TyrLysVal 70  
 DB 2114 CAACACGTTCTGAGAGCTTACATCCACAGCATTTCAAGGCACTTGCTTACAAAGAA 2173  
 QY 70 Ileu-----ThrAlaGlu-----GlnLysAla----- 77  
 DB 2174 ATGTATGACAGTGTGAAGACTTACTTGATACCTCCAGAGAGAGGAGCAATGTGAGCC 2233  
 QY 78 -----LysAlaLeu-----LysGlyG 83  
 DB 2234 AATCTTAAGAGCGTGAAGGCTTGAATATGTCTCAAGTTGATGTTGCTGAGAGAC 2293  
 QY 83 IAsp-----AspPheAsp-----HisProAsp 90  
 DB 2294 ATTATTTGACAGCTTATGAAGGCAAGAGACAGATGAGATTTGAAGATTCATGAGACG 2353  
 QY 91 Ala-PheAsp-----AsnAspLeuMet-----HisArgThr----- 100  
 DB 2354 GCTCTTGAATCATCAACATCTGATGAAGAGTCAATCAAAAGTCAATCACTCTTTTGA 2413  
 QY 101 -----LeuLysAsnIle-----ValGlu-----GlyLysThrVal 110  
 DB 2414 GGTGGCGGCTTGAATTAATCACTCTGTCTGTCGATGATGAATGATGCTTTGATGC 2473  
 QY 111 GluVal-----ProThr-----TyrAspPheValThr-----His-----SerArgLeuPro 124  
 DB 2474 GAAGTTACACAGCACTCTGTATAGATTCTACACCTGATCCCTCTGTGAAGACTCCA 2533

QY 125 GluThr-----ThrValValTyrProAlaAspValVal-----LeuPheGlu----- 138  
 DB 2534 GAAGCAGAAAGTACATCTATGAT--GAGATGTCCAGAGCAACTCTTTAAAGCAA 2591  
 QY 139 -----GlyIleLeuValPheTyrSer-----GlnGluIleArg----- 149  
 DB 2592 GAATGCCGGGACATTCTGCTTCTCTCATCACCAAGAGCTGAAGAGCTGCTGAGACAG 2651  
 QY 150 -----AspMetPheHis-----LeuArg----- 155  
 DB 2652 AAGATGACATGCACACACAGGCTCGAGAGAGAAAGTACGCTGTAATGCTCAACAGC 2711  
 QY 156 -----LeuPheValAspThr--AspSerAspValArgLeuSerArgArg-- 169  
 DB 2712 ATCTGGAAGTCTTATGATACAGAGATGGCGGCTTACCTACCAACCATATCCAAAGATC 2771  
 QY 170 -----ValLeuArgAspValArgArg-----GlyArgAsp----- 179  
 DB 2772 ATGTCCAGCTGTGCGGACAGTGAACCGGACAGTCATCAACATGGGCGGATCATTT 2831  
 QY 180 -----LeuGluGlnIleLeuThrGln----- 186  
 DB 2832 CTGATTAGTCACTTGTGGCATGTATGACAGCCATCTTAACCAAGATGGGTACACAGAC 2891  
 QY 187 TyrThr-----ThrPheValLysProAla-----PheG 196  
 DB 2892 TACTCTCTTACATGAGACCTTCC--AGACCGACTTGAACTTGAGACTTCTTGATGG 2949  
 QY 196 IAspLeuPhe-----Cys----- 199  
 DB 2950 AGACCTTCATCATGTTCAAGAGACTCATTTGAGAAAGAGCTGTACCTGAGAGCTGATGG 3009  
 QY 200 -----LeuPro-----ThrLysLysTyrAlaAspValI 209  
 DB 3010 CCATGAGCATGCTTCAAAACAGGGCTTCTCTGAGACTATCAACAGATTGCGAAGACA 3069  
 QY 209 Le-----IleProArg-----GlyValAspAsnMet----- 217  
 DB 3070 TGAACCAAGATCTCTTAAGAACACAGACTTTGAGTTCCAGCTGTGGAACACTATTTTC 3129  
 QY 218 -----ValAlaIleAsnLeuIleValGln-----His----- 226  
 DB 3130 ATCTGCACTGCTTATATCAACAGATTTCTGTGAGCTGAGACGATTCTCACAGCCA 3189  
 QY 227 -IleGlnAsp-IleLeuAsn-----GlyAspIleCysLys----- 237  
 DB 3190 AATACACAAATCTCGAATTAAGTATGGGAGATAGAGAGCGGTAATTGGCTTCTCATCC 3249  
 QY 238 -----TrpHisArgGlyLysSerAsn-----GlyArgSe 247  
 DB 3250 GTGATATGTGTGAACAGCTTGTGAGAACAAATCTGCTTATCCAGGCAATGTGTGAGAC 3309  
 QY 247 rTyrLysArg-----ThrPhe-----SerGlu--ProGlyAspHis--Pro----- 259  
 DB 3310 CTATATTAAGATGACACTTATCTCTGAGGCTGAGGCTCGGAAAGCCACCATACCAATCT 3369  
 QY 260 -----GlyMetLeu-----ThSerGly-----LysArg 267  
 DB 3370 TCTTGACATGATGCTGTGTGAATATCAAGAAAGTGGGATTTCAAAAGCTTGAAGAG 3429  
 QY 267 gSerHisLeuGluSerSerArg-----Pro-----His 277  
 DB 3430 AATCATCTCTGAAGCTGACCAAGGTAGAAAGGGGGCCGAGCGACGAGCATACAT 3487

RESULT 15  
 US-09-488-725B-8411  
 ; Sequence 8411, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghast  
 ; APPLICANT: Ankura Sanku  
 ; APPLICANT: Chenghua Liu

APPLICANT: Radoje T. Dzmanac  
 TITLE OF INVENTION: Novel Contigs Obtained  
 FILE REFERENCE: 784  
 CURRENT APPLICATION NUMBER: US/09/488,725B  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US 09/004,182  
 PRIOR FILING DATE: 1998-01-07  
 PRIOR APPLICATION NUMBER: US 09/034,341  
 PRIOR FILING DATE: 1998-02-13  
 PRIOR APPLICATION NUMBER: US 09/045,400  
 PRIOR FILING DATE: 1998-03-20  
 PRIOR APPLICATION NUMBER: US 09/321,214  
 PRIOR FILING DATE: 1999-05-26  
 PRIOR APPLICATION NUMBER: US 09/131,598  
 PRIOR FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: US 09/170,294  
 PRIOR FILING DATE: 1998-10-13  
 PRIOR APPLICATION NUMBER: US 09/179,473  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: US 09/181,430  
 PRIOR FILING DATE: 1998-10-28  
 PRIOR APPLICATION NUMBER: US 09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 PRIOR APPLICATION NUMBER: US 09/234,611  
 PRIOR FILING DATE: 1999-01-22  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 10289  
 SOFTWARE: pc\_ct\_genes Version 1.01  
 SEQ ID NO 8411  
 LENGTH: 6057  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc feature  
 LOCATION: (10)...(5536)  
 OTHER INFORMATION: similar to g1504002 in the genepept database release 114,  
 OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
 US-09-488-725B-8411

Alignment Scores:  
 Pred. No.: 3,17e+04 Length: 6057  
 Score: 298.10 Matches: 152  
 Percent Similarity: 15.06% Conservative: 48  
 Best Local Similarity: 11.45% Mismatches: 75  
 Query Match: 20.56% Indels: 1055  
 DB: 1 Gaps: 1

us-09-896-522-2 (1-277) x US-09-488-725B-8411 (1-6057)

Qy	3	Ser1aaglyly	-----Gluasp-----Cysgluser-----	11
Db	1521	AGTCAGAGTGGCTCTCCCTATTGAAGACATGACAGGATCCATCTGCATTCATGTTTCG	1580	
Qy	12	-----	-----Pro1aapro-----	14
Db	1581	ACATCGCTCATCTCTGGAATCTAAAGATTAAGAGAAAGAACTTGGCATGTCTATGT	1640	
Qy	15	Glu1aasparg	-----Pro19	19
Db	1641	GAACCTGATGAAGAGATGGAAGATCTACACGATGATTCATGATTAAGTTGCTCT	1700	
Qy	20	His-----	-----Prophleuile-----	26
Db	1701	CAAGGGGACAGCAAGATGAGATGACAGGCGCATACCTGACCTTCTCTTATCG	1760	
Qy	27	-----Glyvalserglyly-----	-----	31
Db	1761	ACACCATGTGAAAAACAAGGGGCGACGCTGACGAGACTTCACGACTGTTGGGGGCT	1820	
Qy	32	-----Thr1aaserglylys-----Serthr-----Valcysglu-----Lysileme	44	
Db	1821	TTCTGTCAAGCTCCCGGAGATGTGTTCTCATATTTCACCTGTGTGTCTCCACAAAGCTCAC	1880	

Qy	44	tgly-----Leuleugly-----G1	49
Db	1881	TCGAATGCGGCTCTCTGGGTTGCTGAAGGCGTATGAAGCTCACTGCTACAGCA	1940
Qy	49	nasn-----GluValgluIn-----ArgGlnarglys-----Val1alleuser-----	63
Db	1941	GAATTTAGAAAAGATTGAAGTTGTGATGAGAGAAAGTGTGAAGTTCTCCAGATAC	2000
Qy	63	-----	63
Db	2001	TCGTATGCCCTCTTCAACATCATGATGAGACATTCTCAAGTATGATGATCATCTCT	2060
Qy	63	-----	63
Db	2061	CGCTTTGATGCTTGATTTACATATAGACTCATTTGACAGCCGGAATTTGACATTT	2120
Qy	64	-----Glnaspargphe-----Tyrlysva	70
Db	2121	CAACACGCTTCTGAGGCTTACATCCACAGCATTTCAAGCGACCTTGCTTACAAGAA	2180
Qy	70	lleu-----Thr1aaglu-----Glnlysa1a-----	77
Db	2181	ATTGATGACAGTCTGAAGACTTACTTGATACCTCCAGCAGAGGAGCAATGTGAGCC	2240
Qy	78	-----Lys1alleu-----Lysgly	83
Db	2241	AATCTTAGAACCTGAGGCTTTGGAATATGTGTTCAAGTTGCTTGGTGGAGAGAC	2300
Qy	83	lnTyr-----Asnphasp-----Hisproasp	90
Db	2301	ATTATTTTACAGCTTATGAGCAAGAAACAGATGAGATTGGAAGATCATCATGAGACG	2360
Qy	91	Ala-pheasp-----Asnasp1eumet-----Hisargthr-----	100
Db	2361	GCCTTTGATTCATCAACATCTGATGAAAGTCAATACAAACATCCATCTTTTGA	2420
Qy	101	-----Leu1yaseu1le-----Valglu-----GlylythrVal	110
Db	2421	GGTGGCGGCTTTGAATATCATCTCCATCTGCTGATGATGTAAGTGTCTTGATGC	2480
Qy	111	GluVal-----Prothr-----TyraspheValthr-----Serargleupro	124
Db	2481	GAAGTTACTGAGCAACTCTGTATGATGTTCTACACTGATCCCTCTGTAACATCCA	2540
Qy	125	GluThr-----ThrValValTyrPro1aaspValVal-----Leuphegu-----	138
Db	2541	GAAGCAAGAACTACAGCTATGAAAT--GAGATAGTCCAGAGCAACCTTTTAAAGCAA	2598
Qy	139	-----Gly1lleuValPheTyrSer-----Gln1utllearg-----	149
Db	2599	GAATGCCGAGCATCTGCTTCTCTGTCATACCAAGAGCTGAAAGAGCTGCGAGACAG	2658
Qy	150	-----AspmetPhehis-----Leuarg-----	155
Db	2659	AAGATGACATGACAACCAAGTCTGAGAGAGAAATGATGATTCATACAGC	2718
Qy	156	-----LeupheValaspThr--AspSeraspValargLeuserargarg--	169
Db	2719	ATCTTGAGATCTTACTACAGAGATGCGGCTTCACTACCAACATATCAAGAGATC	2778
Qy	170	-----ValleuargaspValargArg-----GlyTargasp-----	179
Db	2779	ATGCTCAAGCTGCTGCGAAGTGAACCGAGACATCATCACTGAGCCGGGATCAATT	2838
Qy	180	-----Leu1leu1leuThr1leu-----	186
Db	2839	CTGATTAAGTCACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG	2898
Qy	187	TyrThr-----ThrPheValLysPro1a-----Pheg	196
Db	2899	TACTCTTCTTACATTTGAGACCTTCC--AGACAGCTCTGAAGCTTGTGAGACTTCTTGTATG	2956

```

QY 196 luGluPhe-----Cys----- 199
Db 2957 AGACCTTCATCATGTTCAAGSACCTCATTTGAAGAAGACGTACCTCGAGACGTGATGG 3016
QY 200 -----LeuPro-----ThrLeuPheTyrAlaAspValI 209
Db 3017 CCATGACATGTTCAAAACAGGGCTTCTCGAGACATCAACAAGTTTGCAAAACCA 3076
QY 209 le-----IleProArg-----GlyValAspMet----- 217
Db 3077 TGAACCAAGAGTTCTTGAACACACGAACTTTAGTTCCAGCTTGGAACAACATATTTTC 3136
QY 218 --ValAlaIleAsnLeuIleValGln-----His----- 226
Db 3137 ATCTGGCAGTGGCTTTATATCAACCGAGATTTCTCGACGTGAGACAGTTCTCACACGCCA 3196
QY 227 --IleGlnAsp--IleLeuAsn-----GlyAspIleCysLys----- 237
Db 3197 AATTAACAACAAATCTGATTAAGTATGAGGACATGAGACGCGTAAATTGGCTTTCATCC 3256
QY 238 -----ThrPheArgGlyGlySerAsn-----GlyTyrGse 247
Db 3257 GGTATATGTGTATCAACCTTGTGCAACAATACTGCTTCATCCAGGACATGTTAGAC 3316
QY 247 rTyTyLysArg-----ThrPhe-----SerGlu--ProGlyAspHis--Pro----- 259
Db 3317 CTATATTAGAGATGACACTTATCTCCCTGAGCTGAGCTCCGAAAGCAACCATACCAATCT 3376
QY 260 -----GlyMetLeu-----ThrSerGly-----LysArg 267
Db 3377 TCTTCGACATGATGCTGTGTAATATCAAGAAAGTGGGATTTCAAAAAGTTGAAACG 3436
QY 267 gSerHisLeuGluSerSerSerArg-----Pro-----His 277
Db 3437 AATATCATCTGAAAGCTGACCCAGAGGTAGAGGGGCGCGAGCGGACGACATGACAT 3494

RESULT 16
US-09-488-725B-7320
GENERAL INFORMATION:
  APPLICATION: US/09488725B
  APPLICANT: Yuanhua T. Tang
  APPLICANT: John Tillinghaast
  APPLICANT: Ankura Slink
  APPLICANT: Chenghua Liu
  APPLICANT: Radoje T. Dmanac
  TITLE OF INVENTION: Novel Contigs Obtained
  FILE REFERENCE: 784
  CURRENT APPLICATION NUMBER: US/09/488, 725B
  PRIOR FILING DATE: 2000-01-21
  PRIOR APPLICATION NUMBER: US 09/004,182
  PRIOR FILING DATE: 1998-01-07
  PRIOR APPLICATION NUMBER: US 09/034,341
  PRIOR FILING DATE: 1998-02-13
  PRIOR APPLICATION NUMBER: US 09/045,400
  PRIOR FILING DATE: 1998-03-20
  PRIOR APPLICATION NUMBER: US 09/321,214
  PRIOR FILING DATE: 1999-05-26
  PRIOR APPLICATION NUMBER: US 09/131,598
  PRIOR FILING DATE: 1998-08-10
  PRIOR APPLICATION NUMBER: US 09/170,294
  PRIOR FILING DATE: 1998-10-13
  PRIOR APPLICATION NUMBER: US 09/179,473
  PRIOR FILING DATE: 1998-10-27
  PRIOR APPLICATION NUMBER: US 09/181,430
  PRIOR FILING DATE: 1998-10-28
  PRIOR APPLICATION NUMBER: US 09/235,076
  PRIOR FILING DATE: 1999-01-20
  PRIOR APPLICATION NUMBER: US 09/234,611
  PRIOR FILING DATE: 1999-01-22
  Remaining Prior Application data removed - See File Wrapper or PALM.
  NUMBER OF SEQ ID NOS: 10289
  SOFTWARE: pt_ct_genes Version 1.01

```

```

; SEQ ID NO 7320
; LENGTH: 2124
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (106)...(1543)
; OTHER INFORMATION: similar to g55701850 in the genepept database release 114,
; US-09-488-725B-7320

Alignment Scores:
Pred. No.: 153 Length: 2124
Score: 297.90 Matches: 129
Percent Similarity: 19.24% Conservative: 49
Best Local Similarity: 13.95% Mismatches: 95
Query Match: 20.54% Indels: 656
DB: 1 Gaps: 4

us-09-488-522-2 (1-277) x US-09-488-725B-7320 (1-2124)
QY 4 AlaGlyGlyGluAspCys---GluSerProAlaProGluAlaAspArg----- 18
Db 10 GCTGAGACAGAGCC-TGCCGCGAAACCCCGGAGCCCGACATCCCTGTCATCCCTCGA 68
QY 19 -----Pro-HisGlnArgProPhe-----LeuIleGlyVal 28
Db 69 ATCCACCGACAGAGCGTCCACCGCGCTGGACCATGCGCATGACTCATGGGCTT 128
QY 29 SerGlyGly-----ThrAlaSerGlyLysSer-----ThrValCys-----Gly 41
Db 129 GCGCGTGAGACAGACAGAAAGCTCGGCTGAGTCTTGACGACACTTGACTTAAAGAA 188
QY 41 uLyStle-----MetGluLeu----- 47
Db 189 GAAATCAACACAGATACCAATGCTGCTGTTCAGAACCAATGCCAATGCAGAAAGAC 248
QY 48 -----GlyGlnAsn-----GluValGluGlnArg 55
Db 249 AGATGAAGAAAGAAAGAGACAGACCTGCCAGCTTACTCAACAGCTGATCAGAG 308
QY 56 Gln-----ArgLysValIleLeuSerGlnAsp-----ArgPhe 67
Db 309 CAACCTTGTGATTAACAACAAGTGAAGTCTTCAGCGGAGATCCAAATCCCTCT 368
QY 67 eTyTyLysValLeuThrAlaGluGln-----LysAlaLysAlaLeuLysGlyGlnTy 84
Db 369 GTACTCGGTGAAGTCTTTGAAGAGCTTGGCGCTGGAACACACACTTCTCAAGAGTCTA 428
QY 84 r-----AsnPheAsp---HisPro-AspAlaPheAspAsn-----AspLeuMet--- 97
Db 429 TGCCATGAGTTTCAATCGTCAATCCCAAGATACAA--GAGAACCATATGCCAGATGCTT 486
QY 98 -----HisArgThr-----LeuLysAsn-----IleValGluGlyLysThr--- 109
Db 487 GCTGAGCCCCCAGACAACTTAATGCCCAGATCTCACTGCTGACT--GCTAAACAGCTGC 545
QY 110 -----ValGlu----- 111
Db 546 CTTCGTCGTCGACATGCTTAGCCAACTAGAACTGGAACAACAAATACCCAGTGTATG 605
QY 112 ----ValProThrTyrAspPheVal-----ThrHisSerArg 122
Db 606 TCTCTCCCAACAGCTATAGCTGCGCTCCCAACAGAGAAAGTATGTAACAATAGGCGCA 665
QY 123 Leu-----ProGluThrThrValValTyr-----Pro 131
Db 666 ATTTTACCTTGAAGTGAAGTGAAGTATGCTGTGTCAGGCAATTAATTGGAAGAGCGCA 725
QY 132 AlaAsp-----ValValLeu-----PheGluGlyIle----- 140
Db 726 GAAGATCAATGACAGATTTGTATTTGACACCCCTGGGACGTGCTGAGTGTGCTCCAA 785

```

```

QY 141 -LeuValPheTyr--SerGlnGlu--IleArgAspMetPheHisLeuArgLeu-----Ph 157
Db 786 GCTCAAGATTGATTCATCCAGAAATCAAGGCTTTGTTGATGATGAGCTGATGATCAT 845
QY 157 eValAspThr-----AapSerAspValArgLeuSerArg----- 168
Db 846 GATAGCCACTCAGGCGCCACCAAGATCAGAGCATCCGATCCAGAGATGCTGCCAGAA 905
QY 169 ----- 169
Db 906 CTGCAGATGCTGCTTTCTCCGCCACCTTTGAAGACTGTGTGTGAAGTTGCCAGAA 965
QY 169 gValLeuArgAsp-----ValArgArg--GlyArgAsp--LeuGlnGlnI 183
Db 966 AGTGTCTCCAGACCCCAACGTTATCAACTGAACGCTGAGAGAGAACCTTGACACCAT 1025
QY 183 eLeuThrGlnTyrThrThrPheValLysProAlaPheGlnGluPhe-----Cys-- 199
Db 1026 C--AAGCAGTACTATGCTGTGTGACAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1082
QY 200 ----- 200
Db 1083 CCTCTACGGGGCCATCAACATTTGCTCAAGCCATGATCTTCTGCATCTCGCAAAAGC 1142
QY 206 aAsp----- 207
Db 1143 TAGTTGGCTGACAGACAGCTCTCAAAAGAGCCACAGGTGCTCTGTAAGTGGGA 1202
QY 208 ----- 213
Db 1203 GATGATGATGAGAGAGAGGCTGACGATGATGATGATGATGATGATGATGATGATGAT 1262
QY 214 -----ValAspMetValAlaIleAsnLeuIleValGlnHisIleGlnAspIle 231
Db 1263 TTGTGTGACCAACCAACGTTGTGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1322
QY 231 uAsnGlyAspIleCysLysTrp----- 239
Db 1323 CAATCTTGATCTTC--CCGTGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY 240 ArgGlyLysSerAsnGlyArgSerTrpLysArg----- 250
Db 1381 CGAGTCGGGCGCAGCGGCGGCTTTGGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY 250 ----- 250
Db 1441 AAGCAGACATGAATCTGTAACAGAAATCCAGAGCATTTTAATAGAGATGAGAAAG 1500
QY 250 ----- 250
Db 1501 TTGACACAGATGATTTGAGAGATTTGAGAAATAGCCACTGAGAGCTCCACAGCC 1560
QY 251 ThrPheSerGluProGlyAspHisProGlyMetLeuThrSerGlyLysArgSerHisLeu 270
Db 1561 ACTGATGCGACGCTCTGCGACTGCGCTGACAGAGAGAGAGAGAGAGAGAGAGAGAG 1620
QY 271 GluSerSer-----SerArg-----ProHis 277
Db 1621 CCGACATCAACCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1673

```

```

RESULT 17
US-09-488-725B-8009/c
; SEQUENCE 8009, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinhuast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radraje T. Dimaanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B

```

```

; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 8009
; LENGTH: 4558
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)....(4559)
; OTHER INFORMATION: n = a,t,c or g
; NAME/KEY: misc feature
; LOCATION: (167)....(2007)
; OTHER INFORMATION: similar to g1458255 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3i00, default parameters
US-09-488-725B-8009

```

```

Alignment Scores:
Pred. No.: 8,41e+03 Length: 4558
Score: 297.60 Matches: 134
Percent Similarity: 15.58% Conservative: 60
Best Local Similarity: 10.76% Mismatches: 77
Query Match: 20.52% Indels: 982
DB: 1 Gaps: 4

```

```
us-09-896-522-2 (1-277) x US-09-488-725B-8009 (1-4558)
```

```

QY 5 GlyLysGluAsp-----CysGlu-----SerPro-- 12
Db 3984 GGTGGGAGAAATGGAAGACAGGGGCAATTTGCTCCAGTATTTTCAATGATCTCTCTGG 3925
QY 13 -----AlaProGluAla--AspArgPro--His----- 20
Db 3924 GAGTTACAGGCTCTCTAGGCGCCAGATTTCTGTTCCACTACTAGTTAGAACTGACAGA 3865
QY 21 -----GlnArgProPheLeu-----IleGlyValSerGly--- 30
Db 3864 TAGTAACTAGGCCCTTTCTAGGGCCCTTCTCAACCCACAGAGAGAGAGAGAGAGAG 3805
QY 31 -----GlyThrAlaSerGly----- 35
Db 3804 TCCTTTGGGAGTTGATTAAGCTGAGCTGGACCTGAGACCGAGAGAGAGAGAGAGAG 3745
QY 36 -----LysSer-----ThrValCys--GluLysIleu 44
Db 3744 CTTGATGAATATATTGAGAGCCCAACCATGCCCCAGCTGCTGTTTGAACGAGAAATCA 3685
QY 44 et-----GlnLeuLeuGlyGlnAsnGluValGlnArgGlyValValIle 62
Db 3684 TGAATGGAACATATG-----TCTTCTTGGAGCCCT--CAGACAACTCATCTCTCT 3632

```

```

Qy 62 userGln---Asp-----ArgPheTyrIleuThrAla-----GluG 75
Db 3631 GGGCCCCGGGAGTACCCCTGCTTAAGGTGGC--AAGTTACTGTTGGCTCCAGTACAGCC 3574
Qy 75 IuIyAla-----LysAlaIeuIyGly-----GlnTyrAspPheAsp--- 87
Db 3573 AGGAATGCTGGCAAAAGATGATGAAGGGGTGGTGAACAGAACACAAATG--GACAAAG 3516
Qy 88 -----HisProAspAla-----PheAsp 94
Db 3515 GCTCAGAGAGAGAAAAGAGACCAAGAGGAGAGTGAAGAGAGAGGCTGAGCTTCTTA 3456
Qy 94 snAspIeuMet-----His-----ArgTh 100
Db 3455 ATGAGGTGAGCTGTGCTACTGAACACAGCTGGAGTGGCTTGGCCCTGAGCAGGG 3396
Qy 100 rIeuIyAsnIleValIgluIyIyThVal]-----Glu 111
Db 3395 CACTGGGAGATGTTCTTCAGT--AAGACTGTGGCAGAGCTGGCATAGAGAGCATCAG 3338
Qy 112 ValProThr-----TyrAspPheValThrHis----- 120
Db 3337 TCACCTTACTTCAGAGGAGTCAAAAGTGTTCAGAGTCTACCT--TTCATGG--CACTTTAA 3281
Qy 121 -----SerArgIeuPro-----GluThr 126
Db 3280 TGGCCTTCAAGCAAAAGTGGCTGAGATGCCCAAGATGGAGACACATTGGGTGTAAAG 3221
Qy 126 ----- 126
Db 3220 CTGGAGATGGCTTCCCTCCCAAAAGAAATTTTCCAAACCTATGTGCACTGCTGCTGT 3161
Qy 126 ----- 126
Db 3160 ACCTTTTGGGATCCAGGCTAGGATGATTTTCTTCTTAATAGTCTCTTCCCTGG 3101
Qy 126 ----- 126
Db 3100 CCTGGCCAGGTAGAAATATAGACTGTGTCATGAAGAACTGAGAGATGGGGCTCACCATATC 3041
Qy 126 ----- 126
Db 3040 AATAACTACTGCCCTCCCTCCGCGCATGGAGCTGCTGTCATGCTCTCCTACTGCTGC 2981
Qy 126 ----- 126
Db 2980 TGAATGATAAGAGATTCTTCAATTTCATGTCATATCAAGATGGGTGCTGGAG 2921
Qy 126 ----- 126
Db 2920 GGCTTGAAGTTAATGCTTGAAGCTGTAAGATTTGTAATAATCACTGACTGGAACATGA 2861
Qy 127 --ThrValVal]-----TyrProAla--AspValIleuPheGluGlyIleuVal 142
Db 2860 ACACTGTGGGTAAAGTTTCTTCCCTATATGATATATCTACTCTTCCACTGATGAATTA 2801
Qy 142 al-PheTyrSerGlnIleuIeArg-----AspMetPheHisIleuValGlu 156
Db 2800 TATAGCTTGAAGCAAAAGTGAAGATGTGCTCAGCTGAGATGATGGGA--CTGATGCTTA 2742
Qy 157 PheValAspThrAspSerAsp---ValArgIeu----- 166
Db 2741 GTGTGAGAGTGAAGTGGACAAAGTGAAGGCTGATTTGGCCCAAGTTCGGGCTCCTCTT 2682
Qy 167 -----SerArgValIleu 171
Db 2681 TCTTCAAGACCATGTGTCTATGACATCAAAAGAAATAGAGGGGAAAAGATATGG 2622
Qy 172 ArgAspValArgArg-----GlyArgAspIeu--GluGln-IleuThrGln 186
Db 2621 AGGAAGTCAGTAGAGAGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2562
Qy 187 Tyr-----ThrThrPheVal--LysPro-AlaPheGluGlu----- 197

```

```

Db 2561 CATACATAAGGACACTGCTTGTACCAAGTCTTGGAAACCAACATCAGCACTCT 2502
Qy 198 -----PheCysIeuPro-----ThrLys----- 203
Db 2501 AAGACTAACCAAGGCTACTGTCTCATTTTGGCTCCCTGCCCATCACTCAAGTGGCTCC 2442
Qy 204 -LysTyr----- 205
Db 2441 CAATATGATGAGCAATGACCTCTCTCAGCAAAAGATTTGGGCTTACCTTATTAGGCT 2382
Qy 206 --AlaAspValIleIleProArgGlyValAsp----- 215
Db 2381 CTGGGGACACATAGACCTTTGGCAGTTGATTAATAGTGGGACCTAACAGCTGGGTC 2322
Qy 215 ----- 215
Db 2321 CAGAGGTCCCATCTCTCTCTCCCCAGAGCTTGAAGATATATGAGAGAGTTCCAAAG 2262
Qy 216 -----AsnMet 217
Db 2261 GCCAGGGGTGTTCCAAAGCTTCCAGATCTGGAGAGAGAAAGCCCTGGAATAATTTA 2202
Qy 218 ValAlaIle-----AsnIeuIle-----ValGlnHisIleGlnAspIleuAsnG 233
Db 2201 AAGCATTTCTGGGAGAAATTTAGTTAATGATTTGGAACACCTGAGACTTGACTCAAG 2142
Qy 233 LysAsp-----IleCysLysTrp 239
Db 2141 GAGATTGTACGTGGCTGAAGATGCTGTGTCGAGGCTGGAAACAAGTGTGCTGGTGGC 2082
Qy 239 LysArg-----GlyGlySerAsnGlyArgSerTyrIleuAsnThr 251
Db 2081 AAAAATGTAAATGCTGAGCAGAGGTGGAGTGAAGAGAGAGAGAGAGAGAGAGAGAG 2022
Qy 252 -----PheSerGluProGly----- 256
Db 2021 GGCAAGAAAGCATTAATGATTTGTTCTCAGAGGTTGGGGAGCCCGCAGTACTCCCAT 1962
Qy 257 -----As 257
Db 1961 TGGGCTCTGGGTGAGGGGCCAACATCTTATCCTTGTGTAATCTCTGCTTTCTTGA 1902
Qy 257 pHisProGlyMetIeuThrSerGlyLysArgSerHisIleuGlu----- 271
Db 1901 ACATCTTTGATGCA--TCAGAGGAGAGAAAGAGATTAACAGCCCGATGATGGGGGC 1843
Qy 272 -----SerSerArgProHis 277
Db 1842 ACACCGGCAAAAGTGAAGGCCACAT 1818

```

RESULT 18  
 US-09-488-725B-5757  
 ; Sequence 5757, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghaast  
 ; APPLICANT: Ankura Sunku  
 ; APPLICANT: Chenghua Liu  
 ; APPLICANT: Radoje T. Drmanac  
 ; TITLE OF INVENTION: Novel Configs Obtained  
 ; TITLE OF INVENTION: From Various Libraries  
 ; FILE REFERENCE: 784  
 ; CURRENT APPLICATION NUMBER: US/09/488, 725B  
 ; PRIOR FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/034,341  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 09/045,400  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/321,214  
 ; PRIOR FILING DATE: 1999-05-26

PRIOR APPLICATION NUMBER: US 09/131,598  
 PRIOR FILING DATE: 1998-08-10  
 PRIOR APPLICATION NUMBER: US 09/170,294  
 PRIOR FILING DATE: 1998-10-13  
 PRIOR APPLICATION NUMBER: US 09/179,473  
 PRIOR FILING DATE: 1998-10-27  
 PRIOR APPLICATION NUMBER: US 09/181,430  
 PRIOR FILING DATE: 1998-10-28  
 PRIOR APPLICATION NUMBER: US 09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 PRIOR APPLICATION NUMBER: US 09/234,611  
 PRIOR FILING DATE: 1999-01-22  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 NUMBER OF SEQ ID NOS: 10289  
 SOFTWARE: pf\_ct\_genes Version 1.01  
 SEQ ID NO 5757  
 LENGTH: 2932  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (152)...(1752)  
 OTHER INFORMATION: similar to g15834428 in the genepept database release 114,  
 OTHER INFORMATION: Run with FASTX 3.3t00, default parameters  
 US-09-488-725B-5757

## Alignment Scores:

Pred. No.: 578 Length: 2932  
 Score: 295.70 Matches: 130  
 Percent Similarity: 17.52% Conservative: 55  
 Best Local Similarity: 12.31% Mismatches: 86  
 Query Match: 20.39% Indels: 788  
 Gaps: 1

us-09-896-522-2 (1-277) x US-09-488-725B-5757 (1-2932)

Qy 1 MetAlaSerAlaGly-----GlyGluAsp-----Cys----- 9  
 Db 34 CTAGCGTTGACGGAGCTGCGCGCGCTGATCTGACCTGTCACCTGCCCCCT 93  
 Qy 10 -----GluSerProAla--ProGluAlaAsp----- 17  
 Db 94 CCGCGCGCGCTGACCCAGAAACCGCGCGCAATCGCGCGCGCACTGAGCTGTTTCAT 153  
 Qy 18 --ArgProHisGluArgProHe-----LeuIleGly--ValSerGlyTyrAl 33  
 Db 154 GCGAGCGCTCAAGAGGCGAGTTTGGGGCCATGTGGGGCGGTGACCGAGGACACG 213  
 Qy 33 aSer----- 34  
 Db 214 TTCAGCGCGCTTTTGGTTTCATTCATAAAACAGCTGAACCTAGTCATCAAGT 273  
 Qy 35 -----GlyLysSer 37  
 Db 274 AGAATAAACAAGAGTCCCAAGAGAGATGGGTGAGACGACCTTAAGAAATTC 333  
 Qy 38 ThrValCys-----GluTyrIleMetGluLeuLeuGlyGluHisGluValAl 53  
 Db 334 ACATTCGTCTATGATGTATAGAGAAACATGTGAGAACTTGACAGCTCAATATTGA 393  
 Qy 53 u-----GlnArgGlnArgLysValValIle--LeuSer 63  
 Db 394 TATTTCACAATAAAGCTATTGGTGTGACGACCAAGGAGAAACCACTGATGCTGGA 453  
 Qy 64 GlnAspArgPhe-----TyrLysValLeu----- 71  
 Db 454 CAAGTATACGTGAGAGCTCTCTACAAATGCTGTGGTGTGCTTGAATTAAGACCAATC 513  
 Qy 72 -ThrAlaGluGlnLysAlaLysAlaLeuLysGlyGlnTyrAsnPhe-----Asp 87  
 Db 514 TACCGTTGAGAGCTTATGTAAGAAATTCAGAGAAATATATATCTTGTCAAGTCCAAAC 573  
 Qy 88 HisProAspAla-----PheAspAsn-- 94

Db 574 AGGCGTTCCACTTAGCACTTACTTCACTGAGTGAAGAACTTGCTGCTCTTGAACATGT 633  
 Qy 95 --AspLeuMetHisArgThrLeu--LysAsn-----IleValGlu 107  
 Db 634 GAGAAAGTTCAAAAGCCCGCTTAAAGAAACAGAGCTTTTGGAGCTATATATTCATG 693  
 Qy 107 Ly-----LysThrValGluVal--ProThrTyr----- 115  
 Db 694 GCTTATTGAGTTTACAGAGAGAGTCAATGAGGTCTTCACTGTACATGTATACAA 753  
 Qy 116 --Asp-----PheValThr--His----- 120  
 Db 754 TGCAGTAGACATGATGCTTTTCAACATGTCATCTTGAATGAGATTAACAATCTGCG 813  
 Qy 121 -----SerArgLeuProGlu--ThrThrValValTyr-- 130  
 Db 814 AATTATTGGAATTCAGATGAAGAAATCTTCAATGTCGAGAGTCTTGAAGATCTATG 873  
 Qy 131 -----Pro-----AlaAspValVa 135  
 Db 874 GCCTATGAAAATCTCTCATAGCGTGAAGAGCTGGGCTTGAAGGTGCCATATCTG 933  
 Qy 135 IleuPheGluGly-----IleuVal-----PheTyrSe 145  
 Db 934 GGTGTTAAGGAGCAAGTCTGCTGATGTTGGGAGCAAAATGTGCTTCCAGATTGACAG 993  
 Qy 145 GlnGluGluAlaArg-----AspMetPhe-----HisLeuArgLeu 156  
 Db 994 CCAAAA-ATACGATGAGAACAGAGATGTTTCTATGATTAATACAGGCCATTAAGTGTGA 1052  
 Qy 157 PheValAsp-----ThrAspSerAspValArgLysSerArg----- 168  
 Db 1053 TTTTCTGATCATGGCGCTTCTCACCAGAGGCTTACAACTTGGCAGAGCAAAACAGTA 1112  
 Qy 169 -----ArgValLeu----- 171  
 Db 1113 TATTATGCTTTGAGAGGCTGTAGATATAGCTGTGCTGTATGCTGCTAAGAGAC 1172  
 Qy 172 -----ArgAspValArgArgGly--ArgAspLeu--GluGlnIleLeuThr 185  
 Db 1173 AATCTTGGAATTAATAAGACTCAGAGAAATGAAACCTTCTTAAGAAAGTAGTACT 1232  
 Qy 186 GlnTyrThrThrPheValLysProAlaPheGluGluPheCysLeuProThrLysLysTyr 205  
 Db 1233 TCTTATGCGCTACTACTTCTGTCACGATTTTGGGGTTA-----TAT 1274  
 Qy 206 AlaAspValIleIlePro-----ArgGly-----ValAspAsnMetValAla-- 1220  
 Db 1275 GCACTTATTTGGAGAGCCAGCGAGAGGATATGCTGAGCTCACTCAGTTCAACCAT 1334  
 Qy 220 eAsn-----LeuIleValGlnHis----- 1228  
 Db 1335 AATATGCCATATTTGTTGCTGCTGATTAAGAGCTGTGTTTCCAAATCGAGAGATTTTG 1394  
 Qy 229 AspIleLeuSerGluAsp-----IleCys-----LysTyrPheHisArg 241  
 Db 1395 GATGCCATGATGAGACTGTGATTCACCTGATCTTTCAGAGATGATGAGAAATG 1454  
 Qy 241 LysIleSerAsnGlyArg-----SerTyrLysArgThrPhe-----Ser 253  
 Db 1455 ACC--AGCAACA--AATTTCTATGAGCTACAGAGACATTCGTATATACAGATGT 1510  
 Qy 254 Glu--ProGly-----AspHis--ProGly--MetLeuThrSerLys-----Lys 266  
 Db 1511 GAGAGCTTCATGAGCCCAAGCACTGACATGGGCGGCTATGGCGGAGAGGCTGAGA 1570  
 Qy 267 ArgSer--HisLeuGluSerSerSerArg-----Pro-His 277  
 Db 1571 AGAGGTGGGATGAGGTCTCGAACCAGAGAGATTTTGTGCGCCGTAC 1620  
 RESULT 19  
 US-09-488-725B-4967

```

; Sequence 4967, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillingshaast
; APPLICANT: Ankura Sinksu
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: From Various Libraries
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIORITY FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc CT _genes Version 1.01
; SEQ ID NO 4967
; LENGTH: 6506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6505)...(246)
; OTHER INFORMATION: similar to gi2224591 in the genepet database release 114
US-09-488-725B-4967

Alignment Scores:
Pred. No.:      5,23e+04    Length:      6506
Score:          294.10     Matches:      137
Percent Similarity: 14.51%   Conservative: 46
Best Local Similarity: 10.86% Mismatches:      83
Query Match:    20.28%     Indels:       999
DB:             1         Gaps:           5

us-09-896-522-2 (1-277) x US-09-488-725B-4967 (1-6506)
QY      2 Alaser-----AlaglygylgluaspygsyluseerPro-----AlaproglualasP-- 17
        |||||              |||||              |||||              |||||
Db      1020 GCCAGTTGAGCGCGGTGTGTGTGCATCAGTCTCCGATCCAGCGACGGGCCCGCC--TCGACGT 1077
        18 -----                                -ArgProHis----- 20
QY      1078 GGAGTGTGTCTCTGTCTTCTTCTCACTCTCTGCGTAGGCGAAGGTCTGCTCATCTCCA 1137
        21 -----                                -GlnArgProHelenille----- 26
Db      1138 CATCTGCATCTTCAGACATTTAATACTGATCATGTCCACACCCTGTGTGTAGAGAGACTCT 1197
        27 ---GIyvalserGIy-----GIyThralaserGIy-----Lysert 38
Db      1198 CTCGGCGTTGTGTGGCAGGCGCCAGCCAGCAGAAGG-GCCTCTGGTGTCGGGAGACAATCTCA 1256
        38 hrvalCyse-----GluyslleMet----- 44

```

Db	1257	CCCACTGCAAAATCCTCTGCTGATGCCATTCGGCATTTGAATGCTTTATGTCCT	1316
Qy	45	-GluLeuLeuGlyGln-----AsnGlu-----ValGluGlnArgGln	57
Db	1317	CGACCTTGCAATGCGAGCTTAAATCACTGTCGAAATCTCGTGTGTGAAACAGGCGCTCA	1376
Qy	57	rglyValVal-----	60
Db	1377	GGAAGGTGTGAGCAGACGCTGTCAAACTGTTGTCACGCGCCGCATTAATGAGACT	1436
Qy	61	-----IleuSerGlnAspArgPhe-----	67
Db	1437	GGGCAATTAAAGTCTTTAGTCGACAGCAACGGAACTTATCCGGGTGAATGTTCTGCCTGC	1496
Qy	68	-----TyrIleValIleuThrIalaglGlnIly	76
Db	1497	CCTTGGCGGTGATCAACGACGATGCCACCGATATGCAAGCTGACCGCA-----	1547
Qy	77	AlAlaValAlaLeuIlysgIlyGln-----TyrAsnPheAspHisProAsp---	90
Db	1548	-----GGTCAGACTCTCCAAATTCATCTCTTGGACCAACCCCGAGTGTG	1592
Qy	91	-----AlaPheAspAsnAspLeuMet-----	97
Db	1593	CGTATCGTAAGCGTTCTTGATGATGCGCATGAAACAGGCCAGCAGAAGTACAACGCGG	1652
Qy	97	-----	97
Db	1653	CACGCTGTTGGAGAGACTTCATTCCTGTGAGACGGGAATGCTGCTGAAGTCTTCAGCA	1712
Qy	97	-----	97
Db	1713	TGTTGGCCTTCAACCCCTGCGGTGCTCGAAACAAGATGCGGCCGACAGCAGAT	1772
Qy	98	-HisArg-ThrLeu-----LysAsnIleVal	105
Db	1773	TCAAGGACCTTGGGGTGTGATCTCCATGGTGAGGAAGTCCGAGACAGCATGCGGCT	1832
Qy	106	GluIlyLysThrValGluValPro-----ThrTyr	116
Db	1833	GCAGGGAATGCAACTTCTTCTCCAGCTGCATCAACCACTCGGGGCCAGATGCATTTCT	1892
Qy	116	spPheValIthrHisSerArgLeuProGluIthrThrValValTyr-----	130
Db	1893	TCAGCATCACCCAC-----CTGCCGACCTTACAGCGGGTATTATTCCTTATCTGCTT	1946
Qy	131	-----Pro--AlaAspValValIleuPheGluGlyIleLeuValPheTyrSerGln-	146
Db	1947	GGTTAAAGCCTTCTGCGACAGCCCGCATTCGATTAAGATGATCTGCTGTGCTGCGCTG	2006
Qy	147	-GluIleAspAspMet-----	151
Db	2007	CAMGGTCTTCGACATGTCACACTGGCATCATTAACGAGCACAAGCATTAAACAGAGAG	2066
Qy	152	-----PheHisLeu-----	154
Db	2067	TGTTGGGCTTCACTCTGTCGCCCACAATTTGGGTGCAAGTGTGAACGCGCTGCTCATATG	2126
Qy	155	-----ArgLeu-----PheValAspThrAsp-----SerAspValArgL	166
Db	2127	ACATGAAAGACTCCCCAAGGTTTGTGAAACAACATGTGGCCANTGGCCACAAGCGCAT	2186
Qy	166	euserArgAspVal-----LeuAspAspValArg-----	175
Db	2187	CGGGCCGAAAGCTCGGATCAGAGCAGAGCGGTGATGCTCGGCCAATGGGTGTTCAG	2246
Qy	176	-----ArgGlyArg-----AspLeu-----	180
Db	2247	GTTTCTTCACTCCAGAGGTAAAGGCACACTGCTCCGGGAGAGCTGTCTGTCAAGCCAGA	2306
Qy	181	-----GluGlnIleLeu--ThrGln-----	186





```

Db      3901 GCAGAAAGCCAGAGGTGAGCAGATGATCCGAGACCTCGAAGCCAGCATCGCCCGCTA 3842
Qy      55 -ArgGlnArgLysValValIleLeuSerGlnAspArgPheTyrIleVal---LeuThrAl 73
Db      3841 CAGAGAGAAATACGCCGCTCGATCTCAGAGGCCAGCCATCAAGGACAGACCTCGAGC 3782
Qy      73 a----GluGlnLys-----AlaLysAlaLeu-----80
Db      3781 TGTCCAGGCAAAAGTAAACCGGAGCACTGCTCTTCTGAAAGCTTGTCTGTGAACGTGA 3722
Qy      81 -----LysGlnIlyrAsnPheAspHisProAspAla-----91
Db      3721 ACCATGGGAAAAACAAGTGAAACTTTCAAAAACAGATGTCCACATGCTGGGAGACTG 3662
Qy      92 -----PheAsp-----AspAsp 95
Db      3661 TCTCTGTGAGCTGCGCTTCAATGCTTACGCGGTTACTTTGACGAGATGCGCTCAGAA 3602
Qy      96 LeuMetHis-----98
Db      3601 CTGTTCACCTACTCGTGTCCATCACTTACAGAACCAATCCAGTTCCTGACAGATAT 3542
Qy      99 ---ArgThr---LeuLysAsn-----103
Db      3541 TGCCAGAGCGGAATACCTTTCATGCTGATGAGCGTCTTCTGCGAGGCGAGCTCCTT 3482
Qy      103 -----103
Db      3481 GCGCTGATGACCTTGTGACAGAAAATGCCATCAGTGAAGATTCATAGGTATCC 3422
Qy      104 ---IleValGlu---GlyLysThrValGlu-----111
Db      3421 GCGATCATTTGACCCCTCTGAGACAGGCCACAGAAATTCATTATGAAATATTAAGATCG 3362
Qy      111 -----111
Db      3361 TAAGATCACAGGACAGCTTCTGTGATGAGCGCTTCAGAAAAGAACTTAGAGATGCACT 3302
Qy      112 -----ValProThrTyrAsp---PheValThr- 119
Db      3301 GAGATTCGATACCCCTCTGTGTCCAGATGTGGAAAGCTACGATCCAGTTTGAACCC 3242
Qy      120 -----HisSerArg-----122
Db      3241 GGTGCTGAACCGTGAAGTGGCGGGAACAGGGGGAGAGTCTGATCACTCTCGGGACCA 3182
Qy      123 -----LeuPro-----GluThrThrValVa 129
Db      3181 GGACATAGACCTGTGCGCATGTTTGCATCTTCTGTGTCACCCGGGATCCACTGTGCA 3122
Qy      129 IlyrProAlaAspValValLeuPheGluGly-----Ile 140
Db      3121 GTTCCACACAGATC-T-CTGTTCCCGGTTACTTTGTAACTTTCACAGTTAACCGGTA 3066
Qy      141 LeuValPheTyrSerGln-----GluIle-----ArgAspMet-----151
Db      3065 GCGATTTTACA-AGCCAGGTCTTAATGAAGTACTTAAAGCAAGCACTGATGTGGAC 3007
Qy      152 -----PheHisLeuArgLeu-----156
Db      3006 GAGAAACGATCTGATCTTCTTAAACTTCAAGGGGAATTTCAAGTCCGTTTCCGTCAGCTG 2947
Qy      157 -----PheValAspThrAspSer 162
Db      2946 GAAAAATCTCTACTACAACTCTGAACAGAGTGAAAGGGCGCATTTTGGATGACGACACG 2887
Qy      163 AspVal-----ArgLeuSerArg-----ArgValIle 171
Db      2886 ATCATTAACCACTCTGAGAACTGAAAGAGAGAGGCTGCAAGGTCCACAGAAAGTTGAG 2827
Qy      171 uArg-AspVal-----ArgArgGlyArg-----178
Db      2826 GAGACGAGCATTTGTCTATGACAGAGGTGAGAACCGTGTCCAGCAGATCACTCCGCTCTCC 2767

```

```

Qy      179 -----AspLeuGluGlnIle-----LeuThr 185
Db      2766 ACCGCGCTGCAGCAGCATCTTACTTACCAGTAGAGTCCCTCAAGAGCATCACTTGTGTAC 2707
Qy      186 GlnTyrThr-----ThrPheVal---LysProAlaPheGlu-----196
Db      2706 CAGTACTCCCTCCAGTTTTTCTCGAGACATTTATCACACAGCTCTTA--TACGAGAACCCGA 2649
Qy      197 ---GluPheCysLeuProThrLysLysTyrAla--AspValIle-----IleP 211
Db      2648 ACCTGAAGGGGTGTCA--CCGACACACACAGCGCTGTCCATTATTAACAAGACACTCTTC 2590
Qy      211 roArgLysValAspAsnMetValAlaIleAsnLeuIleValGln-----225
Db      2589 CAGGTGCGCTT--AACCGAGTGGCTTGAGAGCATGTGCATCAGAGCACATTACCTTTG 2532
Qy      225 -----225
Db      2531 CCATGCTGCTGCAAGATCAAACTGAAGGACACGTGGGGAGGCCACCTAGATGACG 2472
Qy      225 -----225
Db      2471 AATTCCAGCACTTCTTGAGAGAAATGAATGTCTGAGTGTGCTCCACCCGAGGA 2412
Qy      225 -----225
Db      2411 TCCAGGCGCTGACTGTGAGACAGCGGAGCGGTGTGAGGCTGAGCTGCTTCCGCGGT 2352
Qy      225 -----225
Db      2351 TTAAGGACTTGATGAAAGGTTCAAGGACAGACAGCAATTTGGCATCTGCTGAGACGA 2292
Qy      225 -----225
Db      2291 GCTCCCCGAGCAGACTGTGCTCCTTACTGTGAGTGAAGAAACACTGCAACCACTTG 2232
Qy      225 -----225
Db      2231 GCCAGGCATCCACCGCTGTCTGTGATCCAGGCTTTCCGGCCGATGCGCTGTGGCCA 2172
Qy      225 -----225
Db      2171 TGGCCCATGTTTGTTTCAACAACTTGGGAGTCTTTCATGTCAATCATGAGACAGC 2112
Qy      225 -----225
Db      2111 CGCTGCACCTGACCCAAATTTGGGACAGAGGTGAAGCCCAACACTCTGTCTTAATGT 2052
Qy      226 -----HisIleGlnAspIle-----230
Db      2051 GCTGTGTGCTGTGTTATGATGCAATGTCCAGGACCTTGGACGCCAGACAGAAC 1992
Qy      231 -----L 231
Db      1991 CGCAGATCACTTCAATTGCAATCGCTCTGCAGAGGCTTTTAAACCAAGATTAAGCAA 1932
Qy      231 euAsn-----GlyAspIle-----235
Db      1931 TAAACACCGCTGTAAGTGGGCGAGGTGGTGTATGTGTAAGAAATGTCATCTGGCCCA 1872
Qy      236 -----CysLysTrp-----238
Db      1871 GGTGCTGATGACGCTGGAAGAAAGTGTGATCCCTGAGCGCGATGCTGTCCGAC 1812
Qy      239 -----HisArgGly---GlySer---Asn-----GlyArg- 246
Db      1811 TCTTCTCAACATGAGATCAACCCCAAGGTGCTGTGAATGTGCTCGGTGGGGCGCA 1752
Qy      247 -----SerTyrLys-----ArgThrPheSerGlu- 254
Db      1751 TCTTTGTGTTGAGCAGCAGCGCAGGGGTGAAGGCCAACTGTGAGAGAGCTTCAGACAGA 1692

```

```

QY 254 ----- 254
Db 1691 TTCCCGTCTACGAGATATGCAAGTCTCCCAACGAGCGTCCCGCTTGACTTCTGCTGG 1632
QY 255 ProGly-----AspHisProGlyMetLeuThr-----SerGlyLysArg 267
Db 1631 CCTGGTTTACATGCGATCATTCACAGACCGCTTACGATACGACACGACGAGGCGTGTCAAGA 1572
QY 268 Ser---HisLeuGluSer----- 272
Db 1571 AGTATGAAATTTGAGAGCTTGACCTGCGGCTTGCGATACGATGACACGTCGCTGG 1512
QY 273 SerSerArgPro-----His 277
Db 1511 ATGACACGCGCCAGGCGACGCAACAT 1484

RESULT 21
US-09-488-725B-5251
; Sequence 5251, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dimanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 5251
; LENGTH: 2996
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2555)...(2220)
; OTHER INFORMATION: similar to g33880026 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-5251

Alignment Scores:
Pred. No.: 1.26e+03 Length: 2996
Score: 293.60 Matches: 145
Percent Similarity: 12.91% Conservative: 46
Best Local Similarity: 9.80% Mismatches: 84
Query Match: 20.25% Indels: 1208
DB: 1 Gaps: 4

us-09-896-522-2 (1-277) x US-09-488-725B-5251 (1-2996)

```

```

QY 3 SerAla-----GlyGlyGluSerCysGlu-----SerProAla-- 13
Db 475 AGTGAACCTCTTGCAAAAAGGTTTCGAAACATTGTCAAGCTTGGAAGAAGTCCCCACCTTG 534
QY 14 -----ProGlu-----AlaSerPro--- 19
Db 535 ATAAACACTCTAAAGACACCCCGAGGCTTTGAACGAGAGCCCTTCACACAAAGGCCAGCTC 594
QY 20 -----HisGluArg----- 22
Db 595 AGGCTCACCAGCATGTCTGTGCGCAACAAGCTTCCAGCTCCACATACCACTTCCTT 654
QY 23 -----ProPheLeuIleGly 27
Db 655 GAGATCTGCATTAGAGCGCTGAGTCCGAAAGAACATGTTGTGCATTTCCTTAGAGC 714
QY 28 -----ValSerGly---GlyThrAla----- 33
Db 715 TTGACTTTTATTAAGGCTTAGTTCAATCTCATCCAGGAGATTGGGCACTCGAATGAATACA 774
QY 34 -----SerGly-----LysSerThrValCys-- 40
Db 775 CAGATCTGACACATTAAGAGATTAATATACATGTCGCCCAAGCCTGAAATGCTT 834
QY 41 -----GluLysIle---MetGluLeuGlyGlnAsnGluValGluGlnArg 55
Db 835 TTATTAACATACATCAAGGTGTCTCCGACTGTCCAGAAAGACTTGCTCCAGAGG 894
QY 56 GlnArg-----LysValValIleLeuSerGln-----Asp--ArgPhe 67
Db 895 CAGAGAAAGCTGAGGTTCTTATGTATACAAAGCATTTCTTACATAGACGAGGGGT 954
QY 68 TyrLysValLeuThrAlaGluGlnLysAlaLysAlaLeuLys---GlyGln--TyrAsn 85
Db 955 GTTAAAGATCCCATATCACTGAAGAGACTTCCCTCAAAATGAGGCTCTGTACAAC 1014
QY 86 PheAspHisProAspAlaPheAspAsnAspLeu----- 96
Db 1015 CTTC--CATGAGATCTTCAAAAAAAGATCTCATAGCTGTAGGGAAGCGCGTGAC 1072
QY 97 -----MetHisArgThr-----L 101
Db 1073 ATTAACATATATATACAAAAATCATCATTCGTGACGCTCGGGCTTGTGTAATCTC 1132
QY 101 euLysAsnIleValGluGlyLysThr--ValGluValProThrTyr----- 115
Db 1133 TTCACAGTCTGTCTTCCAAAACAGGGCTCCCTGCTGCTTATTTCAAGTAACTAA 1192
QY 116 -----Asp----- 116
Db 1193 GTCAAGATCTGTTTCTTTAGCAGATTCAAGGGGAAAAATATATATTATGGGCTTCT 1252
QY 117 -----PheValThr-----His----- 120
Db 1253 AATTAACATTTCAATACAGATATCAAAATATAGTCAATTTTGAATATATCTATGATA 1312
QY 121 -----SerArgLeuProGlu-----ThrThrValValTyrProAla-- 132
Db 1313 TCCCTGATTAATATCAAGAAATCCAGAGACTTCGTAACACCAAGATTTTCAACAGGGGTG 1372
QY 133 -AspValValLeuPhe-----GluGlyIleLeuValPhe----- 143
Db 1373 AGACCCGCTGTGTTTCTTAGCAGACAGAGAAAGGA--CTAGTATACGGGCAATGTTCTC 1430
QY 144 -----TyrSerGlnGluIle-----ArgAspMet 151
Db 1431 CAGGAAGCCCTGTGAGCAGTACAGTACTGAATTTCTAATCTGAGCCAAATAGATCATG 1490
QY 152 -----PheHisLeu-----ArgLeuPheValAspTh 160
Db 1491 AACGAAATTTCACTGAACTGTATAGTAAATTCATTAACAAAGGCTTCTCTTCAAC 1550

```

```

QY 160 rApSeraspValArgLeuSer-----ArgArg-----ValL 171
    |||||
Db 1551 CCGTGCATCTGTTAACTCTCCGCGCTGTGACAGACATCCAGACAGAAAACATCAGTCC 1610
    |||||
QY 171 eu----- 171
    ||
Db 1611 TGCGTACTGTGAGTTGGGCTAGAGAAAACAAGCCCAAGATCCCTTTCTAAGCTATGA 1670
    ||
QY 172 -----ArgaspValArgArgglArgasp-----LeuGlulnilleuT 185
    |||||
Db 1671 CCMAACCTCGAAAACAGGAGCGTGAAGAGAGAGACAGACAGCTTGAAGAGCTTTGA 1730
    |||||
QY 185 hrglnlyrthrhphrpeVal-----Lysp 193
    |||||
Db 1731 CCCAAGGACACAGATCATAGGGGCGAGGGGACCTGTAGAGTTTATAGTGAAGGAGAGA 1790
    |||||
QY 193 roAlaphegluln----- 197
    |||||
Db 1791 GAGCTTCCGTGTATGCTCGCGAGAGAGTTCTGGAAGGCAACAGCTCTGTGCAAAAAC 1850
    |||||
QY 197 ----- 197
    ||
Db 1851 ACACATCTGGAGTGAATAACAGATCATTAACAAGACCCCAATTTGCTTCTCAAAAC 1910
    ||
QY 197 ----- 197
    ||
Db 1911 AAAATCAAACTTAATAAACTATGCAATAACCTGGGTGACATGAGTAGAGTACACTGG 1970
    |||||
QY 197 ----- 197
    ||
Db 1971 AGAAGTCTGTGAATGAGTGCATCAGCTGAGTCAAGAGAGAGCTGTGTGAAGTCAG 2030
    |||||
QY 197 ----- 197
    ||
Db 2031 CATCCACAGGTGCTACTGCGACCTAAGAGAAAGAGGAGCGGAGGCTTCCAAAC 2090
    |||||
QY 197 ----- 197
    ||
Db 2091 AGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2150
    |||||
QY 198 -----Phec 199
    |||||
Db 2151 GCGCATTTTCATTTGCTGTGAATGAGAAAGCTTCATCTCAGTCTGAGTCAAGTAACT 2210
    |||||
QY 199 yelauProthr-----LysLysLysLysLysLys 208
    |||||
Db 2211 GCATCCCATCCACTCTTCTCTCTTTTGTAGTGAAGCTTCAAGAACTGTGTGAATGT 2270
    |||||
QY 208 lile-----lileProArglYval-----AspAsnMet-----ValAl 219
    |||||
Db 2271 CCTCTCTTAACAACCGTCCCTTCATCAGCAAACTCTTGAAGTGTCTTTAAGTTCAG 2330
    |||||
QY 219 aileauLeuileVal-----Gln-----HisleGlnAspLileuAsn----- 232
    |||||
Db 2331 TCTTCAAAATCATGTATTCACAATAGAGTCCACTGTGAGTCTATCATCTGCTGTA 2390
    |||||
QY 233 -----Glyasp-----lileGlyLysLysLysLysLysLys 239
    |||||
Db 2391 GGGTATTCATTAAGGGGATGCTCTCTGTCAAGTGTGCTGGGCAATCTTCCCTTTGTTCAAT 2450
    |||||
QY 240 Arg----- 240
    |||||
Db 2451 AAGCCGAAGCTGTGTATTCATCTGTCAAGAAATAGACATCTAAGTCCATACATTT 2510
    |||||
QY 241 -----GlyGlySerAsn-GlyArgse 247
    |||||
Db 2511 TCATACAGTCTTGAGAGTACACACACTGTGTAGCCAGTTCAAGGGGCAATAGTGGCAG 2570
    |||||
QY 247 r-----LysLys----- 249
    |||||
Db 2571 TGTCTTTCTTTATAGCTGCTTAGCTTTAAGCTCTGAAGTTTGACGACGAGATTTGATTT 2630
    |||||
QY 250 -----ArgThr----- 251
    |||||

```

```

Db 2631 CTGCTTGAGGCTTTTCATTTCTTAACATGCTGTGAGATCAGATTCAGAACTAGAGCCGG 2690
    |||||
QY 252 -----PheSerGluProGlyAspHisPro----- 259
    |||||
Db 2691 CACATGTTCACTGTTCTGTCTACTTAACT-CCCGACATCATCTCTTCCCTGTTCT 2749
    |||||
QY 260 -----GlyMetLeuThrSer 264
    |||||
Db 2750 GGAACATCCTCTTTGAGGAGTACTATCTGTAGTGTCTTCATTTTCAGGTTGATTAATCC 2809
    |||||
QY 265 -----Gly- 265
    |||||
Db 2810 TGATCACTATTCATCAATGTTCCGACCAATCCATCATCTCAGTGAATATTGGTT 2869
    |||||
QY 266 -----LysArgSer-----His-----Le 270
    |||||
Db 2870 ACTGCCAATTTGTCAGACATTAAGCCCAAAAAGAAACAGTTTCATGACGCTGTCAT 2929
    |||||
QY 270 ugiUserSerSerArgProHis 277
    |||||
Db 2930 ACCATCTCCTGAATAATCCCAAC 2951
    |||||

RESULT 22
US-09-488-725B-8306/c
GENERAL INFORMATION:
APPLICANT: Yuanhua T. Tang
APPLICANT: John Tillinghaest
APPLICANT: Ankura Sunku
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Configs Obtained
FILE OF INVENTION: From Various Libraries
FILE REFERENCE: 784
CURRENT APPLICATION NUMBER: US/09/488, 725B
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pc CT_genes Version 1.01
SEQ ID NO 8306
LENGTH: 2782
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)-(2783)
OTHER INFORMATION: n = a,t,c or g
FEATURE:
NAME/KEY: misc feature
LOCATION: (77)...(714)
OTHER INFORMATION: similar to g13128 in the genepept database release 114,
OTHER INFORMATION: Run with FASTX 3.3c00, default parameters

```



```

Db 779 TTGCTGTGTAGATTTCTGTCCGAGCACCTCGAAGACAGATGCTGTGTGCTTTTG 720
Qy 238 PHIS----- 239
Db 719 GCACCTATGCTGGCAACTGAGCTTCTTCCCTTGAGTACTTTTGTATGTACAAGTAGA 660
Qy 240 ArgGlySerSerangly----- 245
Db 659 AGAAGTACAGATATAGATGTCTGACACTACCGCGGCACACAGCAATGAGTCAAGA 600
Qy 246 -----ArgSer-----TyrLys----- 249
Db 599 AGCCCTCAAGTAGAAGCGCAGATCCAGTTGACAGATACAAGACAGATAGAGCCCA 540
Qy 250 -----ArgThr-----PheSerGluPro-----GlyAspHis----- 258
Db 539 GAAAGAACAGATAGTGGGTGTGTGATCTCGGCTCCCGACGTCTGTCTGATCAATAA 480
Qy 259 -----ProGly-----MetLeuThrSerG 265
Db 479 GCTGCGAAGATAGCAACGACCTCCAGTATGATGAGAAAGTCCAGAGATCTCAAGAG 420
Qy 265 lylYsaYSerHleu-----GluSerSerSerArgProHis 277
Db 419 GAGAGAAATCGTGTATTAATAAATGAGAGGCTCCACAGGACAC 371

RESULT 23
US-09-488-725B-6550/c
; Sequence 6550, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dirmnac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 6550
; LENGTH: 4254
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (219)...(3436)
; OTHER INFORMATION: similar to gi1882215 in the genepept database release 114,
; US-09-488-725B-6550

```

```

Alignment Scores:
Pred. No.: 8, 75e+03 Length: 4254
Score: 291.80 Matches: 145
Percent Similarity: 13.79% Conservative: 44
Best Local Similarity: 10.58% Mismatches: 82
Query Match: 20.12% Indels: 1104
DB: 1 2

us-09-896-522-2 (1-277) x US-09-488-725B-6550 (1-4254)
Qy 2 AlaserlaGlyGlu-----Asp----- 8
Db 2412 GCAAGTACAGCGCGCCAGATGGAGACATCTCCAGGTCAGACCACTATCAAGAGCAC 2353
Qy 8 ----- 8
Db 2352 TGTTAAGACTGTGTGAGACGACCTTTACCTGCCAGAAATATCTTGTCAAGT 2293
Qy 9 -----CysGlu-----SerPro----- 12
Db 2292 CTTGTCAAAAGACTCAACTCTAGCTCTTGCGCTGGAAGTCAAGTCACTCA 2233
Qy 13 -----AlaProGluAlaAsp 18
Db 2232 AAACCTATTCACGCGGGGATGAGATCTTCCGAAACAATGCTCCGAGACTT--CG 2175
Qy 18 GPro-----HisGlnArgPro----- 23
Db 2174 TCCGCAACTTATGTTGATGATGAGGGGTGACTTCCCTTCAACGCTCCCAAGAA 2115
Qy 23 ----- 23
Db 2114 ACGCTTTGGCAATCAGGTCCTGGGCTCTAATATCATGATCCGAACACATGCTCAGT 2055
Qy 24 -----PheLeuIleGlyVal-----SerGlyGly-----ThrAla----- 33
Db 2054 CCCAACTGCTATTCAGAGTCTGTGACAGGGTCCAGATGGGGCATCCACATGCTGCC 1995
Qy 34 --SerGlyLysSer-----ThrVal----- 39
Db 1994 TCTCTGGGATTCCTCACTGTCACAGTCCAGACACAGACAAACAGGACCGTGGGAA 1935
Qy 39 ----- 39
Db 1934 GCATATTTCTGATGATTCAGATCCAGATCTCATGATGTTATATAGTCTGGA 1875
Qy 40 -----Cys-----GluLysIleMetGlu-----LeuLeuGlyGlnAsn 50
Db 1874 GTTGAACACAGACTGCTGAGCTGGAACCACTGTCTCAGATGATGTTCTGGGCACTGAC 1815
Qy 51 GluValGluGlnArgGlnArg-----LysVal-----ValIleLeu-- 62
Db 1814 CAGCGGGCCAGAGGAGCGTCACTGCTCTAAAGTACAGGCGCTGGAATCATCTTCAC 1755
Qy 63 -----SerGlnAspArgPhe----- 67
Db 1754 TTGCACATCGAGCTCTGCTTGAAGGCTTGTAGAGAACGGAACCTTCTCCCA 1695
Qy 68 --TyrLysValLeuThrAlaGluGlnLysAla----- 77
Db 1694 CACTGGGCACTGTGTACTGTAGACACCTTGTCTCTCTGATCATCTGATTTGACAG 1635
Qy 78 -----LysAlaLeuLys-----GlyGlnLysAsnPheAs 87
Db 1634 TTGTACCATAGGCTTGCTTCTTGTCCCTTCAAGCTGTGAGGATCAATTCAGA 1575
Qy 87 P-----His-----ProAsp-AlaPheAsn----- 94
Db 1574 GTTCACATAGGAAGATCTCGGCGCCGATCCAGATGACAACTAAGATGACAGCTGACGG 1515
Qy 95 --AspLeuMetHisArgThrLeuLysAsnIleValGluGlyLysThrValGlu-----ValP 113

```

```

Db 1514 GGGATCTGTCGAGAGGAGACTCCCAAT-----TCGACTGTAGAACCTCTC 1467
Qy 113 rothryrapphevalthr-----HisSerArgLeu----- 123
Db 1466 CAGTTCTCTGCACTGTCAAAAAGTGAAGCCATTCTAGCCTCAAGTGAAGCTGGCCTTG 1407
Qy 124 -----Progu-----ThrThValValTyrp 131
Db 1406 CCCACCTTTGAGAGGAACCATCATCCAGAACCTGACCTGTAAACCTTCCTTACATC 1347
Qy 131 rolaaapval-----Valleuphegluylleuvalpheyr-sergingl 147
Db 1346 CAGCTTCAATCTGCCCAGAAAGTCACTTATCTGATCTTGTTCGAACACTCCACTTC 1287
Qy 147 uillearg-----AspMet---PheHis-----Leu 154
Db 1286 AATCTCTGCCCCCTGGAGCTGTGTACCATCATCAATAGTCTCTCCCACTGTGGGT 1227
Qy 155 ArgLeupheval-----AspThr----- 160
Db 1226 GAGTTCTTCATCATGTACACACATGCTGAGATGTCTGGGTACCCAAAGCACAAGTCATA 1167
Qy 161 -AspSerAsp-----ValArg-----LeuSer-----Ar 168
Db 1166 TGGGTCGACTTGGCCCTCAATCAGGCCCTTCAATATTGTCTTGAAGTCAAGCCCTCG 1107
Qy 168 garyvalleuargapvalarg-----Arglyahapleugluin 182
Db 1106 AGCAGCCAGAGGTGAATTCGAATATGCCCTGGGAGAGGGAGAACGCAATGAGCCAC 1047
Qy 183 lleleu-----ThrInlyrThrThPheVal-----LysPro 193
Db 1046 ATCTTGAAGGTCAAGGACACAGGGGACCAAGTA-ATCGTTGGGCAACACAGAGAGGCA 989
Qy 194 AlaPhegluInphe----- 198
Db 988 GCATGTGAGTCCATGATCATGTGTGTCAGAGTAGTAACTCTGGGATATCCAGCAG 929
Qy 199 -----CysLeu----- 200
Db 928 TTGGTCATCCCTGTCAGTGTATGTAGGGTGGGCGCTCGAATGAGACATTTGACACA 869
Qy 201 ---ProThryls---LysTyralaapvalillelepro----- 211
Db 868 GCCCCACAGAGGAGAGGTCCCAATGA-GTGGCTCCAGTATCACCCGCAAAAGCCATG 810
Qy 212 -----ArgglyValaaspasmevalala-----Iasnleu 222
Db 809 TAGCTGCATGCCCTTGACTCTGCTTGTCAAAAATATTCTTCACTTCCACATCATCTG 750
Qy 223 llevalginhisille-----Glnaspileleu----- 231
Db 749 CACATCACTATCATAGTGAATTCAGTCCAGACGAGATGCTCTTCTCTGACCTGG 690
Qy 232 -----AsnGly----- 233
Db 689 GTGAACCTTGACTCAATGATGCCGAATGGCTTTTACCCAGCTTCACTGCTGAATGT 630
Qy 234 -AspIleCelyslyrThriargglylyserAsnGlyArgserTylys-----ArgT 251
Db 629 AAATGTTTGAGAGTGGGGGT-AGATCCCTTAACAGCCGAGCCACAGTTTCAAGCAGAA 571
Qy 251 hrPheSer-----GluProGly-----AspHisP 259
Db 570 GCTTCTCATATTAATGCGCCAGAGAGGCGCAGACCTGGGCAACATCTTATTTGAGCATT 511
Qy 259 roglymeLeuThrserylylys-----ArgserHisleuG 271
Db 510 CAGCCTTTTCCACGCTGTGGAGGTGACCCAGCAGAGGTAGCTCTGATGACTCATATGA 451
Qy 271 user-----SerSer-ArgPro 276
Db 450 GAGTTTTCGAGTAGAGTCTCTCTGTGTCTCA 418

```

```

RESULT 24
US-09-488-725B-3853/C
; Sequence 3853, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; FROM VARIOUS LIBRARIES
CURRENT APPLICATION NUMBER: US/09/488,725B
PRIOR APPLICATION NUMBER: US 2000-01-21
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pt_ct_genes Version 1.01
SEQ ID NO 3853
LENGTH: 5059
TYPE: DNA
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY:
LOCATION: (2)...(4524)
OTHER INFORMATION: Similar to gi473941 in the genepept database release 114,
US-09-488-725B-3853
Alignment Scores:
Pred. No.: 2,07e+04 Length: 5059
Score: 291.60 Matches: 145
Percent Similarity: 14.08% Conservative: 52
Best Local Similarity: 10.36% Mismatches: 75
Query Match: 20.11% Indels: 1129
Gaps: 5
DB: 1
us-09-896-522-2 (1-277) x US-09-488-725B-3853 (1-5059)
Qy 4 AlaGlylyglu-----AspCysgluser-----ProAlaPro----- 14
Db 2524 GAGGTGAGAGTATCATCCCAACACACTGTGTCAGAAATTCCTGCTGTGTGT 2465
Qy 15 -GluAlaAsp----- 17
Db 2464 CTCTGACAGATGCTTACAAAGCCTCTGCAAGGCTCAACAGCTGATCACTCTCTA 2405
Qy 18 -ArgProHisGlnArgProPheleuIleGlyValserGly-----ThrAlaSer----- 34
Db 2404 GAGACCCAGTGAATTCATTCAGCTTACAGATGATGATCACTTGTCCGGGT 2345
Qy 35 -----Glylys-----SerThyValCysgluysilleme 44

```

```

Db      2344 GCTCTTAGAAGATGCTTGGCAATATGCCAATACACAGAGAAATATGTCTTAAGTGT 2285
Qy      44  |||||-----
Db      2284 TGAATTGGAGATCTGCTGACTGCTGATTTTCTCCAAAGATTGATTATTCCTGCTAGTC 2225
Qy      47  ----LeuGlu-----AsnGluValGluGln-----ArgGln-----
Db      2224 CAGCTTGAGTGAAGAGCCAGACATCTTGAGAGAGACATCCAGGACAGTCCGCAATGTTTC 2165
Qy      57  ----Arg-----LysVal-----ValIleLeuSerGln 65
Db      2164 CGTGCCAGTGTGAGATATTATCATTTGTTATTAAGAGGTGAGAAATTTCTTTCTTGA 2105
Qy      65  sphaRpe-----TyrLysVal-----LeuThr--AlaGluGln 75
Db      2104 CCGAGATATGAAAAGCTTATTAAATCGCTCAGTTCCTGCTTGCGTGAGAGAG 2045
Qy      76  LysAlaLys-----
Db      2044 AGTAAGAGGCCGCCAGGCGAGACCTGTGTCTGCCAGAGTGAATAAGACTGTGATG 1985
Qy      79  ----
Db      1984 CCGGATGTCTGAGCAGACAGCTGTCTCAGGAATCCAGGGCTTCTCTGACAGAGTCT 1925
Qy      80  LeuLysGlyIleTyrAsnPheAspPro-----AspAlaPhe--Asp----- 93
Db      1924 CTCGCACTCATACACACCGGACACCCCGCAGACAGGCTTTTGATCTGACAGCA 1865
Qy      94  AsnAspLeuMetHisArgThrLeuLysAsnIleValGlu-----GlyLysThrV 110
Db      1864 TCTAGCTGAGCCATTAAGAGTTCACTAAGAGACTGAGGCGCTTCCGAGACAGAC 1805
Qy      110  aLglu-ValProThr-----
Db      1804 TCGAGGCTCCGACACTGTCTGACAGATTCACAGGCTTCTTCATGCTGAGATC 1745
Qy      115  ----Tyr-----AspPheValThr-----H 120
Db      1744 ACAGTGTTCAAAATCTACTAATACTGACAGTGCAGACTTCTTAAGCTTCTTC 1685
Qy      120  s-----SerArgLeuPro-----Glu 125
Db      1684 ATCCCGATCTCTCTTCAAGCATTCAGACATGACATCTTCTCAGATCCAACTGTTTC 1625
Qy      126  ThrThrValValTyr-----Pro-----AlaAspValValLeu-- 136
Db      1624 ACCAAGCTGTCTATGTGATTCCTCCCTGAGGGTTGGAAAGGTATGATGTCTGCTTGG 1565
Qy      137  ----PheGluGlyIleLeuValPheTyr----- 144
Db      1564 GTAGAAAAAGCTGATGATTTCTCAGTAAGGTACAGGGGTG--ACTCTATATTAAGAA 1507
Qy      145  ----SerGlnGluIleArgAspMetPheHisLeuArg-----LeuPhe 157
Db      1506 AACGTAGAGACTGTTAATCAGAGCTCCAGGATCT--CTCCAGCAGCACTGGTACAA 1453
Qy      158  ValAspThr--AspSer-----AspValArgLeu-----SerArgArgVal- 170
Db      1452 GTCAACTCCAGACAGTGTGCAAAAGCTGGAAGTCCCTGTGGGGAGACAGAGCGCTTG 1393
Qy      171  ----
Db      1392 TCTAAGCAAGATCAACATATTTCTCTGACACAGAACTTATGCTTAAGAACTTCTGA 1333
Qy      173  pVal---ArgArgGly-----ArgAspLeu--GluGlnIleLeuThrGlnIleTyr--Thr 168
Db      1332 TGTCTCAAGAGAGGGTGTATTCACCTCTCTTTCAGGCAAGTTCTTAACAGAGCTAAGACA 1273
Qy      189  Thr-----PheValLysPro 194
Db      1272 ACATCAAGAGTAAAAACCGGTGTGGGATCTTGGAACTTGGGAGTATTTGTAAAGCCAG 1213

```

```

Qy      194  IapheGluGluPheCysLeuProThrLys-----
Db      1212 GCAATGAACATTAACGTTATTCCTCCACAGAAAGTTTACTGACAGCTGAGGACTGG 1153
Qy      205  ----TyrAlaAsp-----
Db      1152 GCTGCAAAAGTACGATACCTGATTTATTCACACCTTGGCAGACAGATGTGTGAGTAG 1093
Qy      208  ----ValIleIleProArgGly-----ValA 215
Db      1092 ATACGACAGCTGGGAATATATCTCTCTTAATTCATCCAAAGGCGCTGATTAAGCTGG 1033
Qy      215  sphaMetValAla-----
Db      1032 ACCGCTGTGTTTCAAGTATGACTGTGGAGGTACAGCAAGGGGGCAGCATGGGAT 973
Qy      220  ----IleAsnLeuIleValGlnHisIle-----Gln 228
Db      972 CTTTCAACCACTTCAACATTAATTTAC--ACTGAGCATTTGATGAAAAACACACTGAT 914
Qy      229  AspIle-----LeuAsnGlyAsp----- 234
Db      913 GACCTTATCTCTTTCATGATGAGGAGACAGCAATATCATTCATATTAAGCCAG 854
Qy      235  ----IleCys-----Lys-----Trp-----His--Ar 240
Db      853 TTCTGTATGTATTTTGTCTGTTTGAAGCTGTGGCTTGTTGTAATGACATTCATTCAGAG 794
Qy      240  gGlyGlySerAsn-----GlyArgSerTyrLysArgPhePheSerGlu----- 244
Db      793 AACTGCTCAAAATTAGTTATGAAACAAAGACTCTATACATTCGTACACATTGTGG 734
Qy      245  ----GlyArgSerTyrLysArgPhePheSerGlu----- 254
Db      733 CTTTCTTTCAGAAAACTTGTGGCAGAGCCTTAATAATCTTTAAAGTGAAGAT 674
Qy      255  ----ProGlyAsp----- 257
Db      673 GGCATTTGCAATTGAGAAAGGTCCCGGCAAGAAAACAAAATTTTCATCTTCTGTTTC 614
Qy      258  ----HisProGlyMet--LeuThrSer----- 264
Db      613 TTCTATATTTCAATTCATTCATATCTTCTCTCGGGTGGCTTCCCTTTTCTATG 554
Qy      264  ---- 264
Db      553 CTTCCGGGGTACCTGAGAGCTTTAGGCTGTCTTCTTCTTCCGATTCAAGTT 494
Qy      265  ----GlyLysArgSerHisLeuGlu----- 271
Db      493 AGATCTCTGGGCGACAGCTTCTTTAGAGTCTGAATGATTCATCAACATCACTGGGTG 434
Qy      272  ----SerSerSer----- 274
Db      433 GAATPACTGATTTGGCTTACACTGCTGTGACTTCTTAAGCAAAAAAGTAAGCCAGCGGC 374
Qy      275  ----ArgProHis 277
Db      373 ATGAGGCCATAT 361

```

```

RESULT 25
US-09-488-725B-6204
; Sequence 6204, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Configs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784

```





```

QY 176 gelyarpeleuglnleleu-----Thr 185
Db 4461 AACTCAGAAATGATGTATATGTCATGCCATCTCTCCAGAGCCCTTACA 4520
QY 186 GlnTY-----ThrPhe-----190
Db 4521 GGTTCATCATTCAGTCCAGCCGAAATGATGAGACAGACTGATTTCTGTATCT 4580
QY 191 -----ValysProAla-----PheGlnGluPheysleupr 201
Db 4581 CAGAGAAATGCCCGCTCTTGGAAATGCCATGATGTTCCATGTACTGTCATACC 4640
QY 201 oThrlYslyS-----TyrlAlaSP-----207
Db 4641 CGAGAGAAAGACTTATAT-GATCGGTTGGATTCAAGTATCCCGGTAGCAGCCACT 4699
QY 208 -----VallleleProArGlyVal-AspAsmMetValAlaIleAs 221
Db 4700 CCCACCTCAGAAAGTATGATCATGCCAGATGTCAGACAGATATG9--GCTATCAA 4757
QY 221 nleu-----lleValGlnHislleGlnAspIleleuBenglyAspIleCys 236
Db 4758 TATCCATTCACCTCTACAGATGTGACAGAA-----GATGGAACTCCTGT 4802
QY 237 LysTrp-----His-----ArgGly-----GlySerAsn-----244
Db 4803 GCTTGTCCTCCATGTCATGATTTTTCAGAGAGCTGTAAATGATTGTGGAGAGACAG 4862
QY 245 -----GlyArgSerTYr-----248
Db 4863 GCTTCATGTGAATGCTATATTCGTGTGATTTGGACCCACAGCCCTTCACCTTGC 4922
QY 249 -----LysAlaGlnPheSerGlnProGlyAs 257
Db 4923 TATCAAAATCCAGAGAAAGGTTGTAGATGACATGAGGTGTGAGACAGACTCCGCA 4982
QY 257 P-----His-----ProGlyMetLeu-----ThrSer-----264
Db 4983 GCGCAATGACGCCCATCAACTGACAGCTGTCTCCGTCTTCACAGATGAGAGAG 5042
QY 265 -----GlyLys-----ArgSerHis-----269
Db 5043 CTAGGGAAATAGATGATGACTTCTTCCAGTGAAGCCACGCTTAGCAACAAG 5102
QY 270 -----LeuGlnSerSerArgPro-----His 277
Db 5103 AAGCTGATCTCTGGAGGCTTCCACCCATCTGATTTATTCAC 5144

RESULT 26
US-09-488-725B-6655/c
; Sequence 6655, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaet
; APPLICANT: Ankura Sinhu
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dzmanac
; TITLE OF INVENTION: Novel Configs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294

```

```

; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc CT_genes Version 1.01
; SEQ ID NO 6655
; LENGTH: 4182
; ORGANISM: Homo sapiens
; TYPE: DNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (195)..(4027)
; OTHER INFORMATION: similar to g11228047 in the genepept database release 114.
; US-09-488-725B-6655

Alignment Scores:
Pred. No.: 8 41e+03 Length: 4182
Score: 291.10 Matches: 136
Percent Similarity: 16.498 Conservative: 56
Best Local Similarity: 11.684 Mismatches: 84
Query Match: 20.084 Indels: 893
DB: 1 Gaps: 3

us-09-896-522-2 (1-277) x us-09-488-725B-6655 (1-4182)
QY 2 AlaSerAla-----GlyGlyGlnAspCysGlnSer-----ProAlaProGlnAlaAspArg 18
Db 2095 GCGTGGCCAGTGGCGGAGAGACAATTCCTCAAGTTCTCATCTCAGGCCCCACAG 2036
QY 19 ---Pro-----HisGlnArgProPheLeu-----25
Db 2035 TTACCTGTGAGACTGGGCTGTGATGAGCAACTCTGCTGAGACCTCCACGCTCAGTGACT 1976
QY 26 -----lleGlyValSerGlyGly-----31
Db 1975 CCGCTGGCAGCTGTGTTCTCAAGTATGATGAGGCGCATCGATGAGAAATGAGAAAG 1916
QY 32 -----ThrAlaSerGlyLys-----SerThr-----38
Db 1915 GCAAGGTCGGGATGGGTGGGGGCGAGCATGCACTAGCAGCGGCAATGGAGCGAGGCT 1856
QY 39 -----ValCys-----GlnLysIleMetGlu--LeuLe 47
Db 1855 CCCTCACCCAATGAGCTGTCTCCGTCACTGGGAGCAGAGTAGTGTGCGAGCCCTGCT 1796
QY 47 nGly-----GlnAsn--GluValGlnGlnArg-----55
Db 1795 GGGTCTGTGTATACAGATGTCATTCAGACAGCGGTGCCAGCATGATGAGCGCTGT 1736
QY 56 GlnArgLysVal-----VallleuSerGlnAspArgPhe 67
Db 1735 GCCAGCGGGTCCGGGCGCAGAGATGACACACAGCGCTTTGGGAGCCGCGAGTTT 1676
QY 68 TyrLys-----ValleuThrAlaGlnGlnLysAlaLys 78
Db 1675 CGAAGAGAAAGCGCTGCAACGTGATGTGGGGTGTGACAGGCTTCACACAGCTGC 1616
QY 78 sAla-----LeuLysGlyG 83
Db 1615 CGCTGTAGCGGCTGTGCTGCCCACTGAGCTTGTGAGGAGGAGGAGGCTTCAGGGGCT 1556
QY 83 In-----83
Db 1555 AATCGCTTTTCAGGTCGTGCTAGCTCCATCCGGGAGATGTCAATGAGACAGACAGTGTG 1496

```

```

QY      83 ----- 83
Db      1495 AAAAAGCATCTGAAGAGAGATGACACCAAGCCCAAGACAGCAAAAGAGACAGAAC 1436
QY      83 ----- 83
Db      1435 TCCTGATGAGCGGGCACTAGGAGTGAAGTACCGATGAGATGATGCCCACTCCGTGGCC 1376
QY      83 ----- 83
Db      1375 ATGTTCTTCAATGATGACCAAGCTCTGCTGCTTAGGCTTGGCGATTCGCAAGCTTCAACC 1316
QY      84 ----- 84
Db      1315 TCCAGGTTCTACCGGGGTTGAGACCAACTTGTGAGACCAAC-ACATTTCTTAACCC 1257
QY      95 pIueMet-HisArgThrLeuLysAsnIle-----ValGluGly-----Lys 108
Db      1256 AATTAACCAACCAAGGATGGAGAAATCTGCGCCCAATTAGAGGTGGCGCTCAGGCCGAA 1197
QY      108 sThrValGluValProThr-----TyrAspPheValThr----- 119
Db      1196 GATGTGTCAGAGTCCCAACAGACATGACGACGAGCTGAGCACTGTACCAAGGACGACGAG 1137
QY      120 -----His----- 120
Db      1136 GGCAGCCCCCACTTGACTTGACATGTCATCTTCCGGTGAGAGATGATGAGGC 1077
QY      120 ----- 120
Db      1076 AAACAAGATATGATGAGTGTACAGAGGGAGATGAGCTCAGACCAATCTCTCTT 1017
QY      120 ----- 120
Db      1016 GAAGTACGATGACGACGAGCTCTCCGCGAAGGCTGAGTGGGGGTGACAGAG 957
QY      121 -----SerArgLeuPro-GluThrThrValValTyr-----ProIle- 132
Db      956 CATCAGCGGGACGACGAGCTGCGCCAGGAACTTGCGATGTGATGCTGAGAAACAGAGGT 897
QY      133 -----AspValValLeuPheGluGlyIle-----LeuVal-----PheTyr-SerGln 146
Db      896 GATGTGTAGAGACATCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 838
QY      147 GluIleArg-AspMetPheHis-----LeuArgLeu---Ph 157
Db      837 GAACACCAATTAACAAGCTTTGAGTGTGCTGAAGTCTGACAGGTTTATGAGCTCTGCT 778
QY      157 eValAspThrAspSerAspValValArgLeuSer-ArgArg-----ValLeuArgAs 173
Db      777 GGTGATGATGCTCCCAATGATGTCAGATCAGATGAGAAAGCTTCCAGTCAATCTGCGCA 718
QY      173 pValArgArgGlyArgAspLeuGluGlnIleLeu-----ThrGlnTyrThrPheVal 192
Db      717 AGTTCACAGGGGAGACAGACAGGATCATCTAGAGAGTTCCTGAGCTTCTCTTA 658
QY      192 ySProlAlphe-----GluGluAlphe 198
Db      657 GGCCTGGAGAGAGTGGCTACTTGCAGACACAACTCTCAAGCTCTGATCCCAAGC 598
QY      199 CysLeu-----Pro-ThrLys--- 203
Db      597 TGTCTCTCAGACAGTGTTCGAGTCTCTCACCAGTGTGATGCCGGGACAAAGGTG 538
QY      204 -----LysTyr-----AlaAspValIleIleProArgGly---ValAspAsnMetVa 218
Db      537 AACGAATATCACTTACTGCCAGAGAGTCTTGTGCGAG--GGAACACTGAGCACTTAC 480
QY      218 IAlaIleAsnLeuIleValGlnHis-----IleGlnAspIleLeuAsn 232
Db      479 AAATATCTG-CTGAGCATTAAGCACCGGGGACCCACATACCACTCAGG--CTGCTCAGT 423
QY      233 -GlyAsp-----IleCys-----LysTrp-----HisArgGly 241

```

```

Db      422 AGCTCTCTCTTGTGTCGGTCAAGTCCACAGAGTGGGGGAGTAATCCTTACAGGGGT 363
QY      242 Gly-----SerArgGly----- 245
Db      362 GGTGAATTCACAGGTCCTCTTCTGTCAGAGGGAGTTTCAGAGTGGGTACACAGAGC 303
QY      246 ----- 247
Db      302 TAAGATGCAAACTCTGAGAGAGATGAGGATGGATGAGATGACACAGAGAGGCC 243
QY      248 -----TyrLysArgThr-PheSerGlu----- 254
Db      242 ATGTTGTAGAGAGCCAGATATCTTCTCAGCAGACCTTCTCAGTACGAGGTATCCTCAG 183
QY      255 -----ProGly-----AspHisProGlyMet-----LeuT 263
Db      182 CCGAAGTCACCTTGTGCTGCTCCATCCGGAAGTACATGATGATCACCCTGACACACTTGA 123
QY      263 hSer-----GlyLys-----ArgSerHisLeuG 271
Db      122 CAGCACTGACAAAGAACAAACATGTGCAAGTACTGTGTAGAAAGGAGAAAGCACTTAA 63
QY      271 luserSerSerArg-----ProHis 277
Db      62 AAAGAGTAAAGGCTCTGCACAC 39

RESULT 27
US-09-488-725B-8160
/ Sequence 8160, Application US/09488725B
/ GENERAL INFORMATION:
/ APPLICANT: Yuanhua T. Tang
/ APPLICANT: John Tillinghast
/ APPLICANT: Ankura Sanku
/ APPLICANT: Chenghua Liu
/ APPLICANT: Radoje T. Drmanac
/ TITLE OF INVENTION: Novel Configs Obtained
/ TITLE OF INVENTION: From Various Libraries
/ FILE REFERENCE: 784
/ CURRENT APPLICATION NUMBER: US/09/488,725B
/ CURRENT FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/004,182
/ PRIOR FILING DATE: 1998-01-07
/ PRIOR APPLICATION NUMBER: US 09/034,341
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 09/045,400
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: US 09/321,214
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: US 09/131,598
/ PRIOR FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: US 09/170,294
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: US 09/179,473
/ PRIOR FILING DATE: 1998-10-27
/ PRIOR APPLICATION NUMBER: US 09/181,430
/ PRIOR FILING DATE: 1998-10-28
/ PRIOR APPLICATION NUMBER: US 09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ PRIOR APPLICATION NUMBER: US 09/234,611
/ PRIOR FILING DATE: 1999-01-22
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10289
/ SOFTWARE: pc_ct_genes Version 1.01
/ SEQ ID NO 8160
/ LENGTH: 3629
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (97)...(3030)
/ OTHER INFORMATION: similar to g13300094 in the genepept database release 114,
/ OTHER INFORMATION: Run with FASTX 3.3c00, default parameters

```

US-09-488-725B-8160

## Alignment Scores:

Pred. No.: 4.39e+03 Length: 3629  
 Score: 290.00 Matches: 139  
 Percent Similarity: 14.00% Conservative: 65  
 Best Local Similarity: 9.54% Mismatches: 73  
 Query Match: 20.00% Indels: 1186  
 DB: 1 Gaps: 4

us-09-488-522-2 (1-277) x US-09-488-725B-8160 (1-3629)

```

Qy 1 MetAlaSerAlaGly--GlyGluAsp-----CysGluSerProAlaProg 15
Db CTCTCTCTGTAATCTTGGGGAACAGAAATACACCATCACATGATACAGACCAAAACCCG 608
Qy 15 LuAla-----Asp-----ArgProHis-----GluArg 22
Db AGAGCTCCGGTGGATGCCACCTACTTGTACTATGCGGCTCACTGCTGAGACGACGT 668
Qy 23 -----ProHeLeuIleGly-----Val 28
Db 669 GGACTACAGATGTCCTCCACTTGTGTCTCAATGTGATGGCTGGTGTGACTGTGACAG 728
Qy 28 alSerGlyIYThrAlaSerGly--LysSerThr-----ValCys 40
Db 729 TGATCTGGGGACGTCTGTGGATCCAAAATACGCTCCCTGCTGTGGCTTTTATGT 788
Qy 41 -----GluYsIleMetGluLeu----- 46
Db 789 CTGGCAGCGGAGGCTGTGAGAAAGTGTGACATCATATGTGCTGTGAGACCTGGC 848
Qy 47 -----LeuGlyGln-----AsnGluValGlu----- 53
Db 849 CTATCTGACCTTGATGTCTGGGAGGTGGGCGCATCAAAAGTGAATACCGTTCCC 908
Qy 54 --GlnArgGlnArg----- 57
Db 909 CAAGGAGACAGAGGCCCAAGAGCAAGCTGACGCCCATCTGTATGTGGAAATATCTTAC 968
Qy 57 ----- 57
Db 969 CAGCCTTATGCTCTCCCTCAATGTGTACAGAGGGGTTGTGTGTGCGCCGCGGACG 1028
Qy 57 ----- 57
Db 1029 CACACTTCTTTGCTGGAGAGGCCCAAGCTGATGCGGTACCATCGGGAGCAAGGGGGA 1088
Qy 57 ----- 57
Db 1089 GTGTGTGATCAGCCCGACAGACGTCAGATTGTATCCGGACTCAAAAAGCAAGAACAA 1148
Qy 58 -----Lys--ValValIle 61
Db 1149 GCTCACTACTTGAAGAAATTAAGTCTTGTGATAGAGACACCATGAAACCCCATGCTGTC 1208
Qy 62 LeuSerGlnAsp-----ArgPhe-----Tyr-----LysValIle 71
Db 1209 GTCTACCAAGATCTGAGAGATTTCCCAACATCTACCCAAACATCGGAAATATGTAT 1268
Qy 71 uThrAlaGlu--GlnYsAlaIleLeuIleGlyGlnTyr----- 84
Db 1269 TCTGTCTGATTCAGAGAAAAAGGCTTTGA--GAAAGTTATCAACTGTGTTGACCAAGACT 1326
Qy 84 ----- 84
Db 1327 TCAGAAAGCAGACCTACACCGTGTCTCGGATGTGAGAGAGAACCCCGCATGCCCCCT 1386
Qy 85 -----AsnPheAspHisProAsp- 90
Db 1387 GCCCGGCGGAGGCCCGCGGTGATCCATGCTTAAGAGACATGTGCTACATCATCTGAGC 1446
Qy 91 -----AlaPhe----- 92

```

```

Db 1447 ACCTTCTGCTGATGTGGCTGGGTGGCCCTTATCATCATACCTATCCCTGAGCATGATCAG 1506
Qy 92 ----- 92
Db 1507 CAGCAGAGCTCCAGCACACAGAGTTCCAGAAAGAACTGGAAGATTCAGCTCTCCGAG 1566
Qy 93 -----AspAsnAspLeu 96
Db 1567 CAGCAGCAGAGAGCTGCCCTTCCACCACTTGAGACACGCGCTCAGACGCGGAGCTC 1626
Qy 97 Met--His-----ArgThr----- 100
Db 1627 CTGGACACGTCTGGCCCTACTCAGAGAGCTCGGGACACAGACCCCGACAGCTCCCC 1686
Qy 101 -----LeuYsAsnIle--ValGluGly----- 107
Db 1687 AGGGCTTCAACACATGCTCTGCTCCGCGAGCTCTGCTCAAGGCTTGGCAGAGCCCC 1746
Qy 108 -----LysThrValGluVal-----ProThrTyr-----AspPheV 118
Db 1747 TCCCTGGACACAGACGATGAGAGAAACAGCGCTGTGATAGTTGGAAATTTCC 1806
Qy 118 alThrHisSerArgLeuPro-----GluThrThrValValTyr----- 130
Db 1807 TTCTGTCCCAAGATGCTCTGGGCGCATGAGCTGAGGGGCAATTTGTATCCGGGGCATG 1866
Qy 131 -----ProAlaAspVal-----ValLeuPheGluGlyIleLeuValPheT 144
Db 1867 TTTGACAAACGC--GAGTGGCGGTGAAGAGATCCCTCCCGAGT--GTTTGGC--TTGC 1921
Qy 144 YrSerGlnGluIle----- 148
Db 1922 CAGACCGTGAAGTCCAGCTGTTCGAGATCGATGAGCACCCGAAAGTATCCGCTACT 1981
Qy 148 ----- 148
Db 1982 TCTGCAGAGAAAGACCGGCAATTCAGTATCTGCCATCGAGCTGTGACGCCAACC 2041
Qy 149 -----ArgAspMetPheHisLeuArgLeu----- 156
Db 2042 TGCAGAGTATGTGAGACAGAAAGACTTGGCGATCTCGGCTCGAGGCCCATCAGCTTGC 2101
Qy 157 -----PheValAspThr 160
Db 2102 TGCAGAGACCACTCGGCGCTGGCCCACTCCATCCTCAACATCGTTCAAGAGACC 2161
Qy 161 AspSer----- 163
Db 2162 TAAAGCCACACACATCTCATATTCATGCCATGCCAATGACAGGCAAGATCAAGCCATGA 2221
Qy 163 pValArgLeu-----SerArgArgV 170
Db 2222 TCTCCGACTTTGGCCTCGGAAGAAAGCTGGGAGAGACACAGATTTCAGCGCCGAT 2281
Qy 170 alLeu-----ArgAspValArgArgGlyArgAspLeuGlnIleLeu-- 184
Db 2282 --CTGGGCTGCTGGACAGAGGCTGATCGCTCCAGAGATGCTGAGAGAGACTGTAA 2339
Qy 185 -----ThrGlnYrThrThrPheVal----- 191
Db 2340 GGAAGAACCTTACCTTACGATGAGACATCTTTCTGAGAGCTGGCTTTTACTACGTGT 2399
Qy 192 -----LysProAlaPheGluGluPhe----- 198
Db 2400 CTCTGAGGGCAGCAGACCTTTTGGCAGAGTCCCTGACGCGGACAGCCACATCTCCTGGG 2459
Qy 199 -----CysLeuProThrLysLysYrAlaAspValIleIleProArgG 213
Db 2460 TGCCTGACGCTTGAATGCTGTCCACCAAGAGAGACGAAAGCGTATGTCAGAGAAAT 2519
Qy 213 yValAspAsnMetValAlaIle-----AsnLeuIleValG 225

```

```

Db 2520 GATAGAGAAAGATGATTCGATGATCCTCAGAAACGCCCTCAGACGACGCTCAA 2579
QY 225 nhis-----Ilglnaspile----- 230
Db 2580 ACACCCGCTTCTTGAGCCTAGAGAACAGCTCCAGTTCTTCCAGGACGCGACGAC 2639
QY 231 -----Leuasnlglyasp11ecyllys---TrpHisArgglyly--Ser 243
Db 2640 AATAGAAAAGAAATCCCTGGATGGCCGATCTGTAAACAGTTAGAGAGCGCGGAGAGC 2699
QY 244 AsnGly----- 245
Db 2700 CGTGTGAGATGAGTCTGCGGAGGAGAAATCATCTGACCCCTCCAGACAGACCTGCTAA 2759
QY 246 -----ArgSerTyrlys-----ArgThrPheSerGlyPro----- 255
Db 2760 ATTCAGAGACCTAATAAGGTGTGTTCTGTCAAGATCTCC-TCCGAGCCTAGAGAAATAGA 2818
QY 256 -----GlyAspHisProGlyme 261
Db 2819 AGCACCACTACCGGAGAGCTGCTGCAGAGAGTGGCGGAGAGCGTGGGACCCCTCCGACG 2878
QY 261 tleu-----ThrSer-----GlyValArgSerHisleu----- 270
Db 2879 ACTTCGTGTCTACTTCACTGCTGCTGCCCACTCTCCGACACCTACACACCTACCGGGCCA 2938
QY 271 -----GluSerSerArgPro-----His 277
Db 2939 TGGAGCTGTGACGCCAGACGACTCTTCAGCCCTACTACTTCCAC 2985

RESULT 28
US-09-488-725B-8644/C
GENERAL INFORMATION:
APPLICANT: Yuanhua T. Tang
APPLICANT: John Tillinghast
APPLICANT: Ankura Sanku
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Drmanac
TITLE OF INVENTION: Novel Contigs Obtained
FILE REFERENCE: 784
CURRENT APPLICATION NUMBER: US/09/488, 725B
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remainder Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pc_ct_genes Version 1.01
SEQ ID NO 8644
LENGTH: 4493
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature

```

```

LOCATION: (4417)...(845)
OTHER INFORMATION: similar to g15924408 in the genepep database release 114.
OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-8644

Alignment Scores:
Pred. No.: 1.35e+04 Length: 4493
Score: 289.40 Matches: 136
Percent Similarity: 17.03% Conservative: 60
Best Local Similarity: 11.82% Mismatches: 79
Query Match: 19.96% Indels: 883
DB: Gaps: 3

us-09-896-522-2 (1-277) x US-09-488-725B-8644 (1-4493)
QY 3 serIaGly-----GlyIuaspCyvGlu-----SerProAlaPro-----G1 15
Db 4398 ACCGCGGTTTCCACCCCGGAGCTGTCAAGTTGGCTCCGCGCCAGCATGGAG 4339
QY 15 uAlaAspArg-----ProHleGlnArg-----Pro-----PheLeu1 26
Db 4338 AGCTGATATGGGAACACTACATGTGACCTTACAAAAGATTCCAAAGAGATTGGAA 4279
QY 26 leGlyValSerGlyly-----ThrAla-----SerGlylysSerThrVal----- 39
Db 4278 TTGCAGTGTCCGAGGACAGACACACCCCACTTGAAATGAGAAACGTCAATTGTCA 4219
QY 40 -----CyvGluIysIleMetGluLeuGly-----GlnAsnGlu----- 51
Db 4218 TTTCGATGTGTCTCCGCGGTGGGCTGTGATGGCTGTCTCAAGAAATGACAGAGTGG 4159
QY 51 ----- 51
Db 4158 TCATGTCAATGGACACCCCATGAGAGATGCTTATTGCTTGACATTACAGACTCA 4099
QY 52 -----ValGluGlnArgGlnArglyValIle----- 61
Db 4098 GAAAAGTGGGAAGTGTGCTGCTATTGTGTCAAGAGCCCGGAAGTCCAGGTGGCCG 4039
QY 62 -----LeuSerGln-----AspArgPheTyrIysValLeu----- 71
Db 4038 CACTTACGCGACCCCTCCCTGTGATGAGTACCGGGCTTTTGAGGTGACGACGACT 3979
QY 72 -----ThrAla-GluGlnIysAlaIys----- 78
Db 3978 TTGATGCGAAGATTTCGGAGTGGCTACGACGAGAGCCGCTGGAACAGCCATGGGG 3919
QY 79 -----AlaLeuIysGlyGlnTyrAsnPheAspHisProAsp 90
Db 3918 GGCGCAGCCGACCTGAGAGACAGACCCGGAAGGGGGCGTCCCATGAGCGGGCCCGGA 3859
QY 91 AlaPheAspAsnAspLeuMetHis-----ArgThrLeuIysAsnIleVal 105
Db 3858 GCGCGG-GAGCGGAGCCTTACGCGCGGACCGGAGCCGTGGCCGAGCCTGAGCGGGGCTG 3800
QY 106 GluGlyIysThrValGluValPro-----ValThrHisSerArgLeuProGly 125
Db 3799 GACC-AMGACCAATGGCGGACCCGAGACCGGACCGGTGGCCGAGCTTGAGCGGGGCC 3742
QY 114 --ThrTyrAspPhe-----ValThrHisSerArgLeuProGly 125
Db 3741 TGGACCAAGACTTTGGGCGATCCCGGAGACCGGAGACCGTGACCCG-ACCGCGG-CCGAG 3684
QY 126 -----ThrThrValVal----- 129
Db 3683 CATTCACAGACTACAGAGAGACCTATACACCGGCGCTTACAGCCAGACTACAGCGGGC 3624
QY 130 -----Tyr-----ProAla--AspVal----- 134
Db 3623 CTACAGCCGAGATACAGGCGCGGGGCGCGCACGATGCCGCTCTTGGGAGACCCCGAAG 3564
QY 135 -----ValLeuPheGly----- 138

```

```

Db 3563 CCGCAGCCGAGACCCGACCTCACGAGACCCGAGCCGAGCGGCGGCGG 3504
Qy 139 -----GlyIleValPheTyrSerGlnIleArgAspMetHehIleuArgLe 156
Db 3503 GCCCATCGGGGCTCTCTGATGAAAGCA--GAGCG-ACGAGAGATAGTCTCCGGCT 3447
Qy 156 u-----PheValAsp----- 159
Db 3446 TGGGAGTCAGATCTTGTAAGAAATGACCCGAGCGGCTGGCAACTAAGATGGCA 3387
Qy 159 ----- 159
Db 3386 CCTTCAGAGAGACATAATCTCAAGATCAATGGGACTGTAAGAGAACTGCTTT 3327
Qy 160 -ThraPseP-----AspValArgLeuSerArg-----ValIleuArg 172
Db 3326 AACGGATGCTCGAAATTTGATTAAGAAAGTCAAGAGGAAACTAGAGTGTGGTGG 3267
Qy 172 GAAP-----ValArg-----ArgGlyArg 178
Db 3266 AGACAGCCAGACAGACCCCTCATCAACATCCCGTATTAAAGACAGTACTAGAAATGA 3207
Qy 179 -AspLeuGlnIleLeuThr----- 197
Db 3206 AGATATTTCAGAAATAGAGTCAACCCGATCATTTTCTCAGAGAGAGAGATCATGTA 3147
Qy 187 rThr-----ThrPheValys----- 192
Db 3146 TTCTGATTATGATTATCATTCCTCAAGTGAGAAAGCTGAGAAAGGCAAGTTCAGAGA 3087
Qy 193 -----ProIa-----PheGlnIlePheCys-LeuProThr-----LysLysTyrAl 206
Db 3086 GGCAGCCGAGAGAGATGTCAGAGATGGGTGGAGACCCACTCCCTTAAGTCCACAGG 3027
Qy 206 aAspValIle----- 11ProArgGlyVal 214
Db 3026 GGATATTGACAGCAGATGTCCTCCAGACCAACAGAAACCCAGATATCCAGAGAAC 2967
Qy 215 -----AspAsn-----MetVal----- 218
Db 2966 CCCAGCTCTCTCAACCAAAAGCAGCCCGGAGAACTTTCTTCGTCCTAGTCTGAGATGA 2907
Qy 219 -AlaIle-----AsnLeuIleValGlnHis-----IleGlnAsp----- 229
Db 2906 AGCAATATATGCGCCCTAATAC--CAAAATGTAAGTTCAAGAAAGGAGACAGCGTGGC 2849
Qy 230 -----IleLeuAsnGly-----AspIleCysLysTyrHis-----Arg----- 240
Db 2848 CTCGCGGTGGCTGTGGTGGCAATGATGTGGGATATTTGTTGCTGGCATTCAGAAAGGAGC 2789
Qy 241 -GlyGlySerAsnGlyArgSerTyrLysArgThrPheSerGlu----- 254
Db 2788 TCGGCGAGACAGAGGGGCTTCAAGAAAGACAGATTCCTGAAGGTGAACACACAGAT 2729
Qy 255 -----Pro----- 255
Db 2728 TTCAGAGATTAAGTGGGAGAGATGCCGTTCTTACTGTTAGAAATCCCTAAAGGTGA 2669
Qy 256 -GlyAsp-----HisProGlyMetLeu 263
Db 2668 ATGGTACCATTTTAACTCAGAGCCGAGCGAGATGTATAGAGACATCTGGCTTGTGC 2609
Qy 263 hSerGlyLys-----ArgSerHisLeuGlu-----SerSerSerArgP 276
Db 2608 AAGAGGGATTCGTTTTTAAAGAACCACTTGAATGTGAGAAAGAACTCCACAGAC 2549
Qy 276 ro-----His 277
Db 2548 CTGGCCTTCAC 2538

```

RESULT 29  
US-09-488-725B-7478/c  
; Sequence 7478, Application US/09488725B

```

; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Fillinghaas
; APPLICANT: Ankura Sinks
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Configs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 7478
; LENGTH: 3073
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (17)...(2844)
; OTHER INFORMATION: similar to g11019103 in the genepet database release 114,
; OTHER INFORMATION: Run with FASTX 3.3e00, default parameters
US-09-488-725B-7478

Alignment Scores:
Pred. No.: 1.97e+03 Length: 3073
Score: 289.10 Matches: 139
Percent Similarity: 14.57% Conservative: 53
Best Local Similarity: 10.55% Mismatches: 83
Query Match: 19.94% Indels: 1048
Gaps: 2

us-09-486-522-2 (1-277) x us-09-488-725B-7478 (1-3073)

Qy 3 SerAlaGly-----Gly-----GluAspCys----- 9
Db 2525 GCAGAGAGGCTTCGCTCAGATGATGCTGGCAGAGAGTTATCAATCATTCAGAT 2466
Qy 10 -GluSerPro-----AlaPro-----GluAlaAspArg 18
Db 2465 CCAAGACGTCCTGATTAATGTTCAATTCTGACCTCAGGCGCTGTTGCTGAACAGATCTT 2406
Qy 19 Pro-----His-----GlnArgProPheLeu-IleGlyVal 29
Db 2405 CCGTGGCAGACGATTCGGTACAGATATCAACATATCAAGAGCTCTTGGGATTT 2346
Qy 29 eArgGly----- 31
Db 2345 CCATGGGCTATTCACATGGCTCCCATCATCTCCAGTCCATATGATGATCAGAGTCAAGT 2286
Qy 32 -----ThrAlaSerGlyLysSerThrVal-----CysGluLysIleMetGlu 45

```

Db 2285 CACTAATGTTTCAAGTGTAGGTCCAGATTTGGCTCTCTCATGTAAACAGATGTATGAA 2226  
 QY LeuLeuGlyGlnAsn-----GluValGluGlnArgGlnArgValValIleLeuSe 63  
 Db 2225 TGGGAGACCAAAACAGCTGGGAGGTAGTTCCAGACAGACAAAGAAATATCCCTTTC 2166  
 QY 63 r-----GlnAspArg-----  
 Db 2165 CCCTGTCCAAAGTGAACCAAGATGTCTCAATTTTGTCTTCAACCCGAGTTGAGCTTTG 2106  
 QY 67 -----PheTyrLys-----ValLeuThrAlaGluGln---LysA 77  
 Db 2105 TAGGTGCATCTTATTATACGAAGAGCTCCAAAGTCAATCTCAACATCAAGATTCGGACGA 2046  
 QY 77 lAlysAlaLeuLysGly-----GlnTyrAsnPheAsp---HisPro-- 89  
 Db 2045 GGAAGCCTGTGCGGGGTGCATTTCAGCACTGCTTCAAGTAA--GACTCTTATCAAGGC 1987  
 QY 90 -----AspAlaPheAspAsnAsp-----LeuMetHis----- 98  
 Db 1986 TTGTTGATGAATTCAA--AATGACAGGGTACTTGTCCATTATGAATTGTAAAGATTCTAC 1928  
 QY 99 -----ArgThrLeu-----  
 Db 1927 TTTCATTGCAATGACTTCTTACATTCTGAAAACAGAACTCTCGCTTGGACAGGACACAGA 1868  
 QY 102 LysAsnIle-----ValGluGly-LysThrValGlu-----ValPro 113  
 Db 1867 AGGAATGTGGCAATTTTCCATCTTATCCAGGAGCAATTTTCTCCAGTGTCTTCGG 1808  
 QY 114 Thr-----TyrAsp-----PheValThrHis----- 120  
 Db 1807 GTAAAGCTCGCTTATACAGCCCTCAACCCGATGTCAAACTCAGCTGACAGGCTTGTG 1748  
 QY 120 -----  
 Db 1747 GTCACTGGTCTTCAAGGCGCATGTGCTGTGTAATCTAGCTGAGTATGTTCTTCCCTTT 1688  
 QY 120 -----  
 Db 1687 CCAAGATCCGATCACACAGGAGGACAGGCACTTCTCACTGTATCCAGTGTCTC 1628  
 QY 121 -----SerArgLeu-----ProG1 125  
 Db 1627 AGAGCCCGTATCATCTTGTAAAGTGGCTGGAAATGTAGCTCAACCTCTGTGAAGCCTTC 1568  
 QY 125 uThrThrValVal-----TyrProAlaAsp----- 133  
 Db 1567 AAAGACAGTCTTTTGGCGCACCTGAAATTTTCAAGCTGATCATGTGATACAGCATTTGAAA 1508  
 QY 134 ValValLeuPheGlu-----  
 Db 1507 ATCTCTTCTTCGAGAGCTTTTTCATCTTTTCCACATCCAGCTCTTCTATCTGTAGTT 1448  
 QY 138 -----  
 Db 1447 GAGGTCCCCCAGCCACAAAGATCATCATGTGTTGCTGATGTGAGAGGGGGAGGCTTGG 1388  
 QY 138 -----  
 Db 1387 GTCAAGGTGACAAACTGCATTCGAGAACAAATGCTTATATAGTCTGTCTCTCTC 1328  
 QY 138 -----  
 Db 1327 ATACTCTTCAATGTGGGTGCGCAAGTGAATTCACAAAGAGATGTGGTGTGTGAAA 1268  
 QY 138 -----  
 Db 1267 CTGGAACCTGATGCGCAGCCTCCTGTGTGCCATCTCTCCCATGATTCCTGTCCAC 1208  
 QY 139 -----GlyIle-----LeuValPhe---Tyr----- 144  
 Db 1207 AGTCTCGGCTTCCACTTCTGAGATATTAAGCTGCATGCTCTGTGTGACATATTAACAGAG 1148

QY 145 -----SerGlnGluIleArgAspMetPheIleLeuArgLeuPhe-----ValAspThrAs 161  
 Db 1147 CATTAATCCCAACCAAGTCC--GATTAAGCTTCACCTTTGCATATTTGGCATCTGGATGAGA 1090  
 QY 161 P--SerAspValArgLeuSerArgArg--ValLeuArgAspValArgArgGlyAsp 179  
 Db 1089 CCCTGTGACAGAGCTTTGAACCACTTCTCTTGTGGGGTATCGTGAAGAAAGAAAGCT 1030  
 QY 180 --LeuGlnGlnIle-----LeuThrGlnTyrThr-----ThrP 190  
 Db 1029 TCCCTTACTCAGATCAAGCTCTCTGAAACCTTACACAAATAGACATCTGGGGCCTGGATACCA 970  
 QY 190 heValLysProAlaPheGluPhe-----CysLeu--Pro 201  
 Db 969 TGTCTAGCCACAGCCCGAGGCATTTCTTGGGGAGCTGCCATTTATATGATGTATCC 910  
 QY 202 ThrLys-----LysTyr-----AlaAspVal-- 208  
 Db 909 GCAAAAACCTGAAGTTCTGATATAGTGTATCTCTTCTTCTGTAGTATGATGTAT 850  
 QY 209 -----IleIleProArgGly-----ValAsp--AsnMetValAlaIleAsn-- 221  
 Db 849 TTCACAATGTGTATCTGCAAGTCCAAACTTCTGCATGATTAATAATGTA--GCTTGTCCG 792  
 QY 222 -----LeuIleValGln-----HisIleGlnAspIleLeuAsnGlyAspIle----- 235  
 Db 791 ACACTGTGATAGTGAAGAGGAGGACCAACATGATCAATTTTGGACTTGATTTATCTGTCTC 732  
 QY 236 -----CysLys-----Trp--HisArg----- 240  
 Db 731 TTGTTGCAAGCTTTCTGTGTTATCTTGAACCTGTGAGCTTGTGTCCATAGGACATCCCT 672  
 QY 241 -----GlyGlySerAsn----- 244  
 Db 671 TCCCATTTGGTCT--TCAAACCATCAAAAGTTAGAACCACTCCGCAATGTGTGCGTACC 614  
 QY 245 -----GlyArgSerTyrLys----- 249  
 Db 613 TGGCAGGTAACTAGGGCCGAGTTTACACCCGCGGGCGTTGGCATCTCCAGTCCAGCTC 554  
 QY 250 --ArgThrPheSerGlu----- 254  
 Db 553 TGGCAGCTTATACCGAGACAGACAGCAATTCAGATCCCGGGTGCAGAAATCGAAGCC 494  
 QY 255 -----ProGly-----AspHisProGlyMetLeuThrSerGlyLys--- 266  
 Db 493 TGAACAGGCCCTGGCAACTTCTGTGAAGAACATCTGGTGTGTGAACCAAGGCGAGTTG 434  
 QY 267 -----ArgSerHisLeuGlnSerSerSer 275  
 Db 433 GAATACGAGGCTAAGCTCTGTGTGTCCAGCTGAGCGGTACATCTGAGCCAGAGATGTA 374  
 QY 275 rGProHis 277  
 Db 373 GAGTTTCC 366

## RESULT 30

US-09-488-725B-5709/C  
 ; Sequence 5709, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghast  
 ; APPLICANT: Ankura Sanku  
 ; APPLICANT: Chenghua Liu  
 ; APPLICANT: Radoje T. Dirmanc  
 ; TITLE OF INVENTION: Novel Contigs Obtained  
 ; FILE REFERENCE: 784  
 ; CURRENT FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US/09/488, 725B  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07



```

QY      163 pValArgLeuSer-----ArgArgVal-----LeuArgAsp----- 173
DB      2163 TCTGACCTGTCATTCGATTCGCAAGAAATCTGCAAGTCTGAGATGGAAATGCTAG 2104
QY      174 -ValArgArg-----GlyArgAspLeuGluGlnLeuLeuThrG1 186
DB      2103 AGTTGCGTGAACCTTCACAGTCAGATGTCGAGGCGAGAGTCTCAACGCTCTCTCAGGCA 2044
QY      186 rHyThrThrPheVallyProAlaPheGluGluPheCysLeuProThrIlylys----- 204
DB      2043 GTGC-----CAATTCGTCTTCCGAGTGTCAAGGGCCAC 2011
QY      205 -----TyrAlaAspVal----- 208
DB      2010 ACCAGGAGGCTATATGACAC-GTGCCTTAGCAATTCAGTGTCAACCGTCTGTGACAGAG 1952
QY      208 ----- 208
DB      1951 AAGGGTCAGTCATAGATAATACCTGCTAACAAAGCCTGAGTACAAACATCTTACTT 1892
QY      208 ----- 208
DB      1891 TAGTCTCTCTTCTCTCATCGAGGCTAAACTGCTATTGCTGCTCAAGTGTGAATCTTGT 1832
QY      209 -----IleIleProArgGlyValAlaAsp-----AsnMetValAla-Ile-----Asn 221
DB      1831 GAATATAGTGAAGAGTGGAGTGCATATCTTCAACAGCATGCTGATTTAAAGGCACAGAAAT 1772
QY      222 Leu-----IleValGlnHis-----IleGlnAspIleLeu----- 231
DB      1771 CTCTCTGATTTATTTTACAAATTTGTAAGTCTATTTATTCAGTTCATCTTGAATCAC 1712
QY      231 ----- 231
DB      1711 TTCTTTTCTAATAGTGTCTCTTCATGTCATCGAGGCTGGAACAGTATGTCAG 1652
QY      231 ----- 231
DB      1651 CGGACAGACATTCACATTCGTCTTAACTGTGATCATCAATGGGGCTCTAGATTTT 1592
QY      232 -----AsnGlyAspIleCysIlys--Tyr-HisIar 240
DB      1591 CTATCATTTCTTCAGATTCCTTTCTGTGTCGATGTCATGATTTTGAGAAACTGGGACACAG 1532
QY      240 g-----GlyIlySer----- 243
DB      1531 GGCCCTCAGATTCCTCTGTCCTGTCCTGCGGCTGGGTTTCCCCAGAGTTCTGTCAA 1472
QY      244 -----AsnGlyArgSerTyr--- 248
DB      1471 GCTCTAGTCTAATCTATTTCAGGAAGAGAGTCTCCAGAAATGGAAAGATTATACA 1412
QY      249 -----LysArgThrPheSer-----GluPro--GlyAsp--His-- 258
DB      1411 ATTCTGATCTAAGAGAGCTGAATCTTGTAAGTGTGCCAACCTGTGTGTAACATAG 1352
QY      259 -----ProGly-----MetLeuThrSer----- 264
DB      1351 ATTGTAGTTCACAGGTTTTCATTCATTCATTAAGCTGCTTCCTGTGAGATTCGT 1292
QY      265 -GlyIlys-----ArgSer-----HisLeuGluSerSer 273
DB      1291 AGGACAAAGTACAAAGTAAAGAGCTGTCCAGTGAACACTAATTTCACTTGAAGGCTTCC 1232
QY      274 SerArgPro-----His 277
DB      1231 CGATGCTCTGACAGCAT 1214

```

```

RESULT 31
US-09-488-725B-5625
; Sequence 5625, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang

```

```

APPLICANT: John Tillinghaest
APPLICANT: Ankura Sunku
APPLICANT: Chenghua Liu
APPLICANT: Radoje T. Dimanac
TITLE OF INVENTION: Novel Contigs Obtained
FILE REFERENCE: 784
CURRENT APPLICATION NUMBER: US/09/488,725B
CURRENT FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US 09/004,182
PRIOR FILING DATE: 1998-01-07
PRIOR APPLICATION NUMBER: US 09/034,341
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 09/045,400
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: US 09/321,214
PRIOR FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: US 09/131,598
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
REMAINING PRIOR APPLICATION DATA REMOVED - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pc_ct_genes Version 1.01
SEQ ID NO 5625
LENGTH: 4593
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (89)-(4021)
OTHER INFORMATION: similar to gi559703 in the genepept database release 114,
OTHER INFORMATION: Run with FASTX 3.3f00, default parameters
US-09-488-725B-5625

```

## Alignment Scores:

```

Pred. No.: 1.7e+04 Length: 4593
Score: 287.40 Matches: 146
Percent Similarity: 12.78% Conservative: 59
Best Local Similarity: 9.10% Mismatches: 67
Query Match: 19.82% Indels: 1335
DB: 1 Gaps: 7

```

```
us-09-896-522-2 (1-277) x US-09-488-725B-5625 (1-4593)
```

```

QY      5 GlyGly-----GluAspCys 9
DB      597 GGAAGTCTGAGAGCTGAGTACAAATGATGATTCATGATTCACAGAAATGC 656
QY      10 -----GluSerProAlaProGluAlaAspArg----- 18
DB      657 CATTGACGTTCTGCGGGAAGTGAAGCGCCTGTGCAT--GCCGAGAGAGAGAGAC 714
QY      19 -----Pro-----HisGln----- 21
DB      715 TTGCTGTCAGAGCTTACCTGATCACACTGGCAAAATTCATCAACATGTTGCTGCTG 774
QY      22 -----ArgProPheLeuIle-----GlyV 28
DB      775 GAGAGCTGAAGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 834
QY      28 alserGlyGlyThrAlaSerGlyIlySerThrVal----- 39
DB      835 GCTCAGTCTTTTACGTAATAATGAGATCCACAGTCCATCCAGGAATGCAGAAATCTGTCC 894

```



```

QY 39 ----- 39
Db 895 ATGTCCTGGCCATCATTAACAAGATCACAGCTCTGCAGCAGCAGCTCGAAGTGATT 954
QY 40 ----- CysGluYsIleMetGluLeuGluYsGln 50
Db 955 TCTGGCTACGAGAAGCTCTGGCAGATATTGTGAATCTGTGTGTGATTACTACGAGAAC 1014
QY 50 enGluValGluGlnArgGln----- 56
Db 1015 AGGATGTATTTCAGCGCCAGTGAAGAAACACATGCTTCTCAAGTCATGGATTGTGTCTG 1074
QY 57 ----- ArgLysValIle 61
Db 1075 TACCTGATGATGGAGTGTCACTAATCATTTAAGTTGGATGCGCAAGAAATTAAC 1134
QY 62 LeuSerGln--AspArgPheTyrLysValLeu----- 71
Db 1135 TTATCCAAATTCGACAACTTCAAGCAACTCCAGGTGTTCCACTATTGGGGACATG 1194
QY 72 ----- ThrAlaGlu----- GlnLysAlaLysAlaLeuLysGly----- 82
Db 1195 CAATAGAACTGGCAAGATATATCAAGACGAGCGCCCACTACGAGAAATTAATCTCGA 1254
QY 83 ----- GlnTyrAsn----- 85
Db 1255 TGGACGTGCATCTCTCCGCGACGAGCCCTCACTGACAACTCTGCGAGCATGATCCAG 1314
QY 85 ----- 85
Db 1315 ATCCGAGAGACCATGCGCTTCATTTCGAGCTGGCGGCTACAGCAACAGCAGAGTG 1374
QY 86 ----- Phe 86
Db 1375 GTCCAGCGGCTCGGCGCGCAGAGGCCAGAGAAGGACGCGAGTACCGCAAGCTCTTC 1434
QY 87 Asp----- 87
Db 1435 GACCTGGCGCTGCAGGGCTGCAGCTGTTCGCACTGGAGCGCGCATGATGAAGTG 1494
QY 88 ----- HisPro--AspAlaPheAspAsn--Asp----- 95
Db 1495 TATTCTGGAAGCTGTGTGCACCCACGACAGATCTCAACAGAGACTGCCCGACAGC 1554
QY 95 ----- 95
Db 1555 GCTGAAGATGACGAGCGTGCACGCGCTACACTACACGAGGAGAAATTGCTCTA 1614
QY 96 ----- LeuMet----- 97
Db 1615 GTGGAGGTGATGCCCATGATCAAAAGCCTTCAGAGTGTGTATGGCAGAGATGAGAGCGTG 1674
QY 98 ----- HisArg----- Thr 100
Db 1675 TTCAACACGACCATCCGCGACACCGTCTATGCGCACTGCAGAGACTTCTCCAGGTGACC 1734
QY 101 Leu----- LysAsnIleValGlu----- 106
Db 1735 CTTATGAGACCGGTGCGCGAGGCCATCAAGAGAAGAAAGAAAGCTCATCCAGAGTGTCTG 1794
QY 107 --Gly----- LysThrVal----- 110
Db 1795 CAGGCCATCAGAGAAACCGTGTGTGACTGGAGAGCGGGGATAGCCCTTCAATGACCA 1854
QY 110 ----- 110
Db 1855 GCCTTCGGGGGCGAGAAGACCCCAAGAGCGGCTAAGACATAAAGTACACGCGCGGCC 1914
QY 110 ----- 110
Db 1915 GTGGAGCCTTCACGACTGACTTTTACATGTGTGAGAACCATGTCTAGAGTCCCTCATTTGCA 1974
QY 111 ----- GluValProThr-Tyr--Asp 116

```

```

Db 1975 GACAAAAGTGTTCCAAGAAAACCTTGAGAGATGACCTTGAAGGGGCCACCATATTGAC 2034
QY 117 ----- PheValThrHis----- 120
Db 2035 ATGAAAAATTTTCATGAGAGATCATTTCTTACACTACATTGATAAATTTCAAGTAAAGC 2094
QY 121 ----- SerArg----- LeuPro-GluThrThr 127
Db 2095 CTCGACAGTGTGTGACCTTGTGACAGCTGTGTGTCGAGAGTTCGAGAGTTCCTGAGAGTACC 2154
QY 128 ----- ValValTyrProAla--AspVal----- ValLeuPheGluGly 139
Db 2155 ATGGGACAGAGATTCAGATTCCTCCCATTTGAGATGTCATGCTCCGATCTCGACGACACAC 2214
QY 140 IleLeu----- ValPheTyrSerGlnGluLe-- 148
Db 2215 ATCTGGAGACCAAGAGGATCATGATGATGAGTACGATGCTCTCACTCCCTGACCTGTAC 2274
QY 149 ArgAspMetPheHis----- Le 154
Db 2275 AATGACAGCGCCCACTACGCGCTCACACAGTTCACAGAGATTCCTGTACGAGAAAT 2334
QY 154 ValArg----- LeuPheValAspThr----- 160
Db 2335 GAGCGCGAGTGAATCTATGTTTGTGACCAATTTGTTTACAGCTACAGACAGATATT 2394
QY 161 ----- AspSerAspVal 164
Db 2395 GCCTATTATTAAGTTATGCGAGAAAGTTGCTTCTGTATTAACGGTTAGATCAGATGCG 2454
QY 164 LysGlu----- SerArgAspVal--LeuAspAspVal----- 174
Db 2455 AAGAATCAGGAGACCAAGATCCACCTCCGCGCTCAACCGCTACAGAGCTGTGTAAG 2514
QY 175 ArgArg----- GlyArg----- AspLeuGluGlnIleLeuThrGln-- 186
Db 2515 CAGAGCATGTGACGCTCTCGGCAATGATGACTCATATGCTGTGATCACCCAGCCG 2574
QY 186 ----- 186
Db 2575 GTCTCAGACGCATGTATTAAGTCCCTAAGAACTGGAGATTGACGATTTGAAATGAAGAT 2634
QY 186 ----- 186
Db 2635 TTGACCTCCATAGTTGAGTGAATGCGCTTGTGAATCAACCGCATGACCCAAAGCTG 2694
QY 187 ----- Tyr----- ThrThr 189
Db 2695 CTGAGCGCGTACTCTGACGCTGACAGCGCTTCGACGCATGTTCCGGAGGCCAACACACAC 2754
QY 189 rPheValLysPro----- AlaPheGluGlu----- 197
Db 2755 GTGTGACGCGCTTACCGAGAGATCAACCTGCAGAGTCTTCTGGAGGCTCAACTATGACTTC 2814
QY 198 ----- PheCys----- LeuProThrLysLysTyrAlaAspValIleLeuP 211
Db 2815 CTGCCCACTACTGTCACACGCGCTTACCAACCGGTTGTGTG--GACA--GTGTACC 2870
QY 211 o----- ArgGlyValAspAspMetVal----- 218
Db 2871 ATTTTCTCAGAAATTTCAAGAGATTAAGACGCTAATGACAGCCTCAGATATGTCATGG 2930
QY 219 ----- AlaIleAsnLeu--IleValGlnHisIleGlnAspIle----- LeuAsnGly 233
Db 2931 ATCCAAAGCTTTGAAGTGTGACTGCTTACCGCATTTACGCGAGCTACCGGAAGTCTGTGG 2990
QY 234 Asp----- IleCysLys----- Trp-His 239
Db 2991 ACCTCCACATTTCAAGTCACTGCGGCTTCTCGGCTACAGAGGTATGCGGTGTGTAT 3050
QY 240 ArgGlyLysSerAsnLysArg----- SerTyrLysArg 250

```

```

Db      3051 GGAGGAGCTGCTGAAGGTCTGTCAGAGGCTGTGCAAGGACCAATCTCGACGTACGTGAA 3110
Qy      250 gthPheSerGlu-----ProGlyAsp-----257
Db      3111 GACCGCTATGAGGTGATGTCGCCAAGATCTGCCGCTGCCCCGCGACAGATACGGCTCTCC 3170
Qy      258 ----HisProGlyMetLeu-----Threser-----264
Db      3171 TGGTATCTTGAGATTCTTCCACCAACAGCTGAAGACATCTGTGAGTACGACAGCTGAA 3230
Qy      265 -----GlyLysArg-----SerHisLeuGluSers 273
Db      3231 GAGCGTGTGCTTCCAGAACCTGCGGAGAGGTGGAGAGCCATCTCTTCTGCTGCTCAT 3290
Qy      273 eTserArg-Pro 276
Db      3291 CGAGCAGAGGCT 3302

RESULT 32
US-09-488-725B-5785/C
; Sequence 5785, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: PE CT_genes Version 1.01
; SEQ ID NO 5785
; LENGTH: 3022
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (257)..(1107)
; OTHER INFORMATION: similar to gi30821 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-5785

```

```

Alignment Scores:
Pred. No.: 2.04e+03
Score: 287.30
Percent Similarity: 17.40%
Best Local Similarity: 12.30%
Query Match: 19.81%
DB: 1
Gaps: 2

```

```

us-09-896-522-2 (1-277) x US-09-488-725B-5785 (1-3022)
Qy      4 AlaGlyGlyGluAsp-----Cys-----9
Db      2994 GCGGGGGGTGAGGGGTGGCTGATGATGACCAAGCTAATGGCTGATTCGATTCGAAGGGTT 2935
Qy      10 -----GluSerPro-AlaProGluAlaSerPro-----HisGln-- 21
Db      2934 TCATTGGCTCAACCTGGCCCCCAGGACACCAACCCCTGATTGACAGTCTATCAAGA 2875
Qy      21 -----21
Db      2874 AGGTGTGCAAGAGCTCAAGTGTTCAGAGATCTGGGTGATTTATTAAGAAACCTTAGC 2815
Qy      21 -----21
Db      2814 TGAATGAGGGTGGGAGAACAAAGACAAAGACATCTTTTCAGAGGAAACTGAAA 2755
Qy      22 -----ArgProPheLeuIleGly-----ValSerGlyGly 31
Db      2754 GAAAGAGGGAGAGATTAATAAGACATTTCTGGCTGGGACAGGCACTTCAGCAGCTCA 2695
Qy      32 ThrAla-----SerGly-----LysSerThr-----Y 39
Db      2694 ACTGCCAGGGTGACCAAGTGCACCTCTGCAAGTGTCTTCAACAACCTGGTCTTAGACTCG 2635
Qy      39 aLys-GluLysIleMet-----44
Db      2634 TCTGCTGACAAATCTCTGACCTCAAGCCGCGTGAGAGTATTCCTGAGAGATAGCA 2575
Qy      44 -----44
Db      2574 AACATGCCCAACGTAGCCCGCATCTCTGCTGAGCTGTTCAGACATCGCCACACAA 2515
Qy      45 ----GluLeuLeu-GlyGlnAsnGluValGlnArgGlnArgLysValIleLeu-S 63
Db      2514 GGGGAGCTGTAAAGTCCCTCAAGGCGGAAAGCGTCAAGATGAAATTAATTCGCA 2455
Qy      63 eTglnAsp-----ArgPheTyrLysValLeuThrAlaGluGln--Lys 76
Db      2454 GTAAAGATGTGTGTGATTAATAAGCTCAAAAGCTCCCGCGGGAGGATTAACAG 2395
Qy      77 Ala-LysAlaLeuLysGly-----GlnTyrAsnPheAspHis--ProAspAla----- 91
Db      2394 GCTGACTGTCTTCCAGGAAACCCAGCACTTACAGT--AATCATGGCCCAAGATGCCACAG 2337
Qy      92 --PheAspAsnAspLeuMet----HisArgThrLeuLysAsnIleValGlu--Gly-- 107
Db      2336 AAGCTGAAGAGATTTGTGACCCATGACAGTACAGACAGACAGTGAAGAGGCAAT 2277
Qy      108 --LysThrValGluValProThrTyrAspPhe-----ValThrHisSer-- 121
Db      2276 AGACTAGCGTTAAGCTTCATTGGTTCGGTTTGAGAGTAAATGACAAAGAGCTAA 2217
Qy      122 -----ArgLeu-----ProGluThrValValTyrProAla----- 132
Db      2216 TAAACCCGAATAGAGAGAGCCACCCGCGCAAAAGCACACAC--TTCCTCGGCAAGG 2159
Qy      133 -----Asp-----ValValLeuPheGlu-----138
Db      2158 CATTTCTTCTCACACAGATATGATCAGTTCCTTGAATTCGCTAATAAATTAAGAG 2099
Qy      139 -----GlyIleLeu-----141
Db      2098 CCAATTTATCTGTACAGCGGCGGCGCTCTCTTCTTGAAGCAATCATAGTACACC 2039
Qy      142 -----ValPheTyrSerGlnGlu--IleArgAspMetPheHisLeuArgLeuPheVal 158
Db      2038 TCATTCAATTAATTTTCAACAAAGTGGCTCCAGATGATTAATTAACGTCCTTGCTATC 1979
Qy      159 --Asp-ThrAspSer-----162

```

```

Db 1978 CAGATGACGATGACGAGAGTATCTGTGAGAGGACCTGACCTGACGACGCTTATAGC 1919
Qy 163 -----AapVal-----ArgLeuSe 167
Db 1918 TATGCTGTGAGAGATGCAAGACATCATCCTGCTGCTTATGACATCAAGAACTTTC 1859
Qy 167 rArgArVal-----LeuArGApValArGArG-----GlyAr 178
Db 1858 ATATCTCTGACCTGGAGACTACATGGGAGATGAGCTGCTGCTTACAAAAAATGTGTGA 1799
Qy 178 gApLeuGluGln-----LleLeuThrGln-----TyrThrThiPhe----- 190
Db 1798 AGATTCAAAAAGCATGTACTTCAACCCCAAGGAAAGGCAATTTGCGGCTTCATGACA 1739
Qy 191 -----ValLys-----ProAlaPheGluG 197
Db 1738 GCGACTTCCATTGGGAAAGATCAAGTTTCTGCTCATCAGGCTGCTCTCTCTTCAAGC 1679
Qy 197 lApHeCyS-----LeuPro--ThrLysLysTyrAlaAspValAlaIleProArG 213
Db 1678 AACTCATTTTCCCAAGATCTTCCGAGACGAGGAGATATCCAGTTGCTTATCCATGTG 1619
Qy 213 lYValAsp----- 215
Db 1618 CCATTGACGAGGATCTTACTTTAGATGACAAGGAGCGCGCCCAAGATCGGCTTA 1559
Qy 216 -----AsnMet-----ValAlaIleAsnLeuIle-----ValGlnHisIleGlnAspI 230
Db 1558 TCCTTAACCAAGCCCTTGTGACTTCACCTTCCAGCCCTTCAGGCGCCCAAGACCA 1499
Qy 230 eLeu-----AsnGlyAspIleCySlySlyThrPheArgGlyGly----- 242
Db 1498 AATGATGCGCAGGACCCCACTCTCCATCT--TCT--CACCGACAGGCGCAAAACAG 1443
Qy 243 SerAsnGlyArgSerTyrLysArgThrPheSer-----GluPro--GlyAspHis 258
Db 1442 TCMAACCAAGGTCATATAGCATGCGTTTTCGAGGAGCAGAACCCATCGAGGAGCA 1383
Qy 258 s-----ProGlyMetLeuThr----- 263
Db 1382 CAGCCAGTTTGGCGGCAACTGATGTGACTGTCTCTCAGATAC--CTGACCTTCTT 1324
Qy 264 -----SerGlyLys-----ArgSer 268
Db 1323 CTCGAGGACCAAGCAGCAGGTTTCAGACCAAGATCAGGAAGATTACACAGCGGAGCC 1264
Qy 269 -----HisLeuGluSer--SerSerArgProHis 277
Db 1263 GATGCTCACCTGGGTGAGCTTCAAGAAAGG--CAC 1232

```

```

PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: US 09/170,294
PRIOR FILING DATE: 1998-10-13
PRIOR APPLICATION NUMBER: US 09/179,473
PRIOR FILING DATE: 1998-10-27
PRIOR APPLICATION NUMBER: US 09/181,430
PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pt_ct_genes Version 1.01
SEQ ID NO 4150
LENGTH: 4188
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2)...(2777)
OTHER INFORMATION: similar to gi4240253 in the genepept database release 114,
US-09-488-725B-4150

Alignment Scores:
Pred. No.: 1.12e+04 Length: 4188
Score: 286.90 Matches: 143
Percent Similarity: 14.584 Conservative: 54
Best Local Similarity: 10.584 Mismatches: 76
Query Match: 19,794 Indels: 1082
DB: 1 Gaps: 6

us-09-896-522-2 (1-277) x US-09-488-725B-4150 (1-4188)
Qy 4 AlaGly-----GlyGluAsp-----Cys-----GluSe 11
Db 212 GCGAGAGATTACAAAGTTTCAATGATGAGGTACTCTGACCCAGCAGCTGTCTCC 271
Qy 11 rProAlaPro-----GluAlaAsp----- 17
Db 272 TCAGGCCCCAGAGAGACAGAGCTGTATGCTGATGAGAGAGCGCCAGTTTAACTAAAT 331
Qy 18 -----ArgProHis-----GlnArgProPheLeu-----IleGly-----ValSer 29
Db 332 GCGACAGAGGTCCCAACAGCCACACAGACCTTG--ATGACCATGTATCGCGCGCTCTCC 390
Qy 30 GlyGlyThr-----AlaSer----- 34
Db 391 CAGAGATTCAACCCGAATTGGCCAAAGATTTCTGAAAGAGCAAGCCTCGAAGATTCA 450
Qy 35 -----GlyLysSerThrValCys-----GluLysIleMetGluLeu 47
Db 451 CTTTGCTGATATGGGCAAGGATCTGATGTATACGCAACAGAAAGACGGAGCTGTG 510
Qy 47 uGlyGlnAsnGluValGluGlnArgGlnArgLysValAlaIleLeu-----S 63
Db 511 GTTGAAGGCGATCCCGAGAGCATGCTGGGAGCTCTGCTGCTGTCTGAGTGCAT 570
Qy 63 eGlnAspArg-----PheTyrLysValLeuThrAlaGluGlnLysAlaL 78
Db 571 CATGAGAGGCCACACATCTCGGTATATAGACCTTAGTGAGAACTCCATGCGGAA 630
Qy 78 s-----AlaLeuLysGlyGlnTyrAsn-----Phe--AspHisPr 89
Db 631 GTATATATCTCGCCAGAGGAGATTTGAGAGGATTTTACACCGCTCTCCAGAACACC 690
Qy 89 oAspAlaPheAspAsnAsp-----LeuMet- 97
Db 691 A--GCTTTTCAAGATGAATGGCATTCGCTGACTTAAGAGAGTCTTAAACAGCTTATGC 747
Qy 98 -----HisArgThrLeu-----LysAsnIleVal----- 105

```

```

Db      748 TTTTCGAATCCCAACATAGGTAATTGCCAGGCCATGATATTTGACTTCAGTGTCT 807
Qy      105 -----
Db      808 GCTTATAGCAAGAGAGAGAACTTTCTGCTGCTTGTGGCTTTGTGAGCGCATGCT 867
Qy      106 -----
Db      868 CCGAATTAATCAACACAGAGTTGTGGTGACGTGGTGCACGAGCCAGAGTGTCTTTGAGA 927
Qy      111 uVal-----Prothr-----TyrAsp-----
Db      928 GCTAGCAGCAGACTACCTCCACAGCTGTAGACTGTGATGCAAGACCTGGGCGTGAATTC 987
Qy      117 -----PheValThrHis-----SerArgLeuProGluThrTrpVal 128
Db      988 CACCATCTCCCTGCTGTTGCTTCCACATATTTCTGATGATGCTTTTGAAGAGTGC 1047
Qy      128 lValTyrProAlaSerValValLeuPheGluGlyIleLeuValPheTyrSerGln 146
Db      1048 AGTTGTGGTTGTGACTGTTCTTTCTATGAAAGAAATTAAGTGA--TATTCAGTTGGCC 1105
Qy      147 -----GluLeuArg-----
Db      1106 CTAGCTGTGCTGATGCAAAATGTGCAAACTGTTGAATCTGCAAGATGATGGGAGGCC 1165
Qy      150 --AspMetPhe-----
Db      1166 ATGACCCGTTTGGAGAGGTATTTAGACAGTGTGACCAATAAAGACAGACAGCTGCCCTCC 1225
Qy      153 -----HisL 154
Db      1226 ATTCCTCACTCCACTCTCTGCTCAGCGAGATGTGAACTTACCTGAGGTAGACATC 1285
Qy      154 eu-ArgLeu-----PheVal-----
Db      1286 TTTTAGATTCATCAGAACTTCTTACAGAAATTCGGAACTATCCGGGAGATTGATTGAA 1345
Qy      159 --AspThrAspSerAspValArgLeu-----SerArg-----ArgValLeuArgAsp 173
Db      1346 CAGATGA-GATTCAAAACAG--AGACTGAAGATGATCCAGACGCTGAGAGATTAATCGAAAC 1403
Qy      174 -----ValArg-----
Db      1404 GCAACGTGTACGAAACATTTGTGACAGAACTTCCTTACATTGATGAGCTGGAAGAAC 1463
Qy      176 -----ArgGlyArgAspLeuGluGlnIleLeu-----Thr 185
Db      1464 TTTATGTCTTTTCAAGGCAAGAAATCTCACACAGCTGTACTGAGGGGGGAGCAGCAACG 1523
Qy      186 GluTyrThr-----
Db      1524 CGCTGCACCGGACATGACCCAGCTGCCCTTACTGTAAGACATTCGATTCGATTCGAGC 1583
Qy      189 -----
Db      1584 AGTTCAAGGGAATTTGCTCTTCTCTTCTGAGGAGTGTGAATCTCATCTTGACGTTTC 1643
Qy      191 ValLysProAla-----
Db      1644 TGGGCTCCCGCTTGTTCAGTTATTAAGTGAAGAGTCTTTGATTAATTCGCGG 1703
Qy      197 luePhe-----CysLeuPro-----ThrLysLys-----
Db      1704 AGTTGTCTCTGGGCTAAGTGTGATGCTGATGCGAGACCTTACAGAGAAAGCTCAAACTCC 1763
Qy      205 --Tyr-----AlaAsp-----
Db      1764 TGTCAAAATGACAGCTGTGCTGAGCCATCTCTGCAAGATGAAGAACAGATTCTGCTT 1823
Qy      208 -----ValIleIle-----ProArg-----GlyV 214
Db      1824 TTGAAGCACTCAGTACTTCTTTGAAGATATTACCAGGAATGTACACATGTTGTGAT 1883

```

```

Qy      214 aLAspAsn-----MetValAla-----
Db      1884 TGTATAGCAGAAAGAAACAGAGGTGCAGATGATGAGCTTTTACGTTGAGCTTAAGCCAG 1943
Qy      219 -----
Db      1944 ACAAGAGGAAGAGCAATTCACAGAAATTCGTAATTATTGAGACTGTGACTCCAG 2003
Qy      219 -----
Db      2004 AAAATAATCTAAGTCAAGAAATGCAAGATTTTACCAATTAATCAGGGGCACTTCA 2063
Qy      220 lLeuAsnLeuIleValGln-----HisLLeuGln-----
Db      2064 TTGAAGCTGTATAGACAAATGTATACATGTTCCAGCAAGACCCCAATGACAGAGACTGT 2123
Qy      229 -----
Db      2124 ACCATGCCACGAGCAGATGACCAAGCTCTCTGTGAGATTTGGGAGAGTCCGCAAGTTGT 2183
Qy      231 uAsnGlyAspIleCysLys-----Trp-----HisArg 241
Db      2184 TCGTGCCCAAGCCTGCAGAAAGAGGCGGAGCGAGCAGACGATGGCCCTCTGCAACAG 2243
Qy      241 lY-----SerAsn-----GlyArgSerTyr-----
Db      2244 GCATCCAGGCGGTGCTTCTCCAGAAAGAGGCGGAGCCAGCTTACGTGTGAGACTGT 2303
Qy      249 -LysArgThrPheSerGluProGly-----AspHis--Pro-----
Db      2304 TNAGGCCCTGCGGCGAGCTGGCCCCGAGACGAGAGAAACCTCCTTGAGAGACA 2363
Qy      260 -----GlyMetLeuThrSerGlyLysArgSer-----His-- 269
Db      2364 TGGAGGACATCAAGCTGAGAGACTCTCGCCCGGAGCAACGGGGCTGCTCTCATGC 2423
Qy      270 -----LeuGluSerSerArg-----ProHis 277
Db      2424 TGAATCTTACGACAGAACCAAGAGACAGACAGCTTCATGTCCTCAT 2468

RESULT 34
US-09-488-725B-3474
; Sequence 3474, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaast
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20

```



```

QY 251 -----ThrPheSer-----GluPro-----GlyAsp----- 257
Db 1969 TGCACAGCTTTCTGTCGACCTTAATGCTGTACTGTCTGAGCGGTGACGCGCC 2028
QY 258 --His-----ProGlyMetLeu----- 262
Db 2029 TGCATGTACGATATCAGAGTGTGTGTAGCCAGCGCCTTCTCAGAAAGTTGACCA 2088
QY 263 -----Thr-----SerGlybArgSerHisLeuGlyUserSerbArg----- 275
Db 2089 CCTCCACCGCCAGCAGATTCAGTAACCAAGAGTCAACCAATGTMAAACGAGGGGTC 2148
QY 276 -----ProHis 277
Db 2149 TTATCCCTCAT 2159

RESULT 35
US-09-488-725B-3363/c
; Sequence 3363, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OR INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 3363
; LENGTH: 4461
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4464)..(2165)
; OTHER INFORMATION: similar to g1372411 in the genepept database release 114.
; OTHER INFORMATION: Run with FASTX 3.3t00, default parameters
US-09-488-725B-3363

Alignment Scores:
Pred. No.: 1.59e+04 Length: 4461
Score: 286.30 Matches: 145
Percent Similarity: 15.28% Conservative: 55
Best Local Similarity: 11.08% Mismatches: 70
Query Match: 19.74% Indels: 1040
DB: 1 Gaps: 5

us-09-896-522-2 (1-277) x us-09-488-725B-3363 (1-4461)

```

```

QY 7 GluAspCys-----GluSerProAla----- 13
Db 4284 CAGATTTGCTCTCTACTAAGACAGATATGTGTGAGAAACCTTCTTACCGGACTGTGG 4225
QY 14 ProGlyAla-----AspArgProHis-----GlnArgPro----- 23
Db 4224 CCACAGCGCGTGATCATTTAGACAGACACAGAACAGAGGCCAGCTACGCGAGAG 4165
QY 24 -----PheLeuIleGly--ValSer----- 29
Db 4164 AGCGCTTTGCCAAGCAATATATATAGCGCTTTTGTGGATGCTTACTCGCATCATG 4105
QY 30 -----Gly-----GlyThrAlaSerGlybSerThrVal----- 39
Db 4104 ATATTTATGAGTCAAGAACTATGACACCATTCATGGGAAACACGTATTATGGTG 4045
QY 39 ----- 39
Db 4044 TCTTGATATCTATGCTTTGAAATCTTTGACAAACAGTTTGAACAATTCGTATCA 3985
QY 40 -----Cys--GlybIleMetGluLeu-----Gly--GlnAsnGluValG 53
Db 3984 ATTACTGCAATGAGAACTGCAGACACTTATTATTCAGCTGTTTGAAGCAAAACAG 3925
QY 53 IuGlnArgGlnArgbValVal-----IleLeuSerGlnAspArgbPheTyb 69
Db 3924 AGGAATATCCAGCGGAGAGGATCCCTGGAAACATTTAGCTACTTCAACATCAATCA 3865
QY 70 ValLeuThrAla--GluGlnbys----- 76
Db 3864 TTGTTGACCTCGTGAGCAACAGACAAAGGATTCATTCGATTCGATGCTTGCA 3805
QY 77 -----AlaGlybAla-----LeuLys-----GlyGI 83
Db 3804 TGAATGCGCAAGATCAGCATGAATGTTTCTTGAAGCATTAACAGTAATTGGGCA 3745
QY 83 nTybAsn--PheAspHisProAspAla-----PheAsp 94
Db 3744 AACACGCCATTTTTCAGCGCAAGACTCTGTGCTCAGCAAAATTCGAGATTGATC 3685
QY 94 snAsp----- 95
Db 3684 GAGATTTTGCATTCGACATTATGACAGCGATGATGCTATTCGATTTGATTG 3625
QY 96 -----LeuMetHisArgThr----- 100
Db 3624 ACAAAATTAAGATCTTATTTCAGAGTTTCAAGCGCTTATGTATTAACAGTTCAAATC 3565
QY 101 -----LeuLysAsnIle--ValGluGlyLys-----ThrValGluVal-ProThr--- 114
Db 3564 CTGTGCTCAAGATATATGTGCTGAAAGCAAACTGAGCATTACAGAGGTACCAAGGAC 3505
QY 115 -----TyrAsp----- 116
Db 3504 CTCTGACTGCTGACTCTGTTTAAGAATTCATATGCTCTATAGACAACTTGACAT 3445
QY 117 -----PheValThr-----His----- 120
Db 3444 CAAAGAACATATTACGTTCGTTCGATCAAAACCAATGACAAAGAAATCTCCACAGATAT 3385
QY 121 -----SerArgLeuProGluThr----- 127
Db 3384 TTGATGATGAACGCTGCCGCGACCAAGATGAAATATCTTGACTATCGAAGAAATGTGAG 3325
QY 127 ----- 127
Db 3324 TGGGTGGGAGAGATTTGCTTCGCCAGACATACAGAGATTTCTTACAGGATATAGA 3265
QY 127 ----- 127
Db 3264 TGATCTCTGAATTCACCTGCGCCCAACCATGACCTTCTTGACAAAGAGCTGTCAAG 3205

```

```

QY 127 ----- 127
Db 3204 AACTAATGTAAGGTGTGTTTCAGAGTATGATGCTTAATGGAGAACCAAAATTTTCA 3145
QY 128 -----ValValTyr-----ProAla--Asp-----V 134
Db 3144 TTGGAACACCCGAACTGTTTACCTTGAGAGAACTCCGTGCCAGATCTCTATAGGA 3085
QY 134 aValleuphe----- 137
Db 3084 TTGTCTCTTTCTTACAAAAGGTGTGCGGGGACCTTGCCCGCAGTCGTAACAAAGAA 3025
QY 138 -gluGly-----lleuValpheTyr-----SerGln----- 146
Db 3024 CCAAGGAGCTCGACATATACAGTACTACCGGGCCTACAAAGTAAAGTCCGATCC 2965
QY 147 --GluIleargAspMetPheHis----- 153
Db 2964 ACAGAGTGGCCAGACGCTTCATGCGGTCAAGACCATGCGAGACTACGGAGAGCAGTGA 2905
QY 154 -----leuArgleuphe----- 157
Db 2904 AGTGGCCAAAGCCTCTCTAAAGTTCTTCGCGTTTGAGAGGCCCTGACAGCATTTTCA 2845
QY 158 ValAspThrAsp-----SerAspVal----- 164
Db 2844 ATGATGAGAGAGCATCCAGCTCATCAAGACATTCGGGCTCAGACTCCCAAGTCA 2785
QY 165 -----ArgIleu--SerArg--ArgValleuArgAspValArg-----Arg 176
Db 2784 GGCGAAAGGTGTCAGCGGTGGAATGTGAAGGTCAAAAGGCTGACCTCGGGCTCCAGA 2725
QY 177 GlyArgAspleuIleuGlnIleuThrGln-----TyrThr-----Thp 190
Db 2724 GGCGCTGGAGGGCAACTATCTTCTTCAAGCCAGATACACTCAGACCTCAGGCACTT 2665
QY 190 heVal-----lys-----ProAlaPhe-- 195
Db 2664 TTGTCTCTGTGCTAATGATGAAACGGAAGACAAATACATGATGCTCTTCTTCT 2605
QY 196 -----GluGluPhe----- 198
Db 2604 GTCACTGCGTAAGTAATCATGATTAGTAAGTGAAGAGACAGACATTTTGTCACTG 2545
QY 199 -----CysIleu-----ProThrIleuTyr----- 205
Db 2544 ACCGTCACTGTATTAATGATCCACTAAACAGTACAGGTAGAGATATCCCTC 2485
QY 205 ----- 205
Db 2484 TATACATTTGACTGCTGATGCTCTCCATGAGAAAGACCAACTTTGATGTTCCATA 2425
QY 206 -----AlaAspValIleIle-----ProArgGlyVal 214
Db 2424 CGAAGACAAACAAGACCTCATTTGTGCTCTTACAGAAACAGCAACCAAGAGAGTC 2365
QY 215 -----AspAspMet-----ValAlaIleAsn-----Leu 222
Db 2364 GAATTGAGAACTGTGGAGTGTGCTGATCAATTTCAAGATGAGAGAGCCCACTT 2305
QY 223 lleValGln--His-----lleGlnAspIleleuAsnGlyAspIleCys-----L 237
Db 2304 CAAGTGAAAGCTACCAACCCAGTACAGTACAGCTTCAGGGAGAGAGTGCACCGTTC 2245
QY 237 ysTriphIserArgIlyGlySerAsn-----GlyArgSerTyrIlyAspThr-----Phe-- 252
Db 2244 CGTGGAGAGCGGCTCAACACAGCCGACCTTCAACCAAGAAATCGCTGGGCTTCAT 2185
QY 253 -----SerGluProGly-----AspHisPro--GlyMetLeuThrSerGlyIlyAspSerHis 269
Db 2184 CCTCAACGTGCGCGGAAACTGACGCCCGGAGGAGGCTGCGCC--GGAGCCGCGCACAC 2127
QY 270 leuGluSer-----SerSerArgPro 276

```

```

Db 2126 TCCGAGTCTCGGTCCCAAGTCCAGTCTGCTGCTCCCAACCC 2086
RESULT 36
US-09-488-725B-3360
/ Sequence 3360, Application US/09488725B
/ GENERAL INFORMATION:
/ APPLICANT: Yuanhua T. Tang
/ APPLICANT: Ankura Slinku
/ APPLICANT: John Tillinghaast
/ APPLICANT: Chenghua Liu
/ APPLICANT: Radoje T. Drmanac
/ TITLE OF INVENTION: Novel Configs Obtained
/ FILE REFERENCE: From Various Libraries
/ FILE REFERENCE: 784
/ CURRENT APPLICATION NUMBER: US/09/488, 725B
/ CURRENT FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US 09/004,182
/ PRIOR FILING DATE: 1998-01-07
/ PRIOR APPLICATION NUMBER: US 09/034,341
/ PRIOR FILING DATE: 1998-02-13
/ PRIOR APPLICATION NUMBER: US 09/045,400
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: US 09/321,214
/ PRIOR FILING DATE: 1999-05-26
/ PRIOR APPLICATION NUMBER: US 09/131,598
/ PRIOR FILING DATE: 1998-08-10
/ PRIOR APPLICATION NUMBER: US 09/170,294
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: US 09/179,473
/ PRIOR FILING DATE: 1998-10-27
/ PRIOR APPLICATION NUMBER: US 09/181,430
/ PRIOR FILING DATE: 1998-10-28
/ PRIOR APPLICATION NUMBER: US 09/235,076
/ PRIOR FILING DATE: 1999-01-20
/ PRIOR APPLICATION NUMBER: US 09/234,611
/ PRIOR FILING DATE: 1999-01-22
/ Remaining Prior Application data removed - See File wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 10289
/ SOFTWARE: pc_ct_genes Version 1.01
/ SEQ ID NO 3360
/ LENGTH: 7502
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: (2)...(6861)
/ OTHER INFORMATION: similar to g1341386 in the genepept database release 114.
US-09-488-725B-3360

Alignment Scores:
Pred. No.: 9.5e+04 Length: 7502
Score: 266.30 Matches: 138
Percent Similarity: 15.87% Conservative: 59
Best Local Similarity: 11.12% Mismatches: 78
Query Match: 19.74% Indels: 973
DB: 1 Gaps: 3

us-09-488-522-2 (1-277) x us-09-488-725B-3360 (1-7502)
QY 3 SerAlaGlyGlyGluAsp-----CysG 10
Db 3611 TCGTCGGGGAGAGAGACCTCCCTTGATCTCAAACTGGGGCATACAACTGGCTGCG 3670
QY 10 lu-----SerProAlaProGluAlaAspArg-----Pro----- 19
Db 3671 ACAAGTCTTTTCACTCCAGCAAGCAGGCGCAGCAGGAGAGAGCTGTACATTGTGGA 3730
QY 20 -----HisGlnArgPro----- 23
Db 3731 AGCTTAGCCACACATTTCCAGCGCGAAGAGAGAGAGTCTGACCTGTACAGATTACT 3790

```

```

Qy 23 ----- 23
Db 3791 GGATGACCTGAGCATGACGGGAGTGTGACCTGAGTACTGCTCTTAACAGAACT 3850
Qy 24 -----Phe-----LeuileglyValsergly-----G 31
Db 3851 CATCACTTTCGGACACTGGAAGCTCTACTTGGCAGCTCGGGAGTCCCTACCTATGCGG 3910
Qy 31 lYThrAlaSer---GlyLysSerThr----- 38
Db 3911 CAACCTCATCTCAACAGAAATAGCTCTGCTGCGCTGAGGAGGCTACCTGAGTAC 3970
Qy 39 --ValCysGluLysIleMetGluLeu---LeuGlyGlnAsn-----G 51
Db 3971 CGATCTGCAGCAGGGTTATGCCCTTAAAGTCAAGAGCTTCTCTCTCTTTGTGA 4030
Qy 51 uValGlu-----GlnArgGln----- 56
Db 4031 GGTGGAAATCCATCAAAAGACATTTTAAAGTCGCTGGTGGTACTGCTGATGATA 4090
Qy 57 -----ArgLysValValIle-----Leu-----SerGlnAsp 66
Db 4091 CCTGCTGTCGGGAAGCTGTGTGTGACAGGACCAAGCTGATCGATGAGCGCAGGACAT 4150
Qy 66 gPhetyrLysValLeu-----Thr---AlaGluGlnLysAlaLysAlaLeu 81
Db 4151 GCTGCTGAGATGCTGAGAGCATGACATGACAGTACAGATCAAGAACCAAGGCTTCAT 4210
Qy 81 sGly-----GlnTyrAsnPheAspHis---ProAsp----- 90
Db 4211 -GGCTGTGTGATTTGAGACAGCAAGCGCTCAATCTGATGATGACTACCGGACCCGGGT 4269
Qy 91 --AlaPheAspAsnAspLeuMetHis-----ArgThrLeuLysAsnIleValG 106
Db 4270 TCATCTTCGAGAGGCT--CTGCAGCATCATTTATCTCTGAGAGAGATGAAGTACAGATTC 4328
Qy 106 uGlyLysThrValGlu---ValProThr--TyrAspPheValThrHisSerArgLeu 124
Db 4329 TTT--GTGACCTCGAGAAAGATCCCAACAGAAAGACTTCTT--ACAG--GGCAGGATGCC 4384
Qy 124 o-GluThrThrValVal-----Tyr----- 130
Db 4385 TGGGAAACCCGTATATGACAGCAATGAGCCAGGATCGGGCCGTATGAGAGATATAAGAA 4444
Qy 131 -----Pro---AlaAspValVal---LeuPheGlu-----GlyIle----- 140
Db 4445 CAAGATTTTGCAGGACTGTGACTTATGTCGCCCTCTGGAAGATGACAGTGGCATGAGACT 4504
Qy 140 ----- 140
Db 4505 TCTAGTGAACATTAATCATTAATTGTTGACCTTCTGCTGCTGAAGTTTCAAGAAAGT 4564
Qy 141 LeuValIlePheTyr-----SerGlnGluIleArgAspMetPheHisLeuArg-----Le 156
Db 4565 CTGGTGTACACAGATGAGGAGGAGCCCATGATGAGATTGTTATGCTATGCGGGGGCTGCT 4624
Qy 156 u-----PheValAsp-----ThrAspSerAspVal-- 164
Db 4625 GGGCGCATCCACAGAGAGATTCAATGAGTCCCTGACTCTACTACAGATGAAGAAAGAGA 4684
Qy 165 ---ArgLysSer----- 167
Db 4685 TGAAGAAAGAGTGTATTAAGATGGCTGTGTGTATGAGCCAGTGTGGGGCTCGAATGAT 4744
Qy 168 -----ArgArgValLeuArgAspValArgArgGlyArgAspLeu----- 180
Db 4745 GCTTAAACAGACTCGCAGGG--ATCAGAGATTTTCAAGCAGGAGCGCACACTTCTTAACAGTG 4802
Qy 180 ----- 180
Db 4803 CTACTGAATATTGCTCAGTTACTGCTGGAAGTGAAGTCAACCGGACAGCAATGCTGTCAA 4862
Qy 180 ----- 180

```

```

Db 4863 CTGGAATGAACACCTTGAACGTCACTGCGGAGACCTTAAACCTGACCTGTGATGATA 4922
Qy 181 -----GluGlnIleLeuThr----- 185
Db 4923 CAAGAAAGACAGACAGTGGGGGTGACCTGTGCTGACAGGTGCTGTGATCATGATGAG 4982
Qy 186 GlnTyrThrThr-----PheValLysProAlaPheGluGluPhe----- 198
Db 4983 ATTATATCAAGCTGACGCCCAATCTTGAAGCCCTGAGATGAGACAAAGGCAACTCTCT 5042
Qy 199 -----CysLeuProThrLysLysTyrAlaAspVal----- 208
Db 5043 GACAGGTGAACAAGATCAACTGTGTATGCTTGTGACCAAGATCAACAGACACTTGTGCG 5102
Qy 209 -----IleIlePro-----Arg 212
Db 5103 CTCCAACCCCAAGTGTGCTCCAGGCGCTGCTGCAATCATCTCCGATCTTCTTGGAGA 5162
Qy 213 GlyValAspAsn-----MetVal--AlaIleAsnLeuIleValGln-----His 227
Db 5163 GGTGAGAAATACAGATCTTGTGTGAGCGCATTCAAACCATCTGCAACTTGTATTAATA 5222
Qy 227 IeGlnAspIleLeuAsnGlyAsp-----IleCysLys----- 237
Db 5223 TGATGAAGATCAC--AGTGGTATGATATAAGTCTTCTCGGACCTGCTCTGTAAATAGCT 5281
Qy 238 --TrpHisArgGly--GlySerAsnGlyArg--SerTyrLysArgThrPheSerGluPro 256
Db 5282 GCTGGCTCAAGGAAACAACAGCAATGGGACACAGCTGAGAGATCTTGATTTCCAGAA 5341
Qy 256 LysAspHisPro----- 259
Db 5342 GGGATCACCCAGAAATGACATCTGACCTTACATGAAGAAACACATCCCTAGGGCGCAGATT 5401
Qy 260 -GlyMetLeuThrSer----- 264
Db 5402 TGGGATCCGACATCTTGAAGAAAGTTTGTCTTGTGCGCCAGCTTGCATTTATCTTAAG 5461
Qy 264 ----- 264
Db 5462 GCTGCTTGGGGCTGGCCATTCAGACACCTGACACCAAGTTCGTATGAACTGATTC 5521
Qy 265 -----G 265
Db 5522 CATCCCAACCTGATAGCTGAGACAGGTGTCCCACTGATGAGGCACTTGGACCTTGG 5581
Qy 265 LysArgSerHisLeuGluSer----- 272
Db 5582 CAAGAGAACCTGGCTGGAAGCCGTGCGGAAACACCTGACGTAAACAAAGAAATTGACGC 5641
Qy 273 -----SerSerArgPro-----His 277
Db 5642 CAGCCCGCAGGAGAACCCGGGACAGAGAAGAACGCAT 5678

```

RESULT 37  
 US-09-488-725B-769  
 ; Sequence 769, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuanhua T. Tang  
 ; APPLICANT: John Tillinghast  
 ; APPLICANT: Ankura Sunku  
 ; APPLICANT: Chenghua Liu  
 ; APPLICANT: Radoje T. Drmanac  
 ; TITLE OF INVENTION: Novel Contigs Obtained  
 ; TITLE OF INVENTION: From Various Libraries  
 ; FILE REFERENCE: 784  
 ; CURRENT APPLICATION NUMBER: US/09/488,725B  
 ; CURRENT FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/034,341  
 ; PRIOR FILING DATE: 1998-02-13







```

Db      117 GCGCGCGGAGGAGGCGGCGCTGAGGCGGAGCGGCGCGCGGCTTGCGGGGCTCG 176
Qy      9 -CysGluSerProAlaProGluAlaAspArgPro-----HisGln----- 21
Db      177 GTGCGCTCGGCACTGCGCGCGGCGGCTCTCGCGCGCGCATAGTGGCGGCGGCGG 236
Qy      22 -----ArgPro-----PheLeuIle---GlyValSer--G1 30
Db      237 GAGGGGCGTGGGCGCCAGTCGCTTCGCCAGCTACTTGTGATCTGGCGACTGAGACGG 296
Qy      30 yGlyThrAla---SerGlyLys---SerThrValCysGluLysIleMetGluLeuLeu- 47
Db      297 AGACCGGCTGAGACCGGAGAGAGCTGTGGCATTTATGCGAGTACATAC--AGGCTTCTAA 354
Qy      48 -----GlyGlnAsn----- 50
Db      355 AGCCAGGAATGTGCCAGCCCTTCATTTCATGACATGAGAGAGAAATTTTGAACA 414
Qy      50 ----- 50
Db      415 GACACCATGAGAGAAATTCMAATCTAAGTCTTCGACGATATCTTGAGAACGTAGA 474
Qy      50 ----- 50
Db      475 ATGGAATCCCTTGACCAAGATGCAATGAGATGCTATGTATGCCGAAAGGCTGGCATT 534
Qy      51 -----GluValGluGlnArgGln---ArgLysValIleLeuSerGlnAspArg- 66
Db      535 CAAGACCCAGGCTGATCCAGGAGGAGCCCAATTCATGCTTATATACAAAGGAGGA 594
Qy      67 -----PheTyrLysValLeuThrAlaGluGlnIly 76
Db      595 TGGCTCGGACATTTGGGTTTGCCCTCACTTTTATGAAGAGGTGACTAGCAAGCAT 654
Qy      76 salAlaLysAlaLeuLysGlyGlnTyrAsn-----PheAsp-----His- 88
Db      655 CTCAGAGCAATGAGACCTCTTACACATGACATGCAATGTGATGATGCTCTACATGC 714
Qy      89 -ProAspAlaPheAspAsnAsp----- 95
Db      715 TCCCTCGTGATGACAGAGACGAGAGCATGAGAGATGTGTGAGAGACCTCTTGAC 774
Qy      95 ----- 95
Db      775 CAATGCGACGCTTCACTCTTATGACATTAGCCGGGACACTCTTACGTCTTAAGTG 834
Qy      95 ----- 95
Db      835 CATGCGCTCATCACACCATGTCTTTCATGAAGGATGTGAGAGCGTGGAGCAACT 894
Qy      96 -----Leu-----MetHis----- 98
Db      895 CCAACGAGCAGTCACTTCACTGACCCCTCCACTGCCCTTGAGAGTACATATACAA 954
Qy      99 ArgThrLeuLys----- 102
Db      955 CGTACTCTAGAGAGTGGCGCTCCCACTCTCGGCGCGCTCTTGAAGTTTCTGGGGTCTA 1014
Qy      103 -----AsnIleValGluGlyLys-ThrValGluValProThrTyrAspPhe- 117
Db      1015 TGGGCAATATATCTGCGAGAGACCAAGTACCAATGAGCTTCCCTATTGACTTCTGT 1074
Qy      117 ----- 117
Db      1075 CAAGAAGTTTGAACGTCTCGGGGTGAGAAATGTGTTCAGCTTTTACTGTGCGCT 1134
Qy      118 -----Val-----ThrHisSerArgLeuProGluThr-----ThrVal- 128
Db      1135 TCTGAGATTCAATCTGCTCTACTACAGCA--TTACAGAGACTGATGACTGTGGCG 1192
Qy      129 -----ValTyr----- 130
Db      1193 GAGACGATTACAGCTCTCATGTTTCTTCCAGTGGGAGCATGTATGTCCCTATTTCTC 1252

```

```

Qy      131 ProAlaAspValIleLeuPheGluGlyIleLeuValPhe-----TyrS 145
Db      1253 CGAGCTCTCTCTCGCATTTCTTAG--ATGCTCTGTTCATACATCTGATGGGTTGCAAT 1310
Qy      145 ergGluIleArgAspMetPheHisLeuArgLeu-----PheV 158
Db      1311 CCAATGGCTCGATGAGACCGGTCAAAAGCTGAGCTGCTCTCAAGAGCTTAACCTGTCTTG 1370
Qy      158 alaPThrAspSer-----AspVal----- 164
Db      1371 TGGACATTGACCAACCACTTCATTGAGTTGCGAGAGACTTGCCACAGTCCCAACAAT 1430
Qy      165 -----ArgLysSerArgValLeuArg----- 172
Db      1431 TGAAGTTTGCAGAGAACTCTGAGATTCTCATGTGCAATTGGAATTCCTCGAAGGGA 1490
Qy      172 ----- 172
Db      1491 ATCTTCATTCAGTGAAGAGTCCCTCCAAGCTGAAGAGCTGGGCGCTGTGAGCTGTCT 1550
Qy      172 ----- 172
Db      1551 CGGACAGAGAAATGGGACATTTGCTGCTCCCTTTGCAATCTCTACAGACTTCTTAAG 1610
Qy      172 ----- 172
Db      1611 AGAATGAATATTTGCCCGGCTGCAAGCTTGTGTCAAGAGAACTGGGGTAGCCTGAAA 1670
Qy      173 -----AspVal-----Ar 175
Db      1671 AGTTGAAGTGGCTGAAGAACCCCAAGCAATAAGATCTCAAAAGTTCAAGTGTGATGAAG 1730
Qy      175 gArgGlyArgAspLeu-----Glu-----GlnIleLeu-T 185
Db      1731 AAGAACTCAGAGATTACAGCTAAACATTCAGATCCGGGAAGTTTGTGCAAAATCGTTCA 1790
Qy      185 hArgGln-----TyrThrThrPheVal---LysProIle----- 194
Db      1791 CTCAGATGTTTGAGATTATGAGGTGTGTCTATCCAAACCCAGCAGATTAAGAAATCCT 1850
Qy      195 -----PheGluGlu-----PheCys----- 199
Db      1851 GGTTCACCAACAGGAGCAAAATGCAAACTTTATTAAGATCTTTTCTGTGATGACG 1910
Qy      200 -----LeuProThrLys----- 203
Db      1911 CTGAGCCCTACCTGCGCTTCTCTCAAGATTCTCGAGACCCAGATGTTGATCTTCA 1970
Qy      204 -----Lys-----TyrAlaAspValIle 209
Db      1971 TTGACAAACAATAATGTGTGATGATGATGATGAAGAAGCCTGTATCCGGGTATTTG 2030
Qy      210 IleProArg-----Gly----- 213
Db      2031 ATTCCCGAGTTGCAAGATCAAGCTGTGAAATTTGGACCACTACTCTCCGTATATCCA 2090
Qy      214 -----ValAspAsnMet---ValAlaIleAsnLeu----- 222
Db      2091 TGTACAGAAAGTACACATGTGATGATGAAGAGAGAAAGTAATGAGCTGCTGGCAA 2150
Qy      223 -----IleValGln-----HisIleGlnAspIle----- 230
Db      2151 AATTGACATATCTGAAATTCACCACTTTCATTCAGATGAGAAATTTGACAGGAAT 2210
Qy      231 -----LeuAsnGlyAspIle----- 235
Db      2211 ATGAGCGGGCTTCTTCCCTAAGCTCAGTCTGATGATCTTTCACCTGGAGCCAGCA 2270
Qy      236 -----Cys-LysTyr----- 238
Db      2271 ACAATGTGACGAAGAAAGAAATGCGCTGCGCAGTGGAGGCGGAAAGATCGGACAGACAGC 2330

```

```

QY 239 -HisArg----- 240
|||
Db 2331 ACACAGAACCTGCGTTTAGATATAGACAGAGGAGAAATACATCCAGAAACCCAGGA 2390
QY 240 ----- 240
2391 CTATGGCAGACATATCCGCCAGGCCAAATCTCTCCATCAGTATGCCC 2450
QY 240 ----- 240
2451 AGACAAATGGAGATTGTAGAGGCGCTGCTGAAGAGATCCGCAATATAGACCAAGAGA 2510
QY 241 ----G|G|LysSerangly--ArgSer----- 247
|||
Db 2511 TGCTGTGAAAAAATATGCGCCGAGAGCTGTGAGCTAGGSCATGGGAGGTGAACATCA 2570
QY 248 ----TyrLysArgThr-----Phe----- 252
|||
Db 2571 CAGGGGTGGAAGAAACACCTGATTTGCCAGCCTTTTGATCTCTGGAAGAGATCTGA 2630
QY 253 ----SerLysProGlyAsp----- 257
|||
Db 2631 GTCATGACTACAGTGAAGACAGGGGAATCAGCCTTATGTCCACCTGTATACATTATC 2690
QY 257 ----- 257
2691 AGGAAACCGGACAGAAACTACATCAGAGAGCCTCAGTACTCAGGAATACTCTTG 2750
QY 257 ----- 257
2751 ATTGAAACGTAGAGAGTCTGATGCAGCTCATCATGCTCCCTGAGATCTCCCTGA 2810
QY 258 ----HisPro----- 259
|||
Db 2811 TTCAGATATAGCAGCATCGGAGAAATCAGATGATGTGGAAGGCCA 2870
QY 260 ----GlyMetLeuThrSerGlyLysArg-----SerHisLeuGlu-SerSer 273
|||
Db 2871 GAGCATGGGTGCGACTGCTGCATGGAAAAAGTTACTTCCAGACACCTGAGAGCTCC 2930
QY 274 Ser-ArgPro-----His 277
|||
Db 2931 TCTCAGACCATGAGCTCAC 2949

```

```

PRIOR FILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: US 09/235,076
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: US 09/234,611
PRIOR FILING DATE: 1999-01-22
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 10289
SOFTWARE: pt_ct_genes Version 1.01
SEQ ID NO 1107
LENGTH: 4975
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (2) (4975)
OTHER INFORMATION: similar to gi5689519 in the genepept database release 114,
US-09-488-725B-1107
Alignment Scores:
Pred. No.: 2.72e+04 Length: 4975
Score: 285.90 Matches: 152
Percent Similarity: 12.74% Conservative: 53
Best Local Similarity: 9.45% Mismatches: 71
Query Match: 19.72% Indels: 1336
DB: 1 Gaps: 6
us-09-896-522-2 (1-277) x US-09-488-725B-1107 (1-4975)
QY 2 AlaserAlaGlyLys-----GluAsp----- 8
|||
Db 117 GCGCGCGGGAGAGGGCGGCGCTGAGGCGGAGCGGCGCGCGGCTGCGGGGCGCTCG 176
QY 9 -CysGluSerProAlaProGluAlaAspArgPro-----HisGln----- 21
|||
Db 177 GTGCCGCTCCGCACTGCGCGCGCGGTCTCGGCCCGCCAGATGAGCGCGCGCGCG 236
QY 22 -----ArgPro-----PheLeuIle-----GlyValSer--G1 30
|||
Db 237 GAGGGGCGCTGCGCGCCAGTCGCTTCCGCCACTACTGCTGCTGCGAGCTGCAACG 236
QY 30 yGlyThrAla--SerGlyLys--SerThrValCysGluLysIleMetGluLeuLeu- 47
|||
Db 297 AGACCGGGCTGAGCGGAGCGAGAGCTGCGCATTAATGCAATAC--AGCTTCTTA 354
QY 48 -----GlyGlnAsn----- 50
|||
Db 355 AGCCAGGAGATGTGCCAGCCCTTTCATTTCAATGACATGAGAGAAATTTTGAGCA 414
QY 50 ----- 50
415 GACACCATTTGAGAAAGAACTTCAATTAAGTCTTTCACAGATATCTTGAGAACGTA 474
QY 50 ----- 50
475 ATGGAATCCCTTTGACCAAGATGACATGAGAAATCTATGTATGCCAAAGGCTGCGCAT 534
QY 51 ----GluValGluGlnArgGln--ArgLysValIleIleSerGluAspArg- 66
|||
Db 535 CAAAGACCGAGCTGATTCAGAGGAGGCCCAATTCACGCTTATATATCAAGAGGAGA 594
QY 67 -----PheTyrLysValLeuThrAlaGluGlnLys 76
|||
Db 595 TGCGCTCGACATTTGGGTTTGCCCTTCACATTTTATGAAAGAGTGTCTGCAACGAGAT 654
QY 76 sAlaLysAlaLeuLysGlyGlnTyrAsn-----PheAsp-----His- 88
|||
Db 655 CTGAGTGCATGAGACCTCTTACACATGACACAATGCTGAGATATATGCTTACATGTC 714
QY 89 -ProAspAlaPheAspAsnAsp----- 95
|||
Db 715 TCCCGCTGTGATGACAGAGACCGAGACGACATGAGAGATGTGTAAGACACTCTGTGAC 774

```

```

QY 95 ----- 95
Db 775 CAATGACGCGTTCAACTCTATGACATTAGCCGGGACACTCTACGCTCTAAGTG 834
QY 95 ----- 95
Db 835 CATTCGCTGATCACACCAATGCTTTCATGAAAGCATGTGGAGCGTGTGAGCAACT 894
QY 96 ----- 98
Db 895 CCACGAGGACGTACATTCACTCAAGCCCCCTCCACTGCCCCCTTGAGAGCTACATATACAA 954
QY 99 ArgThrLeuLys----- 102
Db 955 CGTACTCTACGAGTGGCCGCTCCACACTCGTGGCCGCTCTGAAGTTTCTGGGGCTCA 1014
QY 103 ----- 117
Db 1015 TGGGCAATATATCTGCGAGACCAAGTACCAATGAGCTTCCCTATTTACATTCTCTGT 1074
QY 117 ----- 117
Db 1075 CAAGAAGTTTGAAGTCTCGGGGTGAGAAATGTGTTTCAAGCTTTTACTGTGCGCT 1134
QY 118 ----- 128
Db 1135 TCTGAGTTTCAATCTGCTCTACTCAACAGCA--TTACCAAGAGACTGATGATGTGGCG 1192
QY 129 ----- 130
Db 1193 GAGACGATTACAGCTCTCATGTTTCTTTCCATGAGCAGACATGCTATATGCCATATCTC 1252
QY 131 ProAlaAspValValLeuPheGluGlyIleValPhe----- 145
Db 1253 CAGGCTCTCTCTGCAATTTCTTAG--ATGCTCTCTTTCCATACCTGANGGTTTGATT 1310
QY 145 ercGlnIuIleArgAspMetPheHisLeuArgLeu----- 158
Db 1311 CCAATGGCTGAGTACCGGTCAAGCTGAGCTGCTCAAGAGGCTAACCTCTGCTTTG 1370
QY 158 aAlaSerThrAspSer----- 164
Db 1371 TGGACATTGACCAACCACTTCATTCAGTTGCGAGAGCACTTGCCACAGTTCCCAACAAAT 1430
QY 165 ----- 172
Db 1431 TGGAGTTTGTCCAGGAAGTCTCTGAGATTCTCATGCAATTGGAAATTCCTCCGTAAGGGA 1490
QY 172 ----- 172
Db 1491 ATCTTCATTGCAATGAGAGTGCCTCCAGCTGAAGAGGCTGGGGGCTCTGAGCTGTCT 1550
QY 172 ----- 172
Db 1551 CGGACAAAGAGAAATGGGAACATTGCTGGGCTCCCTTTGCAATTCCTAAGAGCTTTAAG 1610
QY 172 ----- 172
Db 1611 AGAATGAAAATATATGCGCGCTGCAAGCCTTGCTCAAGAACTGGGGTGAGCTGAAA 1670
QY 173 ----- 175
Db 1671 AGTTGGAAGTGGTGAAGACCCCAAGACGCAATAGAACTCAAAATTCAGTGTGATGAAG 1730
QY 175 gArgGlyArgAspLeu----- 185
Db 1731 AAGAACTCAGGAATTTACAGCTAAACATTCAGATCCGGGAAGTTTGTGAAAACGTTTCA 1790
QY 185 hrcGln----- 194
Db 1791 CTCAGATGTTTGCAATTAATGAGTGTGTCATTCACACCCAGCGAGATTAAGAAATCTC 1850
QY 195 ----- 199
Db 195 ----- 199

```

```

Db 1851 GGTTTACCAACAGAGGACAAATGCAAACTTATATTAAGACTTTTCTCTCAGATCAGC 1910
QY 200 ----- 203
Db 1911 CTGAGCCCTTACTCTGCTCTCTCTCAAGATTCCTGGAGACCAGATGTTGACTTTCA 1970
QY 204 ----- 209
Db 1971 TTGACAAACAAATTAATGTGTCATGATGATGATATTAAGACCTGTACTCCGGGTATTG 2030
QY 210 IleProArg----- 213
Db 2031 ATTCCGAGTTGACAAAGATCAGGCTGTGAAATTTGGACACCTACTCTCCGATACCA 2090
QY 214 ----- 222
Db 2091 TGTACCAAGATGTACCACTGTGATGAAGACAGAGAAAGCAATTTGAGCTGCTGGCAA 2150
QY 223 ----- 230
Db 2151 AAATTGACCAATCTGCAATTCACCACTTACTTGACATGAGATTGACAAAGGAAAT 2210
QY 231 ----- 235
Db 2211 ATGAGCCGGGCTTCTTCCCTAAGCTCAGCTGATGATGATCTTCCACTGGGCGACAGCA 2270
QY 236 ----- 238
Db 2271 ACAAGTGACAGAAAGAAATGCCCCCTGCCAGTGGAGGGGAAAGATCGGACAGACAGC 2330
QY 239 -HisArg----- 240
Db 2331 ACACAGAACACTGCGTTTATATATGACACAGAGGAGAAATCATCCAGAAAGCCAGGA 2390
QY 240 ----- 240
Db 2391 CTATGGGACAGACTATCCGCGACGCCAAACTGTCCAACTCTCTCATCATGATTTGCC 2450
QY 240 ----- 240
Db 2451 AGACCAATTGAAAGTTGTGAGAGGCGCTGTAAGGAATGCCGAATTAAGACCAAGAGA 2510
QY 241 ----- 247
Db 2511 TGTGTGTGAAAAGATGAGGCGCAGAGACTGTGAGAGTGAAGGATGGAGGTGAACATCA 2570
QY 248 ----- 252
Db 2571 CAGGGGTGAAGAGACACCTGATTTGCCAGCTTGTGATCTCTGAAAGGATCTGGA 2630
QY 253 ----- 257
Db 2631 GTCATGACTACAGTGAAGAAACAGGGGAATCAGCCTTATGTGCCACTGTTAATTATTC 2690
QY 257 ----- 257
Db 2691 AGGACAAACCGGACAGAAAACCTCAATCAGAAAGCTCAGTACCTCAGAAATACTTCTTG 2750
QY 257 ----- 257
Db 2751 ATTCAGAACGTAGAAAGTGTATGCCAGCTCACTCATGCTCCCTGAGATTCCTCTGA 2810
QY 258 ----- 259
Db 2811 TTCAGGATATGAGGACATCCAGAAATCGGGGAATCAAGACTGATGTGGGAAAGCCA 2870
QY 260 ----- 273
Db 2871 GAGCATGGGTGAGACTGTCCAGAAAAGTTACTTTCCAGACACCTGAGAGCAGCTCC 2930
QY 274 Ser-ArgPro-----His 277
Db 274 Ser-ArgPro-----His 277

```

DB 2931 TCTCAGACCATGAGCTCAC 2949

RESULT 40  
US-09-488-725B-5599/c  
Sequence 5599, Application US/09488725B  
GENERAL INFORMATION:  
APPLICANT: Yuanhua T. Tang  
APPLICANT: John Tillinghast  
APPLICANT: Ankura Sanku  
APPLICANT: Chenghua Liu  
APPLICANT: Radote T. Drmanac  
TITLE OF INVENTION: Novel Contigs Obtained  
TITLE OF INVENTION: From Various Libraries  
FILE REFERENCE: 784  
CURRENT APPLICATION NUMBER: US/09/488, 725B  
CURRENT FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US 09/004,182  
PRIOR FILING DATE: 1998-01-07  
PRIOR APPLICATION NUMBER: US 09/034,341  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 09/045,400  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: US 09/321,214  
PRIOR FILING DATE: 1999-05-26  
PRIOR APPLICATION NUMBER: US 09/131,598  
PRIOR FILING DATE: 1998-08-10  
PRIOR APPLICATION NUMBER: US 09/170,294  
PRIOR FILING DATE: 1998-10-13  
PRIOR APPLICATION NUMBER: US 09/179,473  
PRIOR FILING DATE: 1998-10-27  
PRIOR APPLICATION NUMBER: US 09/181,430  
PRIOR FILING DATE: 1998-10-28  
PRIOR APPLICATION NUMBER: US 09/235,076  
PRIOR FILING DATE: 1999-01-20  
PRIOR APPLICATION NUMBER: US 09/234,611  
PRIOR FILING DATE: 1999-01-22  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 10289  
SOFTWARE: pt\_ct\_genes Version 1.01  
SEQ ID NO 5599  
LENGTH: 3925  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (1)...(3926)  
OTHER INFORMATION: n = a,t,c or g  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (208)...(2552)  
OTHER INFORMATION: similar to gi2769562 in the genepept database release 114.  
US-09-488-725B-5599

Alignment Scores:  
Pred. No.: 8.7e+03 Length: 3925  
Score: 285.80 Matches: 148  
Percent Similarity: 13.48% Conservative: 62  
Best Local Similarity: 9.50% Mismatches: 66  
Query Match: 19.71% Indels: 1282  
DB: 1 Gaps: 6

us-09-896-522-2 (1-277) x US-09-488-725B-5599 (1-3925)

QY 1 MetAlaSerAlaGly-----GlyGluASP-----CyGluSerProAla 13  
DB 3026 ATGGCGTTCTCAGGAGGCGAGTGGCTCAGAGTCTCGATACGCTGTCCAAAGCGCTGCT 2967  
QY 14 Pro-----GluAlaASPArgPro-----His 20  
DB 2966 CCTCTCATGAAGAAGGCC--AGGCGGAGATCTGAGTTCTCTGGAAGAAGCATGGAACAC 2910  
QY 21 ---GlnArg-----ProHe--LeuIleGlyVal----- 28

DB 2909 TCACAGCGTTATAGCATTTAGCTGTGGGTAGAGAGTGTGTGTGTGACGAGTGAAGG 2850  
QY 29 ---SerGly-----GlyThrAlaSer----- 34  
DB 2849 CTGAGTGGGTTTGAAGATGGCCAAAGAGCTCGAAGACTCAGAGTGTGCTTTGTTT 2790  
QY 34 ----- 34  
DB 2789 TTGCACGAATATATACACAAAACTTCACACTTCTTAACCAAAAAAATATATATA 2730  
QY 35 -----GlyLysSerThrValGlySerGlyLys----- 42  
DB 2729 TATATATATATATATATCTCCCTACATTAAGAAAAAGCGGTGTGCAAAAGTCCCC 2670  
QY 43 --IleMetGluLeuLeuGlyGln----- 49  
DB 2669 ATGTCTTTCATCTCGGTGGAGGCTCCCTCGAAGAGGCCGCCGCTGGGCTGTGAG 2610  
QY 49 ----- 49  
DB 2609 CATGCTTCTCCCGCGCTGTGTTCAGAGCGGTGGCCATGGGAGCGAGGCTCTAT 2550  
QY 49 ----- 49  
DB 2549 CTGAGCGTTCATGTTCTCTCTTAAGTTACTGAGTCAATCACTTGGCGGCGC 2490  
QY 50 -----AenGluValGluGlnArg----- 55  
DB 2489 ATTTCCTGTGCTCTGCGCGGTGGCGCCACTTAAATATATGTCCTCAGAAAGGCGATC 2430  
QY 56 -----GlnArgLysValValIleLeuSerGlnASP-----ArgPheTyr 68  
DB 2429 CCCCCTCTTGTATCAGACAGAGGCGAGTACTTCCGGTAAAGACAGACAGAGATTATAC 2370  
QY 69 LysVal-----LeuThrAlaGlu-----GlnLysAlaLys- 78  
DB 2369 AGGGCCAGGTTGCCAGTCTGCTGACAGAGAGATTCTCGGGAAGAGAGCGGAGA 2310  
QY 79 -----AlaLeuLys 82  
DB 2309 ATTGTTCAATGACCTGTAAATGATGTTCTCCGAGATTATGTCACGCTGTGATG 2250  
QY 82 LysGln---TyrAsnProPheASPHis-----ProAspAla--- 91  
DB 2249 GAGGCCACATGGGTTCTCTCACTCTCAGCTGGGGCTCAGACAGCGCCAGGCTCG 2190  
QY 92 ---PheAspAsnAspLeu-----MetHis 98  
DB 2189 GGTCCATCAAAATGATGATGGAGAGAGCGCGAGCATTTGAGAAACCTGCATCCA 2130  
QY 98 sArg-----ThreLeu-----LysAsnIleValGlu 106  
DB 2129 TCGGCTTGTCTTCCACACAGGTTGCTGAGAGCGCTGATGAATGGGAAGCATTAATGTA 2070  
QY 106 u----- 106  
DB 2069 GGGCTCAGCTCTTCACTTCTGCCACATTTCCCAAAAGTCTTACATTTCTATGAGT 2010  
QY 107 -----GlyLys-----ThrValGlu----- 111  
DB 2009 TCCGCTTCTCTGGGAATTCATTCAGGAGTCCAGAGAGAGGCTTCATGCCGTGAATVG 1950  
QY 112 -----ValPro----- 113  
DB 1949 AGGAACATTCGAGTGTGAGAGATTTCATCTGTGATGTTCCACAGAGGCACTCCAGGA 1890  
QY 114 ---ThrTyrAspPheValThr-----His 120  
DB 1889 GAATCTCATGACCTGTCACATGCTTGTGTCAGAGCTTCTTGTGAGTCACTTCAGCAT 1830  
QY 121 ---SerArg-----LeuProGluThr-----ValValTyrProAlaASP 133

```

Db 1829 GGTCAAGACAAAGCCATCTTGGCCACGCGCTCTGTGTCGTGCTCACTGGCAGAC 1770
Qy 134 -----ValValLeuPheGluGlyIle 140
Db 1769 CAGGGCATTCGACAGGTGACGGCGATCCGCTGANTAGACTCGCTCGCGCGGT 1710
Qy 141 -----LeuVal-----PheTyrSer----- 145
Db 1709 GAGAGATCTGAGAGAGCTCGTTGACCGCGCGTACTGGAATTCACGCTCCGCGGAT 1650
Qy 146 -----GluGluIleArgPhePhe----- 152
Db 1649 GCTGAAGTTCAGAGCGTCAGGACAGATTCCGCTGCACCGTCACTCTGTAGATTC 1590
Qy 152 ----- 152
Db 1589 CATGCATTGACACCACTGTGATTAACCTGCGCGGACGCTTCACTCTGCTGAGCG 1530
Qy 152 ----- 152
Db 1529 GTACTCGGAATTTGTAGTAGAAGAGCGCGCTGCTGCTGCTGATGATTTCTGTC 1470
Qy 153 -----HisLeuArg-----LeuPheVal 158
Db 1469 ATATTGTGGCACTTGAGGCGCGTGAATGACAGCTTCAGGCGCGCAGAGCTGTGCA 1410
Qy 159 AspThrAspSer---AspValArg-----LeuSerArgArgVal---LeuArgAsp 173
Db 1409 ACCGTGATGCGCGGCGATGCAAAAGCAAGTTGATGCCGCGGAGGTGATCTCAGGCG 1350
Qy 174 ValArgArg---GlyArgAsp---LeuGluGluIleLeuThrGluTyrThr----- 189
Db 1349 GTGCTCCGTGAGGCTCCGATGCGATTCAGACACTGCTCTTCGTTTTCACACACTTAC 1290
Qy 190 PheVal----- 191
Db 1289 TTTGTAGGCTGATGATGCTGAGCGCGCAAAAATTCCTCAAAAACCCCGAGAA 1230
Qy 192 -----LysProAlaPhe-----GluGluPhe---Cys----- 199
Db 1229 ACTGACGCGGCTCTCTCAAAAACCCCGAAGATGATGCTGCTTGAAGGCTCG 1170
Qy 200 -----LeuProThrLys-----LysTyrAlaAspVa 208
Db 1169 AATGCTGCTGCGCCCGCTTCCCTTCCCAATCTTGAGATGCTGCACTTCTAGAT 1110
Qy 208 IleIleProArgGlyVal---Asp----- 215
Db 1109 CATGTGCGCCAGATGTCAGGAGCATTAATGTTCCCACTTCTGACAAAGAGGCTCA 1050
Qy 216 -----AsnMetValAlaIleAsnLeu----- 222
Db 1049 GCACCTCCGAGTCACGCTTGAACCTTGTAGTAGTGAGAGCGGCTCCGAGAGATGCCA 990
Qy 223 -----IleValGln---His---IleGlnAspIleAsnGlyAspIle----- 235
Db 989 GGTGTGCGACCTGTGTGACGCTGACCATGACCCCGATGTGCTGTCGACAGCTCAG 930
Qy 236 ---CysLys-----TrpHis----- 239
Db 929 TTGTAGAAGACGAGGAGACCCAGGCTGTCCTTCCACCTGCTGAGAGAAAGCGGCGTGC 870
Qy 240 -----ArgGly---GlySerAsnGly-----ArgSerTyrLysArgT 251
Db 869 CTCGTCTGAATGCTTGAAGGTTCAGGAGCGAGCGAGATTAAAGCGCGCACAGCGGA 810
Qy 251 hr-----PheSerGly----- 254
Db 809 CTCACAGGAGACCCCATCAATCATGCGGCCCAATTTCAAGTAAAGCGAGCGGCTAAGC 750
Qy 255 -----ProGly----- 256
Db 749 CCTGAAGGTGAATCCTTAACAGACACTGCGAGGTGGGTGAAGAGTACTCATCTT 690

```

```

Qy 256 ----- 256
Db 689 CAAAAGCCCCCTGGGTTCTCTTCTCTCATTAANAATTTTGTAAACAGCCGAAAAAG 630
Qy 257 -----AspHisProGly-----MetLeuThr----- 263
Db 629 CTCAGGAACACACCAAGGTGTGCTGAGCTCTCAAGTGTCTGAGGCTTGTGCGGACA 570
Qy 264 -----SerGly-----LysArgSerHisLeuGluSerSerSer 275
Db 569 GCTTCTGCAAGTACTGATGATCAAGCTCCACCGAGTCTGCTGCGAGTGCCTCCA 510
Qy 275 rg-----ProHis 277
Db 509 GGGTCTCGGTCTGTCACAGGCTCTCAC 480

```

```

RESULT 41
US-09-488-725B-3427
; Sequence 3427, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghaet
; APPLICANT: Ankura Sunku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 3427
; LENGTH: 5195
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2)..(3795)
; OTHER INFORMATION: similar to g13327166 in the genepept database release 114,
; US-09-488-725B-3427

```

## Alignment Scores:

```

Pred. No.: 3.46e+04 Length: 5195
Score: 285.00 Matches: 133
Percent Similarity: 14.25% Conservative: 61
Best Local Similarity: 9.77% Mismatches: 82
Query Match: 19.66% Indels: 1086
DB: 1 Gaps: 5

```

us-09-896-522-2 (1-277) x us-09-488-725B-3427 (1-5195)

```

QY      1 MetAlaSerAla-----GlyGlyGlyAspCysGlu-----10...
DB      1053 CTGGCCACCTCATCATACCCCTGAGGAGGAGGACCATGTGCAAAAAAGCTGACGCTCA 1112
QY      11 -----SerPro-----AlaProGluAla-----AspArgPro-----19
DB      1113 GCGGCTGCCAGGCCCTCTGCTCCATCAGCACCAAAAGCAAAATGACATCTCTGTTGCCA 1172
QY      20 -HisGlnArgPro-----PheLeuIle-----26
DB      1173 ACCGAAAGACCGGATTTCTGTGTGCAAGAGATCTGACTTCTCCAGAAAACACCAT 1232
QY      27 -----GlyVal-----28
DB      1233 CCAAGACGACGAGATGCGGAGCAGAAAGCCAGTGTGTGACCTTAGACAGAGT 1292
QY      29 -----SerGlyGly-----ThrAla 33
DB      1293 CTTCGCCAGCTCTCAGAGAGGGGTGCGAGCAGCCCGCAGCCCAAGCTTCCCTCAGCA 1352
QY      34 SerGlyArgSerThrVal-----Cys-----40
DB      1353 GCGGCCAGAGCTCTGTCGCGCAGAGGCGCCACCGCATCCAGAGGCTGTGTAAGCTCT 1412
QY      41 -----GluIleValIle-----MetGluLeuLeuGlyGlnAsnGluValGluGlnArg--GlnArg 57
DB      1413 TCCAGAAAACCTCCGCCATGAGGAGCCTTGGAGCCAAAGGGGCCCAAGAGAAATGAAG 1472
QY      57 GlyValValIle-----LeuSerGlnAspArgPheTyrIleVal-----LeuThr 73
DB      1473 AGGAGTATGACCATCATCCTCTTCCAGTACGGCGGTGTGATGATGATGATGATGATGATG 1532
QY      73 LeuGlnIleValAlaLeuLeuIleVal-----81
DB      1533 CCAAGACGCGGACACTGTGCTGTAAGGGATATCCTGAGAGCCTCCGGGAGAGCTGTGAGC 1592
QY      81 -----81
DB      1593 TCCTCTTCCGGGGCCTGGAATGAGATGTAAGTCAACCCCGGTAAGTATGCTGAGCTGG 1652
QY      82 -----GlyGlnIleTyrAsnPhe-----86
DB      1653 TCGAAGAGTCCACCGGAGAGTACAGCCTGGCCACAGAGAGATGAGCGAGACCTGACACC 1712
QY      87 -----AspHisProAspAlaPheAspAsnAspLeu-----96
DB      1713 GCTCCATGACCCGACACCTT-----GCCCTTCCAGAACGAGCTGGGATGTGCTGCCGAGC 1769
QY      97 -----Met-----HisArgThrLeu-----LysAsnI 104
DB      1770 GGGTGTGATGCTCTATGCTTCCGAAACCCACCATGCTGCTACTGCCAGCAATGAAACA 1829
QY      104 LeuValGlu-----GlyLeuThrValGlu-----111
DB      1830 TCGTACACTGCTGCTCTGCTATGTGCAAGTGAAGAGAGGCTTCTGAGCTCTGCTGCTG 1889
QY      112 -----ValProThrTyr-----A 116
DB      1890 CCTGTGTGAGAGCATGCTGCTGCCACTACTACAAACACAGGGGTGTGGAGCCCTGTGGT 1949
QY      116 SP-----PheVal--ThrHisSerArgLeuPro-----124
DB      1950 ACCAAGGACATCTTGAGAGAGCTACAGAGAGACTTCTGCCAGCTCTCGAGAAAGATGC 2009
QY      124 -----124
DB      2010 AGGACCTGGGGGTATCTCCAGCATCTGCTGTCTCTGATCCACTTCTCTCAGCG 2069
QY      125 -----GluThrThrValVal-----Tyr-----130
DB      2070 TCATGCCCTTGAGAGAGCGGTGTGTCATGTCGATCTTTTCTATAGAGGAGCATCAAG 2129

```

```

QY      130 -----130
DB      2130 TGATCTGCAGGTGGCCCTGGCCGCTCTGAGCGCAACATGAGACACTGTGGGCTGCA 2189
QY      130 -----130
DB      2190 GCGACGAGGCGAGGCATGACATGATGCTGGGAGATATCTGATTAATGTGTCAACAAGC 2249
QY      131 -----P 131
DB      2250 AGAGTCTCTCTCTCTATCCGCACTCCGCTGCTGTGAGCAAGCAGATGACCCCTC 2309
QY      131 roAlaAspValValLeuPheGluGlyIleLeuValPheTyr-----144
DB      2310 CTGACAGGTGACATCTTTGAGCTCTGAAAGTGTCTATGAGAAATTCAGAGCCTGA 2369
QY      144 -----144
DB      2370 GGGCCGAGACATTGAGACAGATGCGGTTTAAACAGAGGCTGAAAGTATCCAGTCTTGG 2429
QY      144 -----144
DB      2430 AGGACACGCGCAAGAGAGATGTGTGCTCGACTATACCTGTGACATTTGTTCTCATTTG 2489
QY      144 -----144
DB      2490 AAGAGCTGAGGACCTTTACATGTGTGTTTAAGCCAAAGACCTTGCTAGCCATCTGGG 2549
QY      144 -----144
DB      2550 GGTGACGCGCAGATGCGCGCGGTCCGGAACCCAGCCTGACCTGAGACAGATACC 2609
QY      145 -----SerGlnGluIleArgAspMetPhe-----152
DB      2610 GATGTATGCAACCGACGCTTCCGGGAACCTTTTCCAGCCTGACACCTTGCGCTGTGGCT 2669
QY      153 -----HisLeu-----ArgLeuPhe-----ValAspThrAspSerAspVal 165
DB      2670 CCCACACACTCTGTGCTGCGAGGCGCATGTTCAAGCTCTCGAGCAGAAACAGACACTCGC 2729
QY      165 rGluLeu-----SerArg-----ArgValLeuAspValArgArgGlyArgAspLe 180
DB      2730 TGATCAACTTCAAGGAGTGTGTGACAGAGATGAGCGGATGTACACAGGGAACCTGACAG 2789
QY      180 uGlu-----GlnIleLeu--ThrGlnTyrThr-----190
DB      2790 AGAAGCTCAAGGCTCTTACAGACTACACCTTCCCAAGCTTGAAGCCAGAGGAGAGCC 2849
QY      190 heValIleAspPro-----AlaPheGluGlu-----197
DB      2850 GAGTTCAAGCTTGAGAGCGACCACTTATTTTACAGAGGAGACAGCTCTCAGAAAGATC 2909
QY      198 -----Phe-Cys-----LeuPro-- 201
DB      2910 TCCTGTGAGCTCATGATGTGATCTTTTCTGCTGCTGAGAGGCTCAAGAGACATACACACA 2969
QY      202 -----ThrIleValTyrAlaAspVal-----208
DB      2970 GGAAGAGCAAGAGAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3029
QY      208 -----208
DB      3030 GGAATATGCGCACTACCTTGAATGTGGGCAAGAGAAAGAGGCTCAGAGAGAGAGAT 3089
QY      209 -----IleIleProArg--GlyValAspAsnMetVal--AlaIleAsnLeuIleValGln 225
DB      3090 TAAGATCTTCCAAAGATGAACAGAGACAGCTTATGAGCTGTGCAAGAGCGTTTCAAA 3149
QY      226 HisIleGln-----AspIleLeuAsnGlyAspIleCysIleValTyr-----HisArgGly 241
DB      3150 CATGTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3207

```



```

Qy 242 -----GlySerAenGlyArgSerTyrLys---ArgThrPheSerGlu 254
Db 3208 AGCCTCTGCTCCGCGATCGAGAGAGTGGGAAAGTTCTCAGCCCGCAAGGAGAG 3267
Qy 255 ProGlyAsp-----HisProGlyMetLeu----- 262
Db 3268 CCCAGGAGACTGCTGCACCTAGAGAGACGACGACCCGAACTGCATCAGAGCGCA 3327
Qy 263 -----ThrSerGly-----LysArgSerHisLeuG1 271
Db 3328 GCCAGGAGCTTACGCCGCCGAGCTGCAGAGAGACCCCAAGCAAGGAGCGAGACACA 3387
Qy 271 userServerArgProHis 277
Db 3388 CACCTCGAAGAAAGCCCAAC 3406

RESULT 42
US-09-488-725B-6263
; Sequence 6263, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Dramanac
; TITLE OF INVENTION: Novel Contigs Obtained
; TITLE OF INVENTION: From Various Libraries
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488, 725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc_ct_genes Version 1.01
; SEQ ID NO 6263
; LENGTH: 6941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (85)...(4217)
; OTHER INFORMATION: similar to gi1043680 in the genpept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-6263

Alignment Scores:
Pred. No.: 8,72e+04 Length: 6941
Score: 285.00 Matches: 152
Percent Similarity: 12.73% Conservative: 44
Best Local Similarity: 9.87% Mismatches: 81
Query Match: 19.66% Indels: 1265
DB: 1 Gaps: 4

us-09-896-522-2 (1-277) x US-09-488-725B-6263 (1-6941)

```

```

Qy 1 MetAlaSerAlaGlyGlyGluAspCysGluSer-----ProAlaProGlu----- 15
Db 98 TTACGACGAGCGCTGTCACAGCGTGCATTCGCCGACGTTCCGCAACACCAACGCTCT 157
Qy 16 --AlaAsp-----ArgPro-----His----- 20
Db 158 TCATCGACGACGAGGAGGCGCAAGTGGGTGAGGTCAAGTCCAAAGCGAGGACATGACGG 217
Qy 21 ---GlnArgProPheLeuIleGlyValSerGlyThrAla----- 33
Db 218 TGTTCAGCGCGCTTTCGTGGGGGGCTGCCCGGAAGTGGCGCGCGGCTCAAGC 277
Qy 33 ----- 33
Db 278 TCACCTGCGCTCGGTGAGGAGAGCGGAGCCCTTCAAGGGGTGAGTTCTGACGTAGGG 337
Qy 33 ----- 33
Db 338 TCACCTGCGCTCGGTGAGGAGAGCGGAGCCCTTCAAGGGGTGAGTTCTGACGTAGGG 397
Qy 34 -----SerGlyLys----- 36
Db 398 CCAACAGCGCGCGGAGAAAGCGCCGTGCGAGCGCGGAGAGCGCGGCGGTGTC 457
Qy 37 -SerThr-----ValCysGluLysIle-----MetGluLeu----- 47
Db 458 CTCACGAGGTGTGTGCTCCGTGTGACGACGACGCGCGTGCAGCTGTCGCAACC 517
Qy 48 -----GlyGln-----AsnGluValGlu----- 53
Db 518 GCGTTCGCGGCGGACGACCTGACGCAAGCAAGCAACAAATGTGGAAGTCTGGGCACTG 577
Qy 54 -----GlnArgGlnArgLysVal-----ValIleIle 62
Db 578 ATGATGCGGACCAAGAAAGAAATATATTGCGACGTTCAAGATCTGAATCTTC 637
Qy 62 eu-----SerGlnAspArgPhe-----Tyr 68
Db 638 TGCTACGACTGTCTCAAAACCCATTCAAGCAGAGTGAATTAATCTGCTCATTT 697
Qy 69 LysValLeu-----ThrAlaGluGlnLysAla 77
Db 698 AAAACCTTCAGAGGAATGAGATGATGCTTCACACTGCGAAATCGCTATTATGCAAT 757
Qy 78 LysAlaLeuLys---GlyGlnTyrAsnPheAspHis-----ProAspAlaPheAs 93
Db 758 CTTGCCCTGAAAATGAGACTGCTCTCTGCT- CATTAATTGGGATCAGGGGCTTTGA 816
Qy 93 P-----AsnAsp-----LeuMet----- 97
Db 817 AGCACTAGTGAGAGCTGTGAATGAGAAAGTTATATATATGCTGCGACGATGTGAAGT 876
Qy 98 His-ArgThrLeuLys-----AsnIle-ValG1 106
Db 877 CACGAGGATCTGCGTCAGACACTCAGGCACTTGACACGCTATGCTGACATATCAATGCA 936
Qy 106 u-----GlyLysThrValGlu-----ValProThrTyrAspPheValT 119
Db 937 TGGGATTTTACACAAAGCGGTACACGCAAGAAATTAATCACTCGGGGTGATGA 996
Qy 119 hr-----HisSerArg-LeuPro-----GlnT 126
Db 997 CTTTTCATATGTGAGGAGTCCAGACAGCGCACTTCCAGGGTCAACAGTCAAGTAA 1056
Qy 126 hr-Thr-----ValValTyr----- 130
Db 1057 CAACTTATGGGCTGTCTCAAGAGGTGTATATTAATAATATGATGAGGCTGAATT 1116
Qy 131 -----ProAla----- 132
Db 1117 ATCTGCACTTGGCAAGCAAGAGATCTTAAGATGAAGATCAATGAGATGAGTGGCATTTAA 1176

```

```

QY 133 -----AspVal1ValIleuPheGlu----- 138
Db 1177 ATGTGAAATGTTCACCTTATGACCAATACCTTTGAAACCCAGAGCTTTCATCTC 1236
QY 138 ----- 138
Db 1237 TTTGCTAAATGAATGCAAGAAAGAACTGGCTCATATCATTTGATTTCCGTACACAGA 1296
QY 139 -----GlyIleuValPhe-----TyrSerGlnIleArg----- 149
Db 1297 GCCAAATGGCTCTATTTATTTAGCCATGGCAAGCCAGACATCAGAAAGATGCCAAGA 1356
QY 150 -----AspMetPhe-----HisIleuArgIle 156
Db 1357 CCCACAGATGATAAGGTGACCTTTTGCTATGAGATGTAGTGGCCACTTCTACT 1416
QY 156 uPheValAsp----- 159
Db 1417 CCTCTGGACATGAGGGGTGAGTACTATATAAAAGCCCTGTTGAAGAAAGTAATGA 1476
QY 160 -----ThrAspSerAspValArg-----IleuSerA 168
Db 1477 TGGAGAAATGTATATCATGTGACTTCCAGAGAGACGAGCGGTACAGTACATTTCTGTCA 1536
QY 168 rArg-----ValIleu----- 171
Db 1537 CACGTTGGGTACTCCCTACACTGCTCTGTGAGAGTGAATTTCTGACCTGATGATGA 1596
QY 171 ----- 171
Db 1597 GTTGTACTGGGGGGGTGCGCAGAAATAAAGTGGCTTGTCTCCACCGAGGTGTG 1656
QY 172 -----ArgAsp-----ValArgArg----- 176
Db 1657 GACTGCTCTGCTCAATATGCTACGTGGCTGCATCGGAGTGGATTTGTCATGTATGGCCA 1716
QY 177 -GlyArgAspLeuGlnIleLeu-----ThrGlnTyrThrThrPheValIysProAla-- 194
Db 1717 AAGCAAGATATCCGGCAATATGCTGAAGTCAACAGTACTCTGTGAAGTGAAGCCTTCTGTG 1776
QY 195 -PheGlnGluPhe-----CysLeu-----ProThrIys----- 203
Db 1777 CTCGAAGGAACACAAACCGTGCCTTACGCAACCTTTCGCAAAACCAATGCGATGTGCGAG 1836
QY 204 -----LysTyrAlaAspValIleIlePro----- 211
Db 1837 GGATGGGTGGAACAGATATG--TCTGTATTTGTTCCGGAACAGGCTATCTTGGCAGGTCC 1894
QY 212 -----ArgGly-----ValAspAsn-----MetValAlaIleAsnLeu 222
Db 1895 TGTGAGAGAGAGGCAACGGTTTGTAGCATATGAGAGCATGTTTGAAGAAATTCAGCTC 1954
QY 223 ---IleValGlnHis-----IleGlnAspIle-----LeuAsnGlyAsp-----IleCysI 237
Db 1955 CCCGTAGCATGATACGAGAGCTGAGATGTTTCTTACCGTTCCGATCCACAGCTGCA 2014
QY 237 ystTPhI.sargGlyGly----- 242
Db 2015 TATGCACTTGTGATGCAACACACTTTAGAGACTGTGTCACACCTCCGCTGGAGCTA 2074
QY 242 ----- 242
Db 2075 GAGCGAGAGCGTGGAAACGTAGCGTCAATCTAGATTGTATCAGGATTAACGTGAATTC 2134
QY 242 ----- 242
Db 2135 AGCAAAAGTCCCGAGACTTTTGTGCTGCTATAACTCAATGATTAACAGAGTGCACACA 2194
QY 242 ----- 242
Db 2195 GTGGGTGTAGTTCCGGCTGGAAGAAAGTTTAAAGTTAACAGTGAACCAACAGGCCATG 2254
QY 243 -----SerAsnGlyArg-----SerTyr----- 248

```

```

Db 2255 ACAGTCAATATGCGAGGTATCATCTAGAGCTGAGTTCATTAACATAGAGCTGCGATC 2314
QY 249 --LysArgThr-----Phe-SerGlnProGlyAsp--His-----Pro----- 259
Db 2315 ATCAGAGAAAGCAGGATCTTCTTCTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2374
QY 260 -----GlyMet----- 261
Db 2375 TTGACATTTATATGAAATGGATATGACCTGTGTAATAATGGCAGCATATGATTACTGT 2434
QY 262 -----LeuThrSerGly-----LysArgSer--HisLeuGlu----- 271
Db 2435 GAGCTTAATGCGAGATTTGGCTTCAGAGAACATCATAGACAGATCTGTCACTTCAAGACC 2494
QY 272 ----- 272
Db 2495 AAATCGAGCTATGTGCTTACCTTACCTTGAACCTTACATCTTATGCACTTTTCTTCT 2554
QY 272 rSerSerArgProHis 277
Db 2555 CAGTTCAAGCAACAT 2570

RESULT 43
US-09-488-725B-6173
; Sequence 6173, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Fillingnaast
; APPLICANT: Ankura Slinku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OR INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; CURRENT FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pc CT_Genes Version 1.01
; SEQ ID NO 6173
; LENGTH: 4927
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22)...(2520)
; OTHER INFORMATION: similar to gi1834495 in the genepept database release 114,
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
; US-09-488-725B-6173

Alignment Scores: 2.76e+04 Length: 4927
Pred. No.:

```



```

Db 2099 AGAAGTGAAGGGCCAGCAGCTGAGATTCTGTGTACGAGAGAGAAACAACCTAACAC 2158
Qy 200 ----- 200
Db 2159 AATATGGTACCGAAAAATTCAGGGGACAAATGCGAGGGTGGGTAAATCCAGTTTCAGA 2218
Qy 201 -----ProThrIys----- 203
Db 2219 AGTAAAGACTTGAAAAAATGCACAGCACTTTTGTAGTCCGAAAAACAGAAATTC 2278
Qy 204 -----LysTyrAlaAsp-ValIleIle-Pro-ArgIlyValAsp-----AsnMetVa 218
Db 2279 CAAGTCAAAATCTGTCCATTAATTCCTGGCCATGCGGATTTGATGTGTGTCACAGTCGT 2338
Qy 218 |A|A|I|e|a|s|n|e|u|l|e|v|a|g|n|-----HisIleGl 228
Db 2339 AGCAGGAGTGTCTCATTTGTGAAGAAATGTCGTGGGGGAAGTTCTCTGTGATCTTACATA 2398
Qy 228 |A|s|p|I|e|l|e|u|-----AsnGly--AspIleCys----- 236
Db 2399 CTCTGTGTGTGACAGCATTTGACAGAGCCCAATGTGTGTGATGG-TGTGATGCTTTGGA 2457
Qy 237 -----LysTrp---His-----ArgIlyGlySerAsnGly 245
Db 2458 CACAGCCTCCCACTAATAAAGTGTATCATGATGACTCAGATGAGGACTCTTGGA 2517
Qy 246 ArgSerTyrIysArgTyrPheSerGluProGly-----AspHis----- 258
Db 2518 ATATCTCTTCAGAGAGCTGAGCCAGCATGATGATGTGGAACACAGTACTCTTACACT 2577
Qy 259 -ProGlyMetLeuThrSerGlyIlyArg-SerHisIleGlu-----SerSer----- 273
Db 2578 CCCTGTGTCTCCCACTTACAGAAATTAATTTCCATTCGAGGAGCCAGCTCTGTTCCT 2637
Qy 274 -----SerArgPro 276
Db 2638 GCTGCTTCATCAAGCA 2656

```

## RESULT 44

```

US-09-488-725B-6286
; Sequence 6286, Application US/09488725B
; GENERAL INFORMATION:
; APPLICANT: Yuanhua T. Tang
; APPLICANT: John Tillinghast
; APPLICANT: Ankura Sanku
; APPLICANT: Chenghua Liu
; APPLICANT: Radoje T. Drmanac
; TITLE OF INVENTION: Novel Contigs Obtained
; FILE REFERENCE: 784
; CURRENT APPLICATION NUMBER: US/09/488,725B
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US 09/004,182
; PRIOR FILING DATE: 1998-01-07
; PRIOR APPLICATION NUMBER: US 09/034,341
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 09/045,400
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 09/321,214
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: US 09/131,598
; PRIOR FILING DATE: 1998-08-10
; PRIOR APPLICATION NUMBER: US 09/170,294
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 09/179,473
; PRIOR FILING DATE: 1998-10-27
; PRIOR APPLICATION NUMBER: US 09/181,430
; PRIOR FILING DATE: 1998-10-28
; PRIOR APPLICATION NUMBER: US 09/235,076
; PRIOR FILING DATE: 1999-01-20
; PRIOR APPLICATION NUMBER: US 09/234,611
; PRIOR FILING DATE: 1999-01-22
; Remaining Prior Application data removed - See File Wrapper or PALM.

```

```

; NUMBER OF SEQ ID NOS: 10289
; SOFTWARE: pt_ct_genes Version 1.01
; SEQ ID NO 6286
; LENGTH: 2340
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (94)-(2121)
; OTHER INFORMATION: similar to g14753778 in the genepept database release 114,
; US-09-488-725B-6286

```

## Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
646	284.60	13.68%	10.39%	19.63%	2340	145	46	81	1126	4

us-09-896-522-2 (1-277) x US-09-488-725B-6286 (1-2340)

```

Qy 3 SerAlaGlyGly-GluAspCysGluSerProAlaProGluAlaAspArgPro-His--- 20
Db 95 GCGGCGGCGCGCGAGGCTTCTGATGTCACCCGGAGCTGAGTAGAGAACCCAGCCATGCT 154
Qy 21 -----GlnArg-----ProPheIleuIleGly-----ValSerGlyGl 31
Db 155 GAACGAAGCCAGAGAAACAGCAGCCTCAACCCCTCTGTGAGGAGGAGTCCAGCAGTGG 214
Qy 31 YThrAlaSerGlyIlyS-SerThrValCys----- 40
Db 215 CAGTGAAGCTCCAAAGATGTTCTGAGATGTTCCACCCCGGCGCTGAGACCCGAGGGCA 274
Qy 41 -----GluIys----- 42
Db 275 TGAGAGACTCCGAGAGAGATGAGCGCGCATTTGAATCTGTGACAAAGTGTCTCCCT 334
Qy 43 -----IleMetGluLeuLeu----- 47
Db 335 GGAATTTCTTCCTCCTCGAATCTGTGAGGAGCTGCAATCTCAAGTTTGAACG 394
Qy 48 ----- 48
Db 395 GATGGCAGCAGTGGCCCCCTTACATAGACGTGACCTGSCACCCAGAGTACCTGG 454
Qy 55 rglInArGlyValIleLeuSerGluAspArgPheTyrIys----- 69
Db 455 CTCAGACAAAGA--GACCTCTTCATGATGATGCGCAGCACCGCGTGAACCTAGTGGC 512
Qy 70 -----ValLeuThrAla--GluGln----- 75
Db 513 CTGAGACATCTCTGACATGACTGTGCGCTGACGCGCTGAGAGAGATCACGGCCAT 572
Qy 76 -----LysAlaIys-----AlaLeuArgGlyGln----- 83
Db 573 CTGACAAAGCTTAAAGCAGCTGGGCTTGAAGAATCATGCGCTGCGGAGAACCAATA 632
Qy 84 -----TyrAsn----- 85
Db 633 GGTGACCAATGGAGAGAGAGAGAGGAGGCTTCAACGACAGTGAAGCTGTGAAGCAC 692
Qy 86 -----PheAsp-----His 88
Db 693 ATCCGAAGTAGTTGTGTGACTACTTGTGACATCTGTGTGAGAGTTACCCCAAGGCCAC 752
Qy 89 ProAspAla-----PheAspAsnAspLeuMetHis----- 98
Db 753 CCGAGACAGGAGACTTTGAGGCTGACCTTAAGACCTTGAAGAAGAGTGTCTGCGGGA 812
Qy 98 ----- 98

```

Db 813 GCCGATTTCATCATCAGCAGCTTTCTTTGAGGCTGACAACTCTTCCGCTTGTGAAG 872  
 Qy 98 ----- 98  
 Db 873 GCATGCACCGACATGGGACATCACTTCCCATCGTGTCCCGGATCTTTCCCATCCAGGCG 932  
 Qy 99 ----- 99  
 Db 933 TACCACCTCCCTTGGCAGCTTTGTGAAGCTGTCCAAAGCTGAGAGTGCCACAGAGATCAAG 992  
 Qy 103 AsnIleValGlu---GlyIysThr-----ValGlu--- 111  
 Db 993 GAGGTATGTAGCCATCAAGAAAGACAGATGCTGCATCCGCAACTAGGATGAGCTG 1052  
 Qy 112 -----ValProThrTyrAspPheVal 118  
 Db 1053 GCCGTGAGCTGTGCGCAGAGCTTCTGCGCATGTGGCTTGTGGCCAGGCTCCACTTCTAC 1112  
 Qy 119 ThrHisSerArgLeuProGluThrThrValValTyr-----ProAlaAspVal----- 134  
 Db 1113 ACCCTCAACCGCAGATGCTACCAAGAGTCTGAAGCGCTGGGATGTGACTGAG 1172  
 Qy 134 ----- 134  
 Db 1173 GACCCAGCGCTCCCTACCTGGGCTCTCAGCGCCACCCCAAGCGCCGAGAGAGAT 1232  
 Qy 134 ----- 134  
 Db 1233 GTAAGTCCATCTTCTGGGCTCCAGACCAAGATTACATCACTGACCCAGAGCTGG 1292  
 Qy 135 -----ValLeuPhe-----GluG 139  
 Db 1293 GACGAGTCCCTTAACGCGCGCTGGGCAATTCCTCTTCCCTGCTTGGGAGCTGAG 1352  
 Qy 139 IylIeuLeu-ValPheTyr-----SerGlnGluIleArgAspMetPhe 152  
 Db 1353 GACTACTACCTCTTCTACCTGAAGAGCAAGTCCCCAAGAGGAGCTGTGAAGATGTGG 1412  
 Qy 153 -----HisLeuArgLeu-----PheVal----- 158  
 Db 1413 GGGGAGAGCTGACCACTGAAGAAAGCGCTTGAAGCTTGTCTTACTCTCGGGA 1472  
 Qy 159 -----AspThr-----AspSerAsp----- 163  
 Db 1473 GAACCAACCGGAAATGTGTCAAAAGTACTTCTGCTGCTGGAACGATGAGCCCTGGCG 1532  
 Qy 164 -----ValArgLeuSerArgArg----- 169  
 Db 1533 GCTGAGACGAGCTGTGAAGAGAGCTGTGGGTGAACGCGCCAGGCGATCTGACC 1592  
 Qy 170 -----ValLeuArgAspValArg----- 175  
 Db 1593 ATCAACTCAGAGCCCAATCAACGAGAGCGGAGCGGCTCCGACCCCATCGTGGCGGGCG 1652  
 Qy 176 -----ArgGly-----ArgAsp- 179  
 Db 1653 CCGAGCGGGGCTATGCTTCCAGAGAGCTTACTAGATTCTTCTCCCGGAGACA 1712  
 Qy 180 -----LeuGlnGluIleLeuThrGlnTyr-----ThrThrPhe-- 190  
 Db 1713 GCGGAGACATCTTCGCAAGTGTGAAGAAAGTACGAGCTCGGGTATATTACACCTTGTG 1772  
 Qy 191 -----ValIys-----ProAlaPheGlu-GluPheCys----- 199  
 Db 1773 AATGTGAAGGCTGAATAACATCAACATGCTGAGTGTGAGCGGATGCTGCACTTGG 1832  
 Qy 200 -----LeuProThrIlySerTyrAla-AspValIle-----IlePro-- 211  
 Db 1833 GGCATCTTCCC-----TGGCGAGAGATCTTCCAGCCCAACCGTAGTGAATCCCGTC 1883  
 Qy 212 -----ArgGly-----ValAspAsnMetVal-----AlaI 220  
 Db 1884 AGCTTATGTTCTTGAAGAGACGAGGCTTGTGCGCTGTGATGTGAGCGGTGGGGAAGACTG 1943

Qy 220 le-----AsnLeuIleValGlnHisIleGlnAsp--IleLeuAsnG 233  
 Db 1944 TATGAGAGAGAGTCCCGCTCCCGACATCATCACTACATCAAGCAACTACTTCTG 2003  
 Qy 233 ly-----AspIleCysIlySerP-----H 239  
 Db 2004 GTCACTGTGTGACATATGACTTCCACTGAGACACTGCTGTGGCAGGTGGAAGAC 2063  
 Qy 239 IAspGlyIlySer-----AsnGlyArgSerTyrIly- 249  
 Db 2064 ACATTGAGCTTCTCAACAGGCCCAACCAAGATGCAAGAAACGAGGCTCATGACCC 2123  
 Qy 250 -----ArgThrPheSerGluPro----- 255  
 Db 2124 TGGCTCTGAGCGCTGCGTGTGAGGCACCTGTCGCCGCTTCTTCCACAGTGTG 2183  
 Qy 256 -----GlyAsp-----HisProGlyMet----- 261  
 Db 2184 CTTCCTTGGGAACTCCACTCTTCGTGTCTTCCACCCGCGCTCCACTCCCCAC 2243  
 Qy 262 LeuThrSerGlyIlyArgSerHisLeuGluSer-----SerArg 275  
 Db 2244 CTGACCAATGGCAGCTAGACTGAGT--GAGGCTTCAGAGCTTCTGCACTGAGTGG 2301  
 Qy 276 ProHis 277  
 Db 2302 CCCAC 2307  
 RESULT 45  
 US-09-488-725B-6100  
 ; Sequence 6100, Application US/09488725B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Yuhua T. Tang  
 ; APPLICANT: John Tillinghaest  
 ; APPLICANT: Ankura Sanku  
 ; APPLICANT: Chonghua Liu  
 ; APPLICANT: Radoje T. Drmanac  
 ; TITLE OF INVENTION: Novel Contigs Obtained  
 ; FILE REFERENCE: From Various Libraries  
 ; FILE REFERENCE: 784  
 ; CURRENT APPLICATION NUMBER: US/09/488,725B  
 ; PRIOR FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US 09/004,182  
 ; PRIOR FILING DATE: 1998-01-07  
 ; PRIOR APPLICATION NUMBER: US 09/034,341  
 ; PRIOR FILING DATE: 1998-02-13  
 ; PRIOR APPLICATION NUMBER: US 09/045,400  
 ; PRIOR FILING DATE: 1998-03-20  
 ; PRIOR APPLICATION NUMBER: US 09/321,214  
 ; PRIOR FILING DATE: 1999-05-26  
 ; PRIOR APPLICATION NUMBER: US 09/131,598  
 ; PRIOR FILING DATE: 1998-08-10  
 ; PRIOR APPLICATION NUMBER: US 09/170,294  
 ; PRIOR FILING DATE: 1998-10-13  
 ; PRIOR APPLICATION NUMBER: US 09/179,473  
 ; PRIOR FILING DATE: 1998-10-27  
 ; PRIOR APPLICATION NUMBER: US 09/181,430  
 ; PRIOR FILING DATE: 1998-10-28  
 ; PRIOR APPLICATION NUMBER: US 09/235,076  
 ; PRIOR FILING DATE: 1999-01-20  
 ; PRIOR APPLICATION NUMBER: US 09/234,611  
 ; PRIOR FILING DATE: 1999-01-22  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 10289  
 ; SOFTWARE: pt\_ct\_genes Version 1.01  
 ; SEQ ID NO 6100  
 ; LENGTH: 7431  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (392)...(5946)

```

; OTHER INFORMATION: similar to g15456754 in the geneSept database release 114
; OTHER INFORMATION: Run with FASTX 3.3c00, default parameters
US-09-488-725B-6100

```

**Alignment Scores:**

Pred. No.:	9.63e+04	Length:	7421
Score:	25.60	Matches:	152
Percent Similarity:	18.20†	Conservative:	57
Best Local Similarity:	8.87†	Mismatches:	67
Query Match:	19.63†	Indels:	1439
DB:	1	Gaps:	7

US-09-896-522-2 (1-277) X US-09-488-725B-6100 (1-7431)

[illegible]

QY	92	-----	92	-----	92
Db	1073	CATCATCATCTGTTACCGCTCCAGTACGACATCCAGAGCCTGATCACTCAACTTATGA	1132		
QY	92	-----	92	-----	92
Db	1133	TATTTGCACCTCAGACGTGTGATCATATATCCAAAGACGAGAGGGAGCTTGAAGCTC	1192		
QY	93	-----	97	-----	97
Db	1193	CATACAAATGATGTAGATAAAGCTTCAGAGTACACAGAGCCTGAATAATGATCTGAT	1252		
QY	97	-----	97	-----	97
Db	1253	ATTTCAGTCGAGAAAATGAAACAGACTGAAAGCTGATCAGGCACTCGAGCTGAACATTA	1312		
QY	98	-----	100	-----	100
Db	1313	TCTAAAAATGAAAGTTATATATGACGAGAAAAACCATGATTGTGAGAAAAACCAAGAC	1372		
QY	100	rleu--lysAsnIleValGlu-----GlyAs-----	108		
Db	1373	ATTGTACGAAACATTGTAGAAAGAAATGTGAACATTGTTGTGAGATATATGGAGAGGG	1432		
QY	109	-----	111	-----	111
Db	1433	ACTACTATTAATGAAAGTCAGATGGCAACTTGGAACTATAGAGATGTGATGACAGT	1492		
QY	112	-----	120	-----	120
Db	1493	GAAATATTCAGCAATGAAATGAAATTCAGAAACCAATTCCTGTGATATACCAATCC	1552		
QY	120	-----	120	-----	120
Db	1553	TTACTGATGATAGATTGTCACTCTTCCATGATATCTCAGAAATGTGAAATCTTCA	1612		
QY	121	-----	124	-----	124
Db	1613	GGACCTTCACCTGGTGTAGTTTCCACATTTTACAAAGAGATGCCCTTCTATATATC	1672		
QY	125	-----	128	-----	128
Db	1673	AGTCATTTGTAAACTGTCAATGAACCACTGTCAAGATGACCAACGATCCAAAGCTC	1732		
QY	129	-----	132	-----	132
Db	1733	CATGAACACTGACCAAGATCTTTCATGACGTTACTCTATCACTTTCGAGAAATGA	1792		
QY	133	-----	143	-----	143
Db	1793	GGACCTATTTTCAGGACAAATGATGATTTAATATCTATTAAGCAAGTATCTTGTGT	1852		
QY	143	eTySerGlnIu-----IleArgSerPheHisLeuArgLeu-----	156		
Db	1853	GCACTTCACAAAAATGAGTCTCATCTGTTCCAGAGGTTTTGAGCTTTCTCTTCTATA	1912		
QY	157	-----	158	-----	158
Db	1913	TTTCTTACTTTGTTCAAATTTTCAGACACATCTGAAGATGCMAATTGAGTGTCTTT	1972		
QY	158	-----	158	-----	158
Db	1973	AAAGAAATTTCTATACATTTTGGAAACTTCTACCAAGCTCATTTGATCACAAAATGATG	2032		
QY	159	-----	168	-----	168
Db	2033	GTTATTCAGACACTGACGAGATTTTGTGCAGATCTCGAAGTGAAGTATTTATGTATA	2092		
QY	169	-----	174	-----	174
Db	2093	AACATGACGTGTGACTTAATATGACCAATATATATTTAAAGCACTGATTAATGATCTATCA	2152		

```
QY 175 -----ArgArgGly----- 177
      |||::|||
Db 2153 AAATTGCTCAAGGAAGGGGAGTCAGAACTTGATGATATGTTCAAGAAATTGAGC 2212
QY 178 -----ArgAspLeuGlu-----GlnIleLeu----- 184
      |||::|||
Db 2213 CTGAGGAAAAAAGGTTTAGAATGCTTAGTGTGATTTTGAAGTATGTTGAATGAGT 2272
QY 185 -----ThrGlnPyr-----ThrThrPhe-----ValysProAlaPhe 195
      |||::|||
Db 2273 AAGGATCAGTATGTAATCCCACTCCAGACCACTCTTGTCAGAAAAAACCCTCAGAG 2332
QY 196 GluGlu-----PheCysLeup 201
      |||::|||
Db 2333 CAAAGATGAGTGAATCAACCAACCTGAGACATAAAGATAGCGAAGTTAAATTCC 2392
QY 201 -----ThrLys-----LysTyrAlaAspVal----- 208
      |||::|||
Db 2393 CTGAGATCAACATCATCATCAGAAATAGCAGCTACAGTACACAGATGCTGCGCACTGAT 2452
QY 209 -----IleTleProArgGlyValAsp 215
      |||::|||
Db 2453 AATCCAGAACAAATTGAGTCTTAAGCAACAAAAAATAATAGAAACAAGGATGCTTGGC 2512
QY 216 -----AsnMetVal-AlaIleAsn-----LeuIleVal 224
      |||::|||
Db 2513 TTATTTATAGAAACCAAGAGAGAAATACAGTACCTCCAGAAACAAGGATGCTTGGC 2572
QY 224 IGIHIsIleGlnAspIleLeuAsn-----GlyAspIle-----CysIly 237
      |||::|||
Db 2573 ACCACACCTGAAAGATATGCCCAATCTTACATCAAGAGAAAGATTAGACTTACTCA 2632
QY 237 sITrPHIsArg-----GlyGlySerAsnGly-----ArgSerTyr----- 248
      |||::|||
Db 2633 GTGGGTAGGGTCCCGGGGGGAT-AATGATTAATTTAACCAAGAGATCATGATGATCAT 2691
QY 249 -----LysArgThrPheSerGlu-----ProGly----- 256
      |||::|||
Db 2692 ATGTGACCAACATGACTTTTCAGAAAAAGACTTCGTTGAGCCCTTCGATGTTCTAG 2751
QY 257 ---AspHis-----ProGly----- 260
      |||::|||
Db 2752 AAGGATTTGCTTCCAGGGGAAAGCTCAGAAAAATCGATCGATTAATGAAAAATTGCTG 2811
QY 260 ----- 260
      |||::|||
Db 2812 CAAGATACCTAGATGCAACCAAGACAACTCTTTGCTAGTGGGATACAGCTTAG 2871
QY 261 -----MetLeuThr-----SerGlyLysArg-- 267
      |||::|||
Db 2872 TTTTGGCTTATTCATTTATGATGTTGACACAGACCTTCACAGTCCACAGGTGAAAAATA 2931
QY 267 ----- 267
      |||::|||
Db 2932 AAATGACAAAGAACATACATTAAGATGATAGAGGTATCAATGACAGTAAAGACCTTC 2991
QY 268 -----SerHisLeu-----GluSe 272
      |||::|||
Db 2992 CTGAAGATATCTATCAGCATCTATATATGAAATAGCTGGAAAAAGATATCAATGAAAG 3051
QY 272 rSerSerArg-----ProHis 277
      |||::|||
Db 3052 AAACAAAGAACTAACATTCCTTAC 3076
```

Search completed: December 12, 2003, 10:36:35  
Job time : 105 secs

**This Page Blank (uspto)**



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 11:17:56 ; Search time 4 Seconds  
(without alignments)  
119.818 Million cell updates/sec

Title: us-09-896-522-2

Perfect score: 1450  
Sequence: 1 MASAGGEDCSPPAEDRPH.....HPGMLTSGKRSKSHLESSRPH 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4515 seqs, 1730228 residues

Total number of hits satisfying chosen parameters: 4515

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

\*8\*pep.\*  
1: /home/sdavid/sdavid-cmp/dectemp/swopes522/US09488725A.pep.\*  
2: /home/sdavid/sdavid-cmp/dectemp/swopes522/6579708.pep.\*  
3: /home/sdavid/sdavid-cmp/dectemp/swopes522/PCITUS0005388.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1450	100.0	277	1	US-09-488-725A-2647 Sequence 2647, Ap
2	1450	100.0	296	1	US-09-488-725A-6219 Sequence 6219, Ap
3	1363	94.0	260	2	US-09-536-647-2 Sequence 2, Appl1
4	1325	91.4	277	2	US-09-536-647-3 Sequence 3, Appl1
5	934	64.4	261	1	US-09-488-725A-1839 Sequence 1839, Ap
6	896	61.8	337	3	PCT-US00-05988-1160 Sequence 1160, Ap
7	889	61.3	335	1	US-09-488-725A-5411 Sequence 5411, Ap
8	92	6.3	199	1	US-09-488-725A-2274 Sequence 2274, Ap
9	92	6.3	224	1	US-09-488-725A-5846 Sequence 5846, Ap
10	82.5	5.7	231	1	US-09-488-725A-3156 Sequence 3156, Ap
11	77.5	5.3	1848	1	US-09-488-725A-5819 Sequence 5819, Ap
12	76.5	5.3	470	1	US-09-488-725A-5453 Sequence 5453, Ap
13	76.5	5.3	470	1	US-09-488-725A-5454 Sequence 5454, Ap
14	76.5	5.3	479	3	PCT-US00-05988-1515 Sequence 1515, Ap
15	76.5	5.3	1770	1	US-09-488-725A-2247 Sequence 2247, Ap
16	76	5.2	387	1	US-09-488-725A-2852 Sequence 2852, Ap
17	76	5.2	396	1	US-09-488-725A-6424 Sequence 6424, Ap
18	73	5.0	469	3	PCT-US00-05988-1494 Sequence 1494, Ap
19	72.5	5.0	745	1	US-09-488-725A-6014 Sequence 6014, Ap
20	70	4.8	738	1	US-09-488-725A-2442 Sequence 2442, Ap
21	69	4.8	490	1	US-09-488-725A-3018 Sequence 3018, Ap
22	69	4.8	507	1	US-09-488-725A-6590 Sequence 6590, Ap
23	69	4.8	507	1	US-09-488-725A-6591 Sequence 6591, Ap
24	69	4.8	3177	1	US-09-488-725A-3448 Sequence 3448, Ap
25	68.5	4.7	796	1	US-09-488-725A-6346 Sequence 6346, Ap
26	68.5	4.7	796	1	US-09-488-725A-6347 Sequence 6347, Ap
27	68	4.7	239	3	PCT-US00-05988-1543 Sequence 1543, Ap
28	66.5	4.6	442	1	US-09-488-725A-2978 Sequence 2978, Ap
29	66.5	4.6	457	1	US-09-488-725A-6550 Sequence 6550, Ap
30	66.5	4.6	777	1	US-09-488-725A-2774 Sequence 2774, Ap

31	66	4.6	372	1	US-09-488-725A-6989 Sequence 6989, Ap
32	66	4.6	883	1	US-09-488-725A-6143 Sequence 6143, Ap
33	66	4.6	888	1	US-09-488-725A-2571 Sequence 2571, Ap
34	66	4.6	1047	1	US-09-488-725A-2464 Sequence 2464, Ap
35	66	4.6	1104	1	US-09-488-725A-6036 Sequence 6036, Ap
36	65.5	4.5	149	1	US-09-488-725A-6728 Sequence 6728, Ap
37	65.5	4.5	545	1	US-09-488-725A-1809 Sequence 1809, Ap
38	65	4.5	337	3	PCT-US00-05988-1372 Sequence 1372, Ap
39	65	4.5	532	1	US-09-488-725A-6870 Sequence 6870, Ap
40	64	4.4	188	1	US-09-488-725A-6619 Sequence 6619, Ap
41	64	4.4	272	3	PCT-US00-05988-1697 Sequence 1697, Ap
42	64	4.4	337	1	US-09-488-725A-3298 Sequence 3298, Ap
43	63.5	4.4	346	1	US-09-488-725A-6792 Sequence 6792, Ap
44	63.5	4.4	603	1	US-09-488-725A-2957 Sequence 2957, Ap
45	63.5	4.4	617	1	US-09-488-725A-6529 Sequence 6529, Ap

#### ALIGNMENTS

```

RESULT 1
US-09-488-725A-2647
; Sequence 2647, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc FL_genes_b Versions 1.0
; SEQ ID NO 2647
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2647

```

Query Match 100.0%; Score 1450; DB 1; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.5e-116;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MASAGGEDCSPPAEDRPHQRFLIGVSGTASGKSTVEKIMELLGQNEVEGRQRKV	60
DB	1	MASAGGEDCSPPAEDRPHQRFLIGVSGTASGKSTVEKIMELLGQNEVEGRQRKV	60
QY	61	ILSDRRYKVLTLAEQAKALKGOYNDHPDAPFNDMLMRLLKNIYEGKTVVPTPDVTH	120
DB	61	ILSDRRYKVLTLAEQAKALKGOYNDHPDAPFNDMLMRLLKNIYEGKTVVPTPDVTH	120
QY	121	SRLETTVVPAVVLFEGLIVFYSGEIRDMFRLFVDTSDSVRLSRVLRDVRGRDL	180
DB	121	SRLETTVVPAVVLFEGLIVFYSGEIRDMFRLFVDTSDSVRLSRVLRDVRGRDL	180
QY	181	EQLITVYTFVKAFFEFCLPTKKYADVILPRGVDMNVAINTLIVQHIQDILNDICKMR	240
DB	181	EQLITVYTFVKAFFEFCLPTKKYADVILPRGVDMNVAINTLIVQHIQDILNDICKMR	240

QY 241 GGSNGRSYKRTFSEBPDHGMKLTSGKSHLESSSRPH 277  
 Db 241 GGSNGRSYKRTFSEBPDHGMKLTSGKSHLESSSRPH 277

# RESULT 2

US-09-488-725A-6219  
 ; Sequence 6219, Application US/09488725A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq Inc  
 ; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 ; FILE REFERENCE: 784FLECT  
 ; CURRENT APPLICATION NUMBER: US/09/488,725A  
 ; CURRENT FILING DATE: 2000-12-22  
 ; PRIOR APPLICATION NUMBER: US/09/488,725  
 ; PRIOR FILING DATE: 2000-01-21  
 ; PRIOR APPLICATION NUMBER: US/09/552,317  
 ; PRIOR FILING DATE: 2000-04-25  
 ; PRIOR APPLICATION NUMBER: US/09/598,042  
 ; PRIOR FILING DATE: 2000-06-20  
 ; PRIOR APPLICATION NUMBER: US/09/620,312  
 ; PRIOR FILING DATE: 2000-07-19  
 ; PRIOR APPLICATION NUMBER: US/09/653,450  
 ; PRIOR FILING DATE: 2000-08-31  
 ; PRIOR APPLICATION NUMBER: US/09/662,191  
 ; PRIOR FILING DATE: 2000-09-14  
 ; PRIOR APPLICATION NUMBER: US/09/693,036  
 ; PRIOR FILING DATE: 2000-10-19  
 ; PRIOR APPLICATION NUMBER: US/09/727,344  
 ; PRIOR FILING DATE: 2000-11-29  
 ; NUMBER OF SEQ ID NOS: 7144  
 ; SOFTWARE: Pf-Genes Versions 1.0  
 ; SEQ ID NO 6219  
 ; LENGTH: 296  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-488-725A-6219

Query Match 100.0%; Score 1450; DB 1; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1,7e-116;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASAGDECSPEADPRHQRPFLLIGVSGTASGKSTVCEKIMELLGONEVEOROKRV 60  
 Db 20 MASAGDECSPEADPRHQRPFLLIGVSGTASGKSTVCEKIMELLGONEVEOROKRV 79  
 QY 61 ILSODRFYKVLTAEQKAKALKGQYNPDHDPADFNDLMHRTLNKIVEGKTEVEPTYPVTH 120  
 Db 80 ILSODRFYKVLTAEQKAKALKGQYNPDHDPADFNDLMHRTLNKIVEGKTEVEPTYPVTH 139  
 QY 121 SRLPETTVVPADVLPFEGILVFYSQEI RDMFHLRLFVDTSDVRLSRVLRDVRGRDL 180  
 Db 140 SRLPETTVVPADVLPFEGILVFYSQEI RDMFHLRLFVDTSDVRLSRVLRDVRGRDL 199  
 QY 181 EQILTYTTFFKPAFEBCFLPTKKYADVILPRGVNMMVAINLIVQHIDILNGDICKMR 240  
 Db 200 EQILTYTTFFKPAFEBCFLPTKKYADVILPRGVNMMVAINLIVQHIDILNGDICKMR 259  
 QY 241 GGSNGRSYKRTFSEBPDHGMKLTSGKSHLESSSRPH 277  
 Db 260 GGSNGRSYKRTFSEBPDHGMKLTSGKSHLESSSRPH 296

## RESULT 3

US-09-536-647-2  
 ; Sequence 2, Application US/09536647  
 ; Patent No. 6579708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ho, Yen Sen  
 ; APPLICANT: Johnson, Randall  
 ; TITLE OF INVENTION: No. 6579708e1 Human Uridine Kinase  
 ; FILE REFERENCE: GP50020  
 ; CURRENT APPLICATION NUMBER: US/09/536,647

CURRENT FILING DATE: 2000-03-27  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 260  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-536-647-2

Query Match 94.0%; Score 1363; DB 2; Length 260;  
 Best Local Similarity 100.0%; Pred. No. 3e-109;  
 Matches 260; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASAGDECSPEADPRHQRPFLLIGVSGTASGKSTVCEKIMELLGONEVEOROKRV 60  
 Db 1 MASAGDECSPEADPRHQRPFLLIGVSGTASGKSTVCEKIMELLGONEVEOROKRV 60  
 QY 61 ILSODRFYKVLTAEQKAKALKGQYNPDHDPADFNDLMHRTLNKIVEGKTEVEPTYPVTH 120  
 Db 61 ILSODRFYKVLTAEQKAKALKGQYNPDHDPADFNDLMHRTLNKIVEGKTEVEPTYPVTH 120  
 QY 121 SRLPETTVVPADVLPFEGILVFYSQEI RDMFHLRLFVDTSDVRLSRVLRDVRGRDL 180  
 Db 121 SRLPETTVVPADVLPFEGILVFYSQEI RDMFHLRLFVDTSDVRLSRVLRDVRGRDL 180  
 QY 181 EQILTYTTFFKPAFEBCFLPTKKYADVILPRGVNMMVAINLIVQHIDILNGDICKMR 240  
 Db 181 EQILTYTTFFKPAFEBCFLPTKKYADVILPRGVNMMVAINLIVQHIDILNGDICKMR 240  
 QY 241 GGSNGRSYKRTFSEBPDHGMKLTSGKSHLESSSRPH 277  
 Db 241 GGSNGRSYKRTFSEBPDHGMKLTSGKSHLESSSRPH 260

## RESULT 4

US-09-536-647-3  
 ; Sequence 3, Application US/09536647  
 ; Patent No. 6579708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ho, Yen Sen  
 ; APPLICANT: Johnson, Randall  
 ; TITLE OF INVENTION: No. 6579708e1 Human Uridine Kinase  
 ; FILE REFERENCE: GP50020  
 ; CURRENT APPLICATION NUMBER: US/09/536,647  
 ; CURRENT FILING DATE: 2000-03-27  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 3  
 ; LENGTH: 277  
 ; TYPE: PRT  
 ; ORGANISM: Human  
 ; US-09-536-647-3

Query Match 91.4%; Score 1325; DB 2; Length 277;  
 Best Local Similarity 91.7%; Pred. No. 5.3e-106;  
 Matches 254; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

QY 1 MASAGDECSPEADPRHQRPFLLIGVSGTASGKSTVCEKIMELLGONEVEOROKRV 60  
 Db 1 MASAGDECSPEADPRHQRPFLLIGVSGTASGKSTVCEKIMELLGONEVEOROKRV 60  
 QY 61 ILSODRFYKVLTAEQKAKALKGQYNPDHDPADFNDLMHRTLNKIVEGKTEVEPTYPVTH 120  
 Db 61 ILSODRFYKVLTAEQKAKALKGQYNPDHDPADFNDLMHRTLNKIVEGKTEVEPTYPVTH 120  
 QY 121 SRLPETTVVPADVLPFEGILVFYSQEI RDMFHLRLFVDTSDVRLSRVLRDVRGRDL 180  
 Db 121 SRLPETTVVPADVLPFEGILVFYSQEI RDMFHLRLFVDTSDVRLSRVLRDVRGRDL 180  
 QY 181 EQILTYTTFFKPAFEBCFLPTKKYADVILPRGVNMMVAINLIVQHIDILNGDICKMR 240  
 Db 181 EQILTYTTFFKPAFEBCFLPTKKYADVILPRGVNMMVAINLIVQHIDILNGDICKMR 240

QY 241 GSGNGRSYKRTFSEPGDHPGMLTSGKSHLESSSRPH 277  
 Db 241 GSPNGRNHKTFFPEPGDHPGMLTSGKSHLESSSRPH 277

RESULT 5  
 US-09-488-725A-1839

/ Sequence 1839, Application US/09488725A  
 / GENERAL INFORMATION:

/ APPLICANT: Hyseq Inc

/ TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

/ FILE REFERENCE: 784FLPCT

/ CURRENT APPLICATION NUMBER: US/09/488, 725A

/ CURRENT FILING DATE: 2000-12-22

/ PRIOR APPLICATION NUMBER: US/09/488, 725

/ PRIOR FILING DATE: 2000-01-21

/ PRIOR APPLICATION NUMBER: US09/552,317

/ PRIOR FILING DATE: 2000-04-25

/ PRIOR APPLICATION NUMBER: US09/598,042

/ PRIOR FILING DATE: 2000-06-20

/ PRIOR APPLICATION NUMBER: US09/620,312

/ PRIOR FILING DATE: 2000-07-19

/ PRIOR APPLICATION NUMBER: US09/653,450

/ PRIOR FILING DATE: 2000-08-31

/ PRIOR APPLICATION NUMBER: US09/662,191

/ PRIOR FILING DATE: 2000-09-14

/ PRIOR APPLICATION NUMBER: US09/693,036

/ PRIOR FILING DATE: 2000-10-19

/ PRIOR APPLICATION NUMBER: US09/727,344

/ PRIOR FILING DATE: 2000-11-29

/ NUMBER OF SEQ ID NOS: 7144

/ SOFTWARE: pc FL\_gene\_b Versions 1.0

/ SEQ ID NO 1839

/ LENGTH: 262

/ TYPE: PRT

/ ORGANISM: Homo sapiens

/ US-09-488-725A-1839

Query Match 64.4%; Score 934; DB 1; Length 261;  
 Best Local Similarity 69.5%; Pred. No. 4,6e-73;

Matches 189; Conservative 27; Mismatches 40; Indels 16; Gaps 4;

QY 8 DCESPPEADRP-ORPFLIGVGSTAGSTVCEKIMELIGONEVEORQRKVILISODR 66  
 Db 4 DSEQTQINQNGPGRGPEFLIGVGSTAGSTVCAKIVOLLGQNEVDYRQKVILISODS 63  
 QY 67 FYKVLTAQOKAKALKQYNEFDHPDAPNDIMHRTLNIVGKTVVEPTVYDFTHSRLPET 126  
 Db 64 FYKVLTAQOKAKALKQYNEFDHPDAPNDIMHRTLNIVGKTVQIPVYDFVSHSRKEET 123  
 QY 127 TVYVPADVLFEGILVYSGEIRDMFHLRFVDTDSVRLSRVLDV-RRGDLLEQILT 185  
 Db 124 TVYVPADVLFEGILVYSGEIRDMFHLRFVDTDSVRLSRVLDV-RRGDLLEQILT 183  
 QY 186 QYTFKPAFEERCLPTKKYADVIIRGVNMAINLIYOHIDILNGDICKWHGSGNS 245  
 Db 184 QYTFKPAFEERCLPTKKYADVIIRGVNMAINLIYOHIDILNGDICKWHGSGNS 242  
 QY 246 RSYKRTFSEPGDHPGMLTSGKSHLESSSRPH 277  
 Db 233 PSKRQT---NGCLNGYTPSRKRQASSESSSRPH 261

RESULT 6  
 PCT-US00-05988-1160

/ Sequence 1160, Application PC/TUS0005988

/ GENERAL INFORMATION:

/ APPLICANT: Craig Roegen,

/ APPLICANT: Steve Ruben

/ TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides

/ FILE REFERENCE: PA101PCT

/ CURRENT APPLICATION NUMBER: PCT/US00/05988

/ CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270  
 EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1160

LENGTH: 337

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (38)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (46)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

FEATURE:

NAME/KEY: SITE

LOCATION: (169)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

PCT-US00-05988-1160

Query Match 61.8%; Score 896; DB 3; Length 337;  
 Best Local Similarity 62.3%; Pred. No. 1e-69;

Matches 188; Conservative 28; Mismatches 40; Indels 46; Gaps 6;

QY 2 ASAGE-----DCESPPEADRP-ORPFLIGVGSTAGSK 36  
 Db 56 AGNGERASVYRTGSGRGAGNHRGQADPAEPAPARRALPYR-----HGTRASK 109  
 QY 37 STVCEKIMELIGONEVEORQRKVILISODRFYKVLTAQOKAKALKQYNEFDHPDAPNDL 96  
 Db 110 SSVCATVOLLGQNEVDYRQKVILISODSFYKVLTAQOKAKALKQYNEFDHPDAPNDL 169  
 QY 97 MHTLNIVGKTVVEPTVYDFTHSRLPETTVYVPADVLFEGILVYSGEIRDMFHLRL 156  
 Db 170 IKTLEITEGKTVQIPVYDFVSHSRKEETTVYVPADVLFEGILVYSGEIRDMFHLRL 229  
 QY 157 FVDTDSVRLSRVLDV-RRGDLLEQILTQYTFKPAFEERCLPTKKYADVIIRGVN 215  
 Db 230 FVDTDSVRLSRVLDV-RRGDLLEQILTQYTFKPAFEERCLPTKKYADVIIRGVN 289  
 QY 216 NVAINLIYOHIDILNGDICKWHGSGNSYKRTFSEPGDHPGMLTSGKSHLESSSR 275  
 Db 290 NVAINLIYOHIDILNGDICKWHGSGNSYKRTFSEPGDHPGMLTSGKSHLESSSR 335  
 QY 276 PH 277  
 Db 336 PH 337

RESULT 7  
 US-09-488-725A-5411

/ Sequence 5411, Application US/09488725A

/ GENERAL INFORMATION:

/ APPLICANT: Hyseq Inc

/ TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

/ FILE REFERENCE: 784FLPCT

/ CURRENT APPLICATION NUMBER: US/09/488, 725A

/ CURRENT FILING DATE: 2000-12-22

/ PRIOR APPLICATION NUMBER: US/09/488, 725

/ PRIOR FILING DATE: 2000-01-21

/ PRIOR APPLICATION NUMBER: US09/552,317

/ PRIOR FILING DATE: 2000-04-25

/ PRIOR APPLICATION NUMBER: US09/598,042

/ PRIOR FILING DATE: 2000-06-20

/ PRIOR APPLICATION NUMBER: US09/620,312

/ PRIOR FILING DATE: 2000-07-19

/ PRIOR APPLICATION NUMBER: US09/653,450

PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US09/662,191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US09/727,344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7144  
 SOFTWARE: pt\_FL\_genes\_b Versions 1.0  
 SEQ ID NO 5411  
 LENGTH: 342  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-488-725A-5411

Query Match 61.3%; Score 889; DB 1; Length 335;  
 Best Local Similarity 63.8%; Pred. No. 4e-69;  
 Matches 190; Conservative 26; Mismatches 46; Indels 36; Gaps 7;

QY 2 ASAGE-----DCESPAEADRP-GRPLIGSGTASGKSTCEK 42  
 DB 52 AGAGEERASVTSGRRGRTMAGSEQTIONHOOPNGEFPLLIGSGTASGKSSVCAK 111  
 QY 43 IMELLIGNEVEQORQKVVILSQDRFYKVLTAEOKAKALKGQYNFDPDAPNDIMHRTLK 102  
 DB 112 IVOLLGQNEVYRQKQVILTSQDSFYRLVTSQKAKALKGQFNDHPAFNELILTKL 171  
 QY 103 NIVEGKTVETPTDFTVTHSRLETTVVYPADVLFEGILVFYSQD-IRDMFHLRFVDT 161  
 DB 172 ETEGKTVQIIVYDFVSHSRKEETVYVPADVLFEGILVFYSQD-IRDMFHLRFVDT 231  
 QY 162 SDVLSRVRVADY-RRGDLFOILLQYV-TVKPAFEFECPTKKYADVILPRGVDNVA 219  
 DB 232 ADTSLSRVLRKDISERGLDQLSSSTLRVFKPAFEFECPTKKYADVILPRGVDNVP 291  
 QY 220 INLIYOHIDILINDICMHRGSGNSGRSYKRTFSPGDHPGLTSGKSHLESSSRPH 277  
 DB 292 INLIYOHIDILINDICMHRGSGNSGRSYKRTFSPGDHPGLTSGKSHLESSSRPH 335

RESULT 8  
 US-09-488-725A-2274  
 Sequence 2274, Application US/09488725A  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq Inc  
 TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 FILE REFERENCE: 784FLPCT  
 CURRENT APPLICATION NUMBER: US/09/488,725A  
 CURRENT FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: US/09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US09/662,191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US09/727,344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7144  
 SOFTWARE: pt\_FL\_genes\_b Versions 1.0  
 SEQ ID NO 2274  
 LENGTH: 200  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-488-725A-2274

Query Match 6.3%; Score 92; DB 1; Length 199;  
 Best Local Similarity 22.5%; Pred. No. 0.032;  
 Matches 34; Conservative 32; Mismatches 65; Indels 20; Gaps 3;

QY 22 RPPLIGVSGGTASGKSTCEKIMELLIGNEVEQORQKVVILSQDRFYKVLTAEOKAKALK 81  
 DB 2 KTFILIGSVGTNSGKTTIAKNLOKHLPNCSV-----ISODDFKPESEIETDK--N 50  
 QY 82 GQYNFDPDAPFNDIMHRTLKNIVEGKTVETPTDFTVTHSRLETTVVYPADVLFEGIL 141  
 DB 51 GFLQYDVLEALNNEKMMASISCMWESARHSVSTDQSAEIP-----ILITIGFL 101  
 QY 142 VFYSQDIRDMFHLRFVDTSDVRLSRVLR 172  
 DB 102 LFNYKPLDTIMNRSYFLTIPEECKRRRSTR 132

RESULT 9  
 US-09-488-725A-5846  
 Sequence 5846, Application US/09488725A  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq Inc  
 TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 FILE REFERENCE: 784FLPCT  
 CURRENT APPLICATION NUMBER: US/09/488,725A  
 CURRENT FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: US/09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US09/662,191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US09/727,344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7144  
 SOFTWARE: pt\_FL\_genes\_b Versions 1.0  
 SEQ ID NO 5846  
 LENGTH: 225  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 NAME/KEY: misc feature  
 LOCATION: (1)..(224)  
 OTHER INFORMATION: Xaa = any amino acid or nothing  
 US-09-488-725A-5846

Query Match 6.3%; Score 92; DB 1; Length 224;  
 Best Local Similarity 22.5%; Pred. No. 0.037;  
 Matches 34; Conservative 32; Mismatches 65; Indels 20; Gaps 3;

QY 22 RPPLIGVSGGTASGKSTCEKIMELLIGNEVEQORQKVVILSQDRFYKVLTAEOKAKALK 81  
 DB 7 KTFILIGSVGTNSGKTTIAKNLOKHLPNCSV-----ISODDFKPESEIETDK--N 55  
 QY 82 GQYNFDPDAPFNDIMHRTLKNIVEGKTVETPTDFTVTHSRLETTVVYPADVLFEGIL 141  
 DB 56 GFLQYDVLEALNNEKMMASISCMWESARHSVSTDQSAEIP-----ILITIGFL 106  
 QY 142 VFYSQDIRDMFHLRFVDTSDVRLSRVLR 172  
 DB 107 LFNYKPLDTIMNRSYFLTIPEECKRRRSTR 137

RESULT 10  
 US-09-488-725A-3156  
 Sequence 3156, Application US/09488725A



```

Best Local Similarity 26.9%; Pred. No. 2;
Matches 36; Conservative 16; Mismatches 33; Indels 49; Gaps 8;

QY 2 ASAGGDEC-ESPAPEA-----DRPHORPLIIV-----SGGTASGKSTVECKI 43
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 36 AAAPGEQAVVAPSTVPSSTSKDRPVSPSLVSGSKPPPARSGSG-SSAKPQBER 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 44 MELLIGONEVQRQRKVVILSGD-RFYKVLTAQKAKALKQGVNFDHPDAPNDIMHRTLK 102
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 95 QQ---QDDIELLETKAVGMSNDGRFLK-----FDIEIGRGSFK 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 103 NIVEG---KTVEV 112
   |||:|||||:
Db 130 TVYKGLDTETTV 143

RESULT 13
US-09-488-725A-5454
; Sequence 5454, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 5454
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5454

Query Match 5.3%; Score 76.5; DB 1; Length 470;
Best Local Similarity 26.9%; Pred. No. 2;
Matches 36; Conservative 16; Mismatches 33; Indels 49; Gaps 8;

QY 2 ASAGGDEC-ESPAPEA-----DRPHORPLIIV-----SGGTASGKSTVECKI 43
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 36 AAAPGEQAVVAPSTVPSSTSKDRPVSPSLVSGSKPPPARSGSG-SSAKPQBER 94
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 44 MELLIGONEVQRQRKVVILSGD-RFYKVLTAQKAKALKQGVNFDHPDAPNDIMHRTLK 102
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 95 QQ---QDDIELLETKAVGMSNDGRFLK-----FDIEIGRGSFK 129
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 103 NIVEG---KTVEV 112
   |||:|||||:
Db 130 TVYKGLDTETTV 143

RESULT 14
PCT-US00-05988-1515
; Sequence 1515, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides

```

```

; FILE REFERENCE: PA101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1515
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-05988-1515

Query Match 5.3%; Score 76.5; DB 3; Length 479;
Best Local Similarity 20.8%; Pred. No. 2.1;
Matches 71; Conservative 46; Mismatches 120; Indels 105; Gaps 17;

QY 9 CESAPAPEA-----DRPHORPLIIVSGGTASGKSTVECKIMELLQO-----49
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 67 CRGLAVEAKKTVYRDKPHVN---VGTIGHVDHGKTLTLTAITKILAEQGAKEKYBEID 123
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 50 NEVEQRQRKVV-----LSQDRFYKVLTAQKAKALKQGVNFDHP-----DAFDND 95
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 124 NAEERARAGITINAAHYEYSTAARHYAHTDCPGHADYVKNMTGTAPLDGCIIVVANDG 183
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 16MRTLNIVEGKTVBEVPTDFVTHSRLEPPTVY--PADVLPFGILVFYSOEIRDMFH 153
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 PMQTRHLLAIOIGV-----EHVVYVNNKADAVODSEVELVEIRHLLT 231
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 154 LRLFVDTSDVRLSRRLV---RDVRRG-RDLBQILLQYTTFYK-PAFE---EPCLETKK 204
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 232 EFGYKGETVIVIGSALCALEGRDPELGKSVOKLDAVDTYIPVPARDLEKEFLPVEA 291
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 205 YADY-----IIPGVNMAINLYVGHIDIINGDI CKMHGSGNR-----246
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 292 VYSPGRGYVTGTLEKGI-----LKKGDCELLGHSKNIRVVTGTIEMF 336
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 247 --SYKRTFSEPGDHPGMLTSG-KRSHLE-----SSSRPH 277
   |||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 337 HKSLER--AEAGDVLGALVGLKREDLRGLVNVKPSIRPH 376
   |||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
US-09-488-725A-2247
; Sequence 2247, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_FL_genes_b Versions 1.0
; SEQ ID NO 2247
; LENGTH: 1771
; TYPE: PRT
; ORGANISM: Homo sapiens

```

US-09-488-725A-2247

Query Match 5.3%; Score 76.5; DB 1; Length 1770;

Best Local Similarity 20.5%; Pred. No. 12; Indels 85; Gaps 14;

Matches 60; Conservative 42; Mismatches 105;

QY 12 PAFBAPD-RPHQRPFLVSGGTASGKSTVCEKIMELIGONEVEFORQKVVILSODRFYK 69  
 DB 249 PTFQNALITHTFPIITLKAS-EKKTKVASISFDMSKAKBSQSGFKITVAKESYS 305  
 QY 70 ULTAQKAKALKQYVNFDPDAPDNDIMHRTLNKIVEGKT-VEVPTDYVTHSRLEPTT 127  
 DB 306 KLEIPYQAEVLDTGLGFDHA-ATLFHIRDSPADPVERPYYLTNTFS- 350  
 QY 128 VVYPADVLEGLVFPVSGEIRDMFHLR-LFPDTGSDVLSR 168  
 DB 351 -PALIHDVLL-PBEAKTFKYNFSKPVLLIPNBSGYITLLFMPSTSSMHDN 403  
 QY 169 RVLRDVRGRDLRLQIITQYTTFYKPA-FEEFCLPTKRYADVIIIPGVDMNV- 218  
 DB 404 NIL-LITNASKFHLPRVYVYTGFDYFVLPK-IEEFIDRGVLSAT 447  
 QY 219 -AINLIYOHIDILND-ICKMHRGSGNSGRSYKRTSEPGDHGMLTS 264  
 DB 448 EASNILFA-IINSNPILAIKSWHIIG-DGLSIELVAVERGNGRTTIISS 494

RESULT 16

US-09-488-725A-2852

Sequence 2852, Application US/09488725A

GENERAL INFORMATION:

APPLICANT: Hyseq Inc

TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides

FILE REFERENCE: 784FLPCT

CURRENT APPLICATION NUMBER: US/09/488, 725A

CURRENT FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US/09/488, 725

PRIOR FILING DATE: 2000-01-21

PRIOR APPLICATION NUMBER: US09/552,317

PRIOR FILING DATE: 2000-04-25

PRIOR APPLICATION NUMBER: US09/598, 042

PRIOR FILING DATE: 2000-06-20

PRIOR APPLICATION NUMBER: US09/620,312

PRIOR FILING DATE: 2000-07-19

PRIOR APPLICATION NUMBER: US09/653,450

PRIOR FILING DATE: 2000-08-31

PRIOR APPLICATION NUMBER: US09/662,191

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: US09/693,036

PRIOR FILING DATE: 2000-10-19

PRIOR APPLICATION NUMBER: US09/727,344

PRIOR FILING DATE: 2000-11-29

NUMBER OF SEQ ID NOS: 7144

SOFTWARE: pc FL\_gene\_b Versions 1.0

SEQ ID NO 2852

LENGTH: 388

TYPE: PRT

ORGANISM: Homo sapiens

US-09-488-725A-2852

Query Match 5.2%; Score 76; DB 1; Length 387;

Best Local Similarity 23.9%; Pred. No. 1.7; Indels 44; Gaps 6;

Matches 33; Conservative 22; Mismatches 39;

QY 17 DRPHQRPFLVSGGTASGKSTVCEKIMELIGONEV-EQORQKVVIL- 62  
 DB 225 ERTROLFLVVDISGFLSSHTQYRTAFETIILTKLELYKEBLQKRPALLAVNKDLPD 284  
 QY 63 SODRFYKVLTAQKAKALKQYVNFDPDAPDNDIMHRTLNKIVEGKTVEVPTDYVTHSR 122  
 DB 285 AODKFHLSQLOPK-DFLHLEKXMIPEPTVE-FOH- 320  
 QY 123 LPETTVVYPADVLPFGI 140

DB 321 -IIPISAVTGEI 332  
 RESULT 17  
 US-09-488-725A-6424  
 Sequence 6424, Application US/09488725A  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq Inc  
 TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 FILE REFERENCE: 784FLPCT  
 CURRENT APPLICATION NUMBER: US/09/488, 725A  
 CURRENT FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: US/09/488, 725  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US09/662,191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US09/727,344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7144  
 SOFTWARE: pc FL\_gene\_b Versions 1.0  
 SEQ ID NO 6424  
 LENGTH: 396  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-488-725A-6424

US-09-488-725A-6424

Query Match 5.2%; Score 76; DB 1; Length 396;

Best Local Similarity 23.9%; Pred. No. 1.8; Indels 44; Gaps 6;

Matches 33; Conservative 22; Mismatches 39;

QY 17 DRPHQRPFLVSGGTASGKSTVCEKIMELIGONEV-EQORQKVVIL- 62  
 DB 234 ERTROLFLVVDISGFLSSHTQYRTAFETIILTKLELYKEBLQKRPALLAVNKDLPD 293  
 QY 63 SODRFYKVLTAQKAKALKQYVNFDPDAPDNDIMHRTLNKIVEGKTVEVPTDYVTHSR 122  
 DB 294 AODKFHLSQLOPK-DFLHLEKXMIPEPTVE-FOH- 329  
 QY 123 LPETTVVYPADVLPFGI 140  
 DB 330 -IIPISAVTGEI 341

RESULT 18

PCT-US00-05988-1494

Sequence 1494, Application PC/TUS0005988

GENERAL INFORMATION:

APPLICANT: Craig Rosen,

APPLICANT: Steve Ruben

TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides

FILE REFERENCE: PA101PCT

CURRENT APPLICATION NUMBER: PCT/US00/05988

CURRENT FILING DATE: 2000-03-08

EARLIER APPLICATION NUMBER: 60/124,270

EARLIER FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1890

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1494

LENGTH: 469

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE  
LOCATION: (299)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
PCT-US00-05988-1494

Query Match 5.0%; Score 73; DB 3; Length 469;

Best Local Similarity 21.5%; Pred. No. 4;  
Matches 48; Conservative 31; Mismatches 92; Indels 52; Gaps 9;

QY 7 EDGSPAPDR-----PHORPLGVGGTASGKSTVCCKIMELGQ-----49  
DB 230 EEMTRKQPDVDRVTKYKRNIEPTHAFLIEKSRSGGRKSLQPTPPMPLISQSEAKNP 289  
QY 50 --NEVEGORORVLTLSODRFYKVLTAQOKAKALGOVNF-----HPDAFDN 94  
DB 290 RINOLSRKQVLLALEROKLADLDRLELEFANFDPVDRKKYMRMHKSRVM 349  
QY 95 DLMRTLKNIIVEGKTVPEVTVYTHSRLEPTTVVYPADVLF-----EGILVFS-----145  
DB 350 DFPFRIDKD-QDGKITRQEPIDGILASKFPITTKLEMAVADIFRDGDGYIDYEFVAL 408  
QY 146 QEIRDMFHLFLVTDSDVLSRRVLDVNRGR-----DLEQI 183  
DB 409 HPNMDAYR---PTTDAD-KLIEDEVTRQVQCKCAKRFQVEOI 446

RESULT 19

US-09-488-725A-6014  
Sequence 6014, Application US/09488725A  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
FILE REFERENCE: 784FLPCT  
CURRENT APPLICATION NUMBER: US/09/488,725A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US/09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: US09/598,042  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: US09/620,312  
PRIOR FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: US09/653,450  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US09/662,191  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US09/693,036  
PRIOR FILING DATE: 2000-10-19  
PRIOR APPLICATION NUMBER: US09/727,344  
PRIOR FILING DATE: 2000-11-29  
NUMBER OF SEQ ID NOS: 7144  
SOFTWARE: pc\_fl\_genes\_b Versions 1.0  
SEQ ID NO 6014  
LENGTH: 749  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-488-725A-6014

Query Match 5.0%; Score 72.5; DB 1; Length 745;

Best Local Similarity 23.1%; Pred. No. 8.1;  
Matches 53; Conservative 33; Mismatches 78; Indels 65; Gaps 12;

QY 9 CESA-PEADRPORPLIGSGGTASGKSTVCCKIMELGQNEVEGORORVLTLSODRF 67  
DB 191 COSGMFLPLDKVRPR-----IAGITAMLOQSLBGLLEGLQTSDDV-----IIRHCLRT 239  
QY 68 YKVLTAQOKAKALG-----QYNPDHPADF--NDLMH-----RTLKNI 104  
DB 240 YATIDKRDALAGQVLKPEYIDEVLTIEQVESHPRGLQVMYKLLFVPHHCRLLREV 299  
QY 105 VEG-----KTVEVPTVDFVTHSRLEPTTVVYPADV-LFEGILVFSQEIRDMFHLFLV 158

DB 300 TGAISSEKGNTPGYDFLVNS-----VWPOIVQGLEBKLPFLNPNNDPAFHEKYTI 352  
QY 159 DTSDVRLSRV--LNDVRRGRDLEQILNQYTFVWPAFEFCLPTKXY 205  
DB 353 SMDVRLERQCGSQASVKRLR-----AHPAYHSF--NKKW 386

RESULT 20

US-09-488-725A-2442  
Sequence 2442, Application US/09488725A  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
FILE REFERENCE: 784FLPCT  
CURRENT APPLICATION NUMBER: US/09/488,725A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US/09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: US09/598,042  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: US09/620,312  
PRIOR FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: US09/653,450  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US09/662,191  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US09/693,036  
PRIOR FILING DATE: 2000-10-19  
PRIOR APPLICATION NUMBER: US09/727,344  
PRIOR FILING DATE: 2000-11-29  
NUMBER OF SEQ ID NOS: 7144  
SOFTWARE: pc\_fl\_genes\_b Versions 1.0  
SEQ ID NO 2442  
LENGTH: 739  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-488-725A-2442

Query Match 4.8%; Score 70; DB 1; Length 738;  
Best Local Similarity 23.3%; Pred. No. 13;  
Matches 50; Conservative 31; Mismatches 72; Indels 62; Gaps 11;

QY 22 RPLIGVSGGTASGKSTVCCKIMELGQNEVEGORORVLTLSODRFYKVLTAQOKAK 81  
DB 197 RPRRAGI---TAMLOQSLBGLLEGLQTSDDV-----IIRHCLRTYATIDKRDALV 247  
QY 82 G-----QYNPDHPADF--NDLMH-----RTLKNIVEG-----KTVEVP 113  
DB 248 GQVLKPEYIDEVLTIEQVESHPRGLQVMYKLLFVPHHCRLLREVTCGAISSEKGNTPV 307  
QY 114 TYFVTHSRLEPTTVVYPADV-LFEGILVFSQEIRDMFHLFLVTDSDVRLSRV--170  
DB 308 GYDFLVNS-----VWPOIVQGLEBKLPFLNPNNDPAFHEKYTISMDVRLERQCGS 360  
QY 171 LNDVRRGRDLEQILNQYTFVWPAFEFCLPTKXY 205  
DB 361 QASVKRLR-----AHPAYHSF--NKKW 380

RESULT 21

US-09-488-725A-3018  
Sequence 3018, Application US/09488725A  
GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
FILE REFERENCE: 784FLPCT  
CURRENT APPLICATION NUMBER: US/09/488,725A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US/09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317



```

; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 3018
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3018

```

```

Query Match
Best Local Similarity 20.6%; Score 69; DB 1; Length 490;
Matches 53; Conservative 38; Mismatches 78; Indels 88; Gaps 15;

```

```

QY 9 CESPAEADRPHQRPFLIGVSGGTASGKSTVCEKIMELLQNEVEQRORRVILSODRFY 68
DB 276 CESPKRPSRPE-----LTILSPTSENNKKLFNDLFR-KNNARAENTERK---QONQYFM 326
QY 69 KVLTAQKAKALKQGYNDFHPDAPNDLMHRTIKNIIVEGKTV-EVPTYDFVTHSRLEPPT 127
DB 327 EWTVE-----GVVDY-----LMV-----VGRVVFQVDDW---LHLLMGTR 360
QY 128 VVYPADVLFEGILVYS-----QETRDMEHLRLFVDTSDVRLSRVLRDVR 175
DB 361 -----ILFKNTLEMTYTYIQLCKLEQLFQEHRLVSLITLRLDAIFCENTERPSIQDKQ 413
QY 176 RGRDLEQILLTYTFVKPAFEER-----CLPTK-KYADV-IIPRGVD----- 215
DB 414 KG-----AKQTFEEMNNYIPDLVVKIGSEETKYSIRLLPDLQOPVLANKQL 460
QY 216 NNVAINTLYOHIQDILN 232
DB 461 TVVLDIVIQELFPELNL 477

```

```

RESULT 22
US-09-488-725A-6590
; Sequence 6590, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0

```

```

; SEQ ID NO 6590
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6590

```

```

Query Match
Best Local Similarity 20.6%; Score 69; DB 1; Length 507;
Matches 53; Conservative 38; Mismatches 78; Indels 88; Gaps 15;

```

```

QY 9 CESPAEADRPHQRPFLIGVSGGTASGKSTVCEKIMELLQNEVEQRORRVILSODRFY 68
DB 293 CESPKRPSRPE-----LTILSPTSENNKKLFNDLFR-KNNARAENTERK---QONQYFM 343
QY 69 KVLTAQKAKALKQGYNDFHPDAPNDLMHRTIKNIIVEGKTV-EVPTYDFVTHSRLEPPT 127
DB 344 EWTVE-----GVVDY-----LMV-----VGRVVFQVDDW---LHLLMGTR 377
QY 128 VVYPADVLFEGILVYS-----QETRDMEHLRLFVDTSDVRLSRVLRDVR 175
DB 378 -----ILFKNTLEMTYTYIQLCKLEQLFQEHRLVSLITLRLDAIFCENTERPSIQDKQ 430
QY 176 RGRDLEQILLTYTFVKPAFEER-----CLPTK-KYADV-IIPRGVD----- 215
DB 431 KG-----AKQTFEEMNNYIPDLVVKIGSEETKYSIRLLPDLQOPVLANKQL 477
QY 216 NNVAINTLYOHIQDILN 232
DB 478 TVVLDIVIQELFPELNL 494

```

```

RESULT 23
US-09-488-725A-6591
; Sequence 6591, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 6591
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6591

```

```

Query Match
Best Local Similarity 20.6%; Score 69; DB 1; Length 507;
Matches 53; Conservative 38; Mismatches 78; Indels 88; Gaps 15;

```

```

QY 9 CESPAEADRPHQRPFLIGVSGGTASGKSTVCEKIMELLQNEVEQRORRVILSODRFY 68
DB 293 CESPKRPSRPE-----LTILSPTSENNKKLFNDLFR-KNNARAENTERK---QONQYFM 343
QY 69 KVLTAQKAKALKQGYNDFHPDAPNDLMHRTIKNIIVEGKTV-EVPTYDFVTHSRLEPPT 127

```

```

Db      344 EVNTVE-----GVTDY-----LMT-----VGWVVCQVPM---LHLLMGTR 377
Qy      128 VVVPADVLEFEGILVFS-----OEIRDMFHLRFVDTSDVLSRRVLRDV 175
Db      378 -----ILFKNTLWMTDYVYLQCKLEQLQEHRLVSLITLBDALFCEHTERPSRLQDKQ 430
Qy      176 RGEDEQLTQYTTFKVPAEEF-----CLPTK-KYADV-IIPRGVD-----215
Db      431 KG-----AKQTEEMNNYLPDLLVKCIGETEYESIRLLFDGLQDPVINKOL 477
Qy      216 NMVAINLVQHIDILN 232
Db      478 TVVLDIVIOELPEELN 494

```

```

RESULT 24
US-09-488-725A-3448
; Sequence 3448, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 3448
; LENGTH: 3178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3448

```

```

Query Match      4.8%; Score 69; DB 1; Length 3177;
Best Local Similarity 22.4%; Pred. No. 1.1e+02;
Matches 45; Conservative 36; Mismatches 92; Indels 28; Gaps 7;

Qy      26 IGVSAGTASGKSTVCEKIME---LIGONEVEORQRKRVIL-----SODRFYKVLTAEQ 75
Db      312 LGFAGGELANIGLALDFVENHPTFRAGSRVEBGPQVLVLISAGPSDELRIGVVALKQ 371
Qy      76 KAKALKGQYNPDHPDAFNDMLMHTLKNIVEGKTVVEPTYDFVTHSRLEPTTVVPADV 135
Db      372 ---ASVFSFGAGQAASRAELQHTATDNLVFTVPEFSPDLOEKLLPIYGVAAQRHIV 428
Qy      136 LFEGLIVFYSOEI--RDMFHLRFVDTSDVRLSR-----RYLADVRRGRDLBQI- 183
Db      429 LKPPITIVQVEVNNRQDIVFL---VDSGSLGLANFNAIRDFIAKVIGRLQRLBQIQA 485
Qy      184 LTOYTFVKPAEEFCLEPTK 204
Db      486 VAQYADIVREPEFYENTHPTKR 506

```

```

RESULT 25
US-09-488-725A-6346
; Sequence 6346, Application US/09488725A

```

```

; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 6346
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6346

```

```

Query Match      4.7%; Score 68.5; DB 1; Length 796;
Best Local Similarity 18.7%; Pred. No. 19;
Matches 49; Conservative 45; Mismatches 97; Indels 71; Gaps 10;

```

```

Qy      13 APEADRPQRPFILVSG-----GTASGKSTVCEKIME-----LIGONEVEORQRK 58
Db      384 AVETQRKHLAVILADQQLGAGTLNLSQVVRRTQRKSTITALLFGEEDLEALKAK 443
Qy      59 VVLSQDRFYKVLTAEQKAKALGQYNPDHPDAFNDMLMHTLKNIVEGKTVVEPTYDFV 118
Db      444 NIKQTE-----LVADIREALIVARHPQCTDRKGSVSRQLPGL-----483
Qy      119 THSRLEPTTVVPADV---LFEGLIVFYSOEIRDMFHLRFVDTSDVRLSRVLRDV 174
Db      484 ----LPTVLTLPPTPLVGLXSLWQELPDSMESHQDHENYVACSRSHRRRAKALLDFE 539
Qy      175 R-----RGDLEQLTQYTTFKVPAEEFC-----LPTKXADYIIPRGVD 215
Db      540 RHDDELGFRRKNDIITVSQK-----DEHCWVGLNGLRGWFPA-KFEVLDERSK 590
Qy      216 NMVA-INLVQHIDILNGIC 236
Db      591 YSINGDDSVTEGVTLVRGITLC 612

```

```

RESULT 26
US-09-488-725A-6347
; Sequence 6347, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450

```

```

; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 6347
; LENGTH: 796
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6347

```

```

Query Match 4.7%; Score 68.5; DB 1; Length 796;
Best Local Similarity 18.7%; Pred. No. 19;
Matches 49; Conservative 45; Mismatches 97; Indels 71; Gaps 10;

```

```

QY 13 APEADPRHQRPPFLIGVG-----GTASGKSTVCEKIME-----LLGONEVEQRQRK 58
DB 384 AVETQRKHLAYLLADGQLGAGTTLNLSQVARRRQRKSTTALLFGEEDLEALKAK 443
QY 59 VLLSQDRFYKVLTAQKAKALKGQVNFHDAFNDLMHRTLNIVEGKTVFVPTDFV 118
DB 444 NIKQTE-----LVADLRBAILRVARHFCQTDPRNCSVSRQLPGL----- 483
QY 119 TSHRLPETTVYPADVY---LEGLIVFYSGEIRDMFHLRLFYDTSVRLSRVLRDV 174
DB 484 ----LPTALTLPPLPLVGLYSIMQELTPDYSMSHQDRHENVYACSRSHRRRAKALLDFE 539
QY 175 R-----RGRDLEQILTYTTFVVKAPFEFC-----LPTKXYADVILPRGVD 215
DB 540 RHDDDELGFRRKNDITTVSOK-----DEKCVGSLNGLRGWFA-KTVEVLDESKSE 590
QY 216 NMVA-INLIVQHIQDILANGDIC 236
DB 591 YSIAGDDSVTEGVTDLVRGTLG 612

```

```

RESULT 27
PCT-US00-05988-1543
; Sequence 1543, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: PAL01PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1543
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-05988-1543

```

```

Query Match 4.7%; Score 68; DB 3; Length 239;
Best Local Similarity 23.0%; Pred. No. 4.3; Indels 20; Gaps 4;
Matches 29; Conservative 21; Mismatches 56;
QY 39 VCEKIMELLGQNEVEQRQRKRVLLISDRFYKVLTAQKAKALKGQVNFHDAFNDLMH 98
DB 134 VCEINIDIVLCGNKVDIKRVRKAKS-IVFRRKKNLQYDISASNTVFBRPLM----- 186
QY 99 RLTKNIVEGKTVFVPTDFVTHSLRPETTVYPADVYLFEGILVFSQEIRDMFHLRLFV 158
DB 187 ----LARDLIGDPMLEFVAMPALA-----PPEVMDPALAAQYEHDL-EVAQTALP 233
QY 159 DTDSDV 164

```

```

DB 234 DEDDDL 239

```

```

RESULT 28
US-09-488-725A-2978
; Sequence 2978, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 2978
; LENGTH: 443
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2978

```

```

Query Match 4.6%; Score 66.5; DB 1; Length 442;
Best Local Similarity 27.5%; Pred. No. 13;
Matches 36; Conservative 13; Mismatches 47; Indels 35; Gaps 6;

```

```

QY 159 DTDSVRLSRV-----LRDVRGRDLEQILTYTTFVVKAPFEFCPTPK----- 204
DB 182 DKES-VLANKRVAEBQVECVKTRRELQHRQRLAKQQLKQVQLCLPDKDKREMDLRNL 240
QY 205 YADVILPRGVNNAVNLIVQHIQDILANGDICMKHRRGSSNGRSYKRTFSEPDHPEMLTS 264
DB 241 WRDSIIPRSLDNL-GYNL-----YHPLGSELASIRRAC-----DHMPSLMS 280
QY 265 GKSHLESSSR 275
DB 281 SKVEELARSLR 291

```

```

RESULT 29
US-09-488-725A-6550
; Sequence 6550, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31

```

```

; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 6550
; LENGTH: 457
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6550

Query Match
Best Local Similarity 27.5%; Pred. No. 14;
Matches 36; Conservative 13; Mismatches 47; Indels 35; Gaps 6;

4.6%; Score 66.5; DB 1; Length 457;

QY 159 DTSDVRLSRV-----LRDVRGRDLQILQYTTFFVAPAEPCLPK----- 204
D 197 DKES-VLNKRVAEQLVECKTRELQERQLAKQLQVQLCLPLDKKPEMDLRNL 255
QY 205 YADVIIPRGVDNVAIIVQHIQDILNGDICKMHRGSGNGSYKRTFSEPDHPCMLTS 264
D 256 WRDSIIPRSLDNL-GYNL-----YHPLGSELASIRAC---DHMPSLMS 295
QY 265 GKRSHESSSR 275
D 296 SKVEELASLR 306

RESULT 30
US-09-488-725A-2774
; Sequence 2774, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 2774
; LENGTH: 778
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2774

Query Match
Best Local Similarity 18.7%; Pred. No. 28;
Matches 49; Conservative 45; Mismatches 97; Indels 71; Gaps 10;

4.6%; Score 66.5; DB 1; Length 777;

QY 13 APEADRPQRPLIGVSG-----GTAAGKSTVCEKIME-----LLGQNEVEQQRK 58
D 365 AVETQRRRLTLVLAADQQLGAGTLTNLSQVRRRTQRRKSTYALLFGDDLEALKAK 424
QY 59 VVILSQDRFVKVLTAEQAKALKGQYNDHPDAFNDMLMRTLKNIVGKTVVEPTYDVF 118

```

```

D 425 NIKQTE-----LVADLREALLVARHFQCTDPKNSVSRQLPGJ----- 464
QY 119 THSRLETTYVYADV-----LFEGLIVFYSQIRDMFHLKLFVDPDSDVRLSRVLRDV 174
D 465 ----LPRYALTPPTPLPVGLCSLMQBELTPDYSMSHQRDHENNVYACSRSHRRRAKALDFE 520
QY 175 R-----RGRLDQLQYTTFFVAPAEPC-----LPTKQYADVIIPRGVD 215
D 521 RHDDDELGRKNDIITIVSQK-----DEHCWGEIINGLRGWPFA-KVEVLDERSKE 571
QY 216 NMVA-INLVQHIQDILNGDICK 236
D 572 YSIAGDSDVTEGVTDLVRGTLIC 593

RESULT 31
US-09-488-725A-6989
; Sequence 6989, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 6989
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6989

Query Match
Best Local Similarity 25.9%; Pred. No. 11;
Matches 36; Conservative 18; Mismatches 47; Indels 38; Gaps 7;

4.6%; Score 66; DB 1; Length 372;

QY 2 ASAGGEDCESPAPADRPQRPLIGVSGTASGKSTVCEK-IMELLGQNEVEQQRKRV 60
D 14 ASAGSH-CHAPPTARAPPIF-----GSKSNMATLKDQLLYNLKKEQTPQNKITVV 66
QY 61 -----ILSQDRFVKVLTAEQAKALKGQYNDHPDAFNDMLMRTL-----KN 104
D 67 GVGAVGNACASISIMKCLADELALVDVIEDLKGEM-----MDLQHGSLFLRTPKI 117
QY 105 VEGKTVVEPTYDVFYTHSRRL 123
D 118 VSGK-----DYNTVANSKL 131

RESULT 32
US-09-488-725A-6143
; Sequence 6143, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT

```

[illegible]

```

QY      116 DFVTH-SRLPBTIVYADVVLPFGILVFSQBIKDMFHLRLFYDTSQVRLSRV-LRD 173
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      949 DGLVKGKYGSGSNIAHWYQVEFEDSQIAMKRE--DIYTL-----DEELPKRVAKRF 998
QY      174 VRRGR 178
      |  :  :  :
Db      999 VSAGR 1003

```

```

RESULT 35
US-09-488-725A-6056
; Sequence 6056, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 6056
; LENGTH: 1105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6056

Query Match
Best Local Similarity 4.6%; Score 66; DB 1; Length 1104;
Matches 38; Conservative 38; Mismatches 73; Indels 36; Gaps 10;

QY      9 CESPAPEADRPORHPEFLIGVS---GGTASQKSTVCEKIMELIQONEVEORQ-----K 58
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      897 CAHAGVLMEDDDMYVNNICFRHKVNPVKSKACEKVIS-VGQTVITKRNTRYSCR 955
QY      59 VVLSQDRFYKVLRAEQAKALKGQYNDFDPAFNDLMAHTLKNI---VEGKTYVEPTY 115
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      956 VMAVTSQCFYEVEMFD-----GSFS--RDTPEDIVSDCLKGPAPAGEVVQVWMP 1005
QY      116 DFVTH-SRLPBTIVYADVVLPFGILVFSQBIKDMFHLRLFYDTSQVRLSRV-LRD 173
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      1006 DGLVKGKYGSGSNIAHWYQVEFEDSQIAMKRE--DIYTL-----DEELPKRVAKRF 1055
QY      174 VRRGR 178
      |  :  :  :
Db      1056 VSAGR 1060

```

```

; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 6728
; LENGTH: 149
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6728

Query Match
Best Local Similarity 4.5%; Score 65.5; DB 1; Length 149;
Matches 31; Conservative 17; Mismatches 49; Indels 19; Gaps 5;

QY      24 FLIGVSGGTASGKSTVCEKIMEL-LGONEVEORQKVV---IISQDRFYKVLRAE----- 74
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      19 FLVGLTGSGISGSSSVYQVQLGCAVIDVNAHRHVGDPYPAHRRIVVFGTEVILEN 78
QY      75 -QAKALKGQYNDFDPAFNDLMAHTLKNIVEGKTV--EVPYDFTVHSRLPBT 127
      |  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db      79 GDINRKVLGDLINQPD-----RQQLNAITHPEIRKEMMETFTYFLRERTS 127

RESULT 37
US-09-488-725A-1809
; Sequence 1809, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT FILING DATE: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 1809
; LENGTH: 546
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-1809

Query Match
Best Local Similarity 4.5%; Score 65.5; DB 1; Length 545;
Matches 62; Conservative 44; Mismatches 102; Indels 123; Gaps 15;

```

```

QY 12 PADEADPHORPFLIGSGTAGSKTYCEKIMELLGONEVEORQKRVLLSDRFYKVL 71
Db 211 PPRGRIRP-----APGG-----C-----IQRGPIEVOYQIAILTK----- 242
QY 72 TAEOKAKALKGQYNFDPH-----DAPDNDLMHRTLNKNIVEGKTEVEPTVDFVTHSR 122
Db 243 -----LDHPNVKLVLEVDDDPREDLTVYVFEVLVNGQPMVEVPTLKPLSE-- 286
QY 123 LPETVVYPADVLFEGILVFYSGEI--RDMFHLRLVDVDDSDVRLSRVLDRRRDL 180
Db 287 --DQARFYPD--LTKGIEVLYQKIHRIKPSNLLVGBDGHKIDFGVSNFKGSD- 341
QY 181 EQLITQYTFVKPAF-----EEFCL 200
Db 342 -ALLSNVVG--TAFMAPESLSETRKIFSGKALDVAMAGVTLVFCVGGCPFMDERIMCL 398
QY 201 PTK-----KYADV-----IIPRGVDNMVAINIYOHIDILNGDICKMHRG--S 243
Db 399 HSKIKSQALEFPPOPIADIEDLKDLITMLDKNPESRIYVEIKILVMTIRKSGFNPFE 458
QY 244 NGRSVKRTFSEPGDHPGMLTSGKSHLESS 274
Db 459 GSRREKSLSPGN--LTKKPTRECESLS 486

RESULT 38
PCT-US00-05988-1372
; Sequence 1372, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: P101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1372
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US00-05988-1372

Query Match 4.5%; Score 65; DB 3; Length 327;
Best Local Similarity 25.0%; Pred. No. 12;
Matches 24; Conservative 15; Mismatches 33; Indels 24; Gaps 4;

QY 46 LIGONEVEORQKRVLLS---QDRFYVVLTAQKAKALKGQYN---FDHDAFD----- 93
Db 136 LFGSGPAERKERLNILSVGTALKTKKODESKSKSKKEVQQTWYHEGPNLSLKVARLW 195
QY 94 --NDLMHRTLNKNIVEGKTEVEPTVDFVTHSRPLPETT 127
Db 196 IANYSLPRAMKRLSEAR-----LHKEIPETT 221

RESULT 39
US-09-488-725A-6870
; Sequence 6870, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20

```

```

; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 6870
; LENGTH: 522
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-6870

Query Match 4.5%; Score 65; DB 1; Length 522;
Best Local Similarity 24.9%; Pred. No. 22;
Matches 48; Conservative 21; Mismatches 56; Indels 68; Gaps 11;

QY 112 VPTY-DEVTHSRLPETVVYPADVLFEGILV-FYSGEIRDM-----FHLRLFD- 159
Db 178 IPYRDWEMVGRYYEE--FPINLKTGEANLTQIYLQELADFIKQARHHPFLYMAVDA 234
QY 160 TSDVYLSRRVLDVVRGRDLEQILTYTTFFVKPAEERFCLPTKYADVLIIPGVNMA 219
Db 235 THAPVYASRKLFTSGRSGR-----YGDV--REIDD--S 264
QY 220 INLIYOHIDILNGD-----ICKMHRGSGNSRSY--KRTFSEPGDH----- 258
Db 265 IGLTIELDQLVHADVTFFVFTSDNGAALISAPEQSGSNPFLCGKQTTTEGGHREPALA 324
QY 259 --PGMLTSGKRSRSH 269
Db 325 WMPGHVTAQGVSH 337

RESULT 40
US-09-488-725A-6619
; Sequence 6619, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 6619
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-6619

Query Match 4.4%; Score 64; DB 1; Length 198;

```

	Query Match	4.4%	Score 64;	DB 3;	Length 272;	
	Best Local Similarity	21.8%	Pred No. 11;			
	Matches	31;	Conservative	24;	Mismatches	53; Indels 34; Gaps 6
QY	12 PAPEADPHRHPFLIGVSGTASGKST--VCSEKIMELLIGONEVEORQRKVLLISQDREY	68				
Dp	1 PAPA-----HVGNGPGDAAPAAATGAATAAASLTAAAGSDAEAKVLATLVGLTVKMF	53				
QY	69 KYLTLAEQAALKKGQYNF-DHPDAFDNDLMERT-----LKNIYEKTVETPYDF	117				
Dp	54 NV-----RMNGYGFINRDITDEDFVHQTAIKNNPRKYLSVSGGETVE---EDV	100				
QY	118 VTHSRLPETVVYPADVILFEQ	119				
Dp	101 VEGEKGAAEAANYTGPDGVPEEG	122				

	Query Match	4.4%;	Score 64;	DB 1;	Length 337;	
	Best Local Similarity	24.7%;	Pred. No. 15;			
	Matches	43;	Conservative	19;	Mismatches	48;
					Indels	64;
					Gaps	9
Cy	130 YPADVVLFEGLIV-FYSGEIRDM-----FHILFVD-TDSQVLSRRLVDVRGR	178				
	: : :	:	:	:	:	:
Db	9 FPIMLKTGEANLTQIYLQDALDFIKQRGRHHPFLYMAVDATHAEVYASKPFLGTSQGR	68				
Cy	179 DLEQLITOTTFFVKPAFEFECLPTKKYADVLIIPKVDNMVAINLVQHIODLIND----	234				
	: : : : : :	:	:	:	:	:
Db	69 -----YDAV--REIDD-SIGKLELLQDIAVDNFTV	98				
Cy	235 -----ICKMHRGGSGNGRSY--KRTPSPRGH-----PGMLTSGSKRSX	269				
	: : : : :	:	:	:	:	:
Db	99 FFTSDNGAALLSAPBGGSGNGPFLCGKQTTEGTGGRRBPALAMWPHAVTAGOVSH	152				

```

RESULT 43
US-09-488-725A-6792
; Sequence 6792, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
;

```



```

; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 6792
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: mic_feature
; LOCATION: (1)...(346)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-6792

```

Query Match 4.4%; Score 63.5; DB 1; Length 346;

Best Local Similarity 27.4%; Pred. No.17; Mismatches 44; Indels 13; Gaps 4;

```

QY 182 QILQVYTFVFP--AFEEFCL--PTKKYADVIIIRGVNVAIINLIQHIQDILNDIC 236
DB 202 QPLASITTAGPBEAIIICCCMBGPAMDTSQIIITTSQDGNRV-----WKIVGCEIDVC 255
QY 237 KW--HRCGSNGRSYKRTFSEPDHHPMLTSGKSH 269
DB 256 SWTASRRGAPGSASKPRKPVGESEPCLESRRGRXH 290

```

RESULT 44

```

US-09-488-725A-2957
; Sequence 2957, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 2957
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2957

```

Query Match 4.4%; Score 63.5; DB 1; Length 603;

Best Local Similarity 22.3%; Pred. No.35; Mismatches 67; Indels 49; Gaps 9;

```

QY 42 KIMELLQONEVEQR--QRKV---ILSDRFYKVLTAQOKAKALKGQYNFDHPDAFNDL 96
DB 421 KOLEMLTDPVSQOINPRNTIDTKDYSTRHLYGVLSGENKKEL-----FL 466
QY 97 MHTTLKNIYE-----GKTVEVPYTDFTYHSRLPETTVYVPADVLLFEG--ILVF 143
DB 467 THGNLEVAEKIKONISLVODQLAVSAQESHFSLSKRNKDVMICD---TLYGGNQLL 523
QY 144 YSOEIRDMFHL-----RLFVDTSDVRLSRVLRDVRGRGDEQLITQ--YTFPVK 192

```

DB 524 SDQELTEQFHKVESQNLKLNHLITDILADVKTXRKTLAN---NKLHOMEREFFVYVFLK 578

RESULT 45

```

US-09-488-725A-6529
; Sequence 6529, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_fl_genes_b Versions 1.0
; SEQ ID NO 6529
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-6529

```

Query Match 4.4%; Score 63.5; DB 1; Length 617;

Best Local Similarity 22.3%; Pred. No.36; Mismatches 67; Indels 49; Gaps 9;

```

QY 42 KIMELLQONEVEQR--QRKV---ILSDRFYKVLTAQOKAKALKGQYNFDHPDAFNDL 96
DB 435 KOLEMLTDPVSQOINPRNTIDTKDYSTRHLYGVLSGENKKEL-----FL 480
QY 97 MHTTLKNIYE-----GKTVEVPYTDFTYHSRLPETTVYVPADVLLFEG--ILVF 143
DB 481 THGNLEVAEKIKONISLVODQLAVSAQESHFSLSKRNKDVMICD---TLYGGNQLL 537
QY 144 YSOEIRDMFHL-----RLFVDTSDVRLSRVLRDVRGRGDEQLITQ--YTFPVK 192
DB 538 SDQELTEQFHKVESQNLKLNHLITDILADVKTXRKTLAN---NKLHOMEREFFVYVFLK 592

```

Search completed: December 12, 2003, 11:18:12

Job time : 8 secs





```

us-09-896-522-3 (1-834) x US-09-488-725A-2647 (1-277)

QY 1 ATGGCTTCGGCGGAGGCGAAGACTGCGAGAGCCCGCGGAGCGGACCGTCCGAC 60
Db 1 MetAlaserIaGlyGluAspCysGluSerProAlaProGluIaAspArgProHis 20
QY 61 CAGGGGCCCTCTCTGATAGGGGTAGCGGCGGCACTGCGACGGGAAAGTGCACCTGTCT 120
Db 21 GlnArgProPheLeuIleGlyValSerGlyValThrAlaSerGlyLysSerThrValCys 40
QY 121 GAGAAATCATGAGTGTCTGGGACAGAACAGAGGTGAAACAGCGGACGCGAAGGTGCTC 180
Db 41 GluIleMetGluLeuLeuGlyGlnAsnGluValGluGlnArgGlnArgValVal 60
QY 181 ATCTGAGCCGAGACAGGTTCTACAGAGTCTTGAACGCGACAGACGAGGCGGACCTTG 240
Db 61 IleuSerGlnAspArgPheThrLysValLeuThrAlaGluGlnLysAlaLysAlaLeu 80
QY 241 AAAGGACGATCAATTTTGAACCATCCAGATGCGCTTGTATGATTTGATGACAGGACT 300
Db 81 LysGlyGlnIlyrAsnPheAspHisProAspAlaPheAspAsnLeuMetHisArgThr 100
QY 301 CTGAAGAACATCTGAGGCGCAAAACGCTGAGAGTGCAGACTATGATTTTGTGACACAC 360
Db 101 LeuLysAsnIleValGluGlyLysThrValGluValProThrIlyrAspPheValThrHis 120
QY 361 TCAAGTTACCAAGACCAAGCGTGTCTACCTTGGCGACGTGTCTGTGAGGCGATC 420
Db 121 SerArgLeuProGluThrValValIlyrProAlaAspValIleuPheGluGlyIle 140
QY 421 TTGGTGTCTACAGCAGAGATCCGGGACATGTTCCACCTGCGCTTGTGTGACACCC 480
Db 141 LeuValPheIlyrSerGlnIleGlnIleArgAspMetPheHisLeuArgLeuPheValAspThr 160
QY 481 GACTCCGACGTCAAGGCTGTCTCGAAGAGTTCTCCGGAAGTGCAGCGGACGAGGACCTG 540
Db 161 AsperAspValAlaGluSerArgArgValLeuArgAspValAlaArgGlyAlaArgPhe 180
QY 541 GAGCAGATTCTGACGACATCAACACTTGTGAAGCCGCGCTTGCAGAGATTCTGCTTG 600
Db 181 GluGlnIleLeuThrGlnIlyrThrThrPheValLysProAlaPheGluGluPheCysLeu 200
QY 601 CCGCAAGAGATGACCGATGATGATCATCCACAGAGAGTGAACAATGAGTGGCCATC 660
Db 201 ProThrLysLysIlyrAlaAspValIleIleProArgGlyValAspAsnMetValAlaIle 220
QY 661 AACCTGATCTGACGACATCCAGAGACATCTGATGAGTGAATCTGCAAAATGGCACCGA 720
Db 221 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysLysThrHisArg 240
QY 721 GAGAGGTCATAGGCGGAGCTACAGCGGACCTTTTCTGAGCCAGGAGGACACCTGGG 780
Db 241 GlyLysSerAsnGlyArgSerIlyrLysArgThrPheSerGlnProGlyAspHisProGly 260
QY 781 ATGCTGACCTTGGCAACGCTCACTTTGGAGTGCACAGACAGACCCAC 831
Db 261 MetLeuThrSerGlyLysArgSerHisLeuGluSerSerArgProHis 277

RESULT 2
US-09-488-725A-6219
; Sequence 6219, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20

; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc FL_Versions 1.0
; SEQ ID NO 6219
; LENGTH: 286
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-488-725A-6219

Alignment Scores:
Pred. No.: 1:46e-30 Length: 296
Score: 1450.00 Matches: 277
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 93.23% Indels: 0
DB: 1 Gaps: 0

us-09-896-522-3 (1-834) x US-09-488-725A-6219 (1-296)

QY 1 ATGGCTTCGGCGGAGGCGAAGACTGCGAGAGCCCGCGGAGCGGACCGTCCGAC 60
Db 20 MetAlaserIaGlyGluAspCysGluSerProAlaProGluIaAspArgProHis 39
QY 61 CAGGGGCCCTCTCTGATAGGGGTAGCGGCGGCACTGCGACGGGAAAGTGCACCTGTCT 120
Db 40 GlnArgProPheLeuIleGlyValSerGlyValThrAlaSerGlyLysSerThrValCys 59
QY 121 GAGAAATCATGAGTGTCTGGGACAGAACAGAGGTGAAACAGCGGACGCGAAGGTGCTC 180
Db 60 GluIleMetGluLeuLeuGlyGlnAsnGluValGluGlnArgGlnArgValVal 79
QY 181 ATCTGAGCCGAGACAGGTTCTACAGAGTCTTGAACGCGACAGACGAGGCGGACCTTG 240
Db 80 IleuSerGlnAspArgPheThrLysValLeuThrAlaGluGlnLysAlaLysAlaLeu 99
QY 241 AAAGGACGATCAATTTTGAACCATCCAGATGCGCTTGTATGATTTGATGACAGGACT 300
Db 100 LysGlyGlnIlyrAsnPheAspHisProAspAlaPheAspAsnLeuMetHisArgThr 119
QY 301 CTGAAGAACATCTGAGGCGCAAAACGCTGAGAGTGCAGACTATGATTTTGTGACACAC 360
Db 120 LeuLysAsnIleValGluGlyLysThrValGluValProThrIlyrAspPheValThrHis 139
QY 361 TCAAGTTACCAAGACCAAGCGTGTCTACCTTGGCGACGTGTCTGTGAGGCGATC 420
Db 140 SerArgLeuProGluThrValValIlyrProAlaAspValIleuPheGluGlyIle 159
QY 421 TTGGTGTCTACAGCAGAGATCCGGGACATGTTCCACTGCGCTTGTGTGACACACC 480
Db 160 LeuValPheIlyrSerGlnIleArgAspMetPheHisLeuArgLeuPheValAspThr 179
QY 481 GACTCCGACGTCAAGGCTGTCTCGAAGAGTCTCCGGGACGTGCGGACGAGGAGGACTG 540
Db 180 AsperAspValAlaGluSerArgArgValLeuArgAspValAlaArgGlyAlaArgPhe 199
QY 541 GAGCAGATTCTGACGACATCCACACTTGTGAAGCGGCGCTTGCAGAGATTCTGCTTG 600
Db 200 GluGlnIleLeuThrGlnIlyrThrThrPheValLysProAlaPheGluGluPheCysLeu 219
QY 601 CCGCAAGAGATGATGCGGATGATGATATCCACAGAGAGTGAACAATGAGTGGCCATC 660
Db 220 ProThrLysLysIlyrAlaAspValIleIleProArgGlyAlaAspAsnMetValAlaIle 239
QY 661 AACCTGATCTGACGACATCCAGAGACATCTGATGAGTGAATGATCTGCAAAATGGCACCGA 720

```

```

Db      240 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysIleStrpHisArg 259
QY      721 GGAGGTCCTCAATGGCGGAGCTACAGCGAAGCTTTTCTGAGCCAGGGAGACCTTGGG 780
Db      260 GlyGlySerAsnGlyAspSerTyrLysArgThrPheSerGluProGlyAspHisProGly 279
QY      781 ATCTGACCTCTGGCAAAACGGTCACTTTGAGTCCAGAGGAGACCCAC 831
Db      280 MetLeuThrSerGlyLysArgSerHisLeuGluSerSerArgProHis 296

RESULT 3
US-09-536-647-2
; Sequence 2, Application US/09536647
; Patent No. 6579708
; GENERAL INFORMATION:
; APPLICANT: Ho, Yen Sen
; APPLICANT: Johnson, Randall
; TITLE OF INVENTION: No. 6579708e1 Human Uridine Kinase
; FILE REFERENCE: GP50020
; CURRENT APPLICATION NUMBER: US/09/536,647
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 260
; TYPE: PRF
; ORGANISM: Human
US-09-536-647-2

Alignment Scores:
Pred. No.: 2,06e-28 Length: 260
Score: 1353.00 Matches: 260
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 87.64% Indels: 0
Gaps: 0

us-09-896-522-3 (1-834) x US-09-536-647-2 (1-260)
QY      1 ATGGCTTCGGCGGAGCGGAGAACTGCGAGAGCCCGCGCGGAGCGGACCGTCCGCAC 60
Db      1 MetAlaSerAlaGlyGlyLysArgCysGluSerProAlaProGluAlaAspArgProHis 20
QY      61 CAGCGGCCCTTCTCTGTAAGGGGTGAGCGGCGGCACTGCCAGCGGAGAAAGTGCACCGTGTCT 120
Db      21 GlnArgProPheLeuIleGlyValSerGlyThrAlaSerGlyLysSerThrValCys 40
QY      121 GAGAAATCATGAGTGTCTGGGAGAGAAAGAGTGGAGAGCGGCGAGCGGAGGTGTCT 180
Db      41 GlnLysIleMetCyluLeuLeuGlnGlnAsnGluValGlnGlnArgGlnArgLysValVal 60
QY      181 ATCTTGAGCCAGAGAGGTTCTTCAAGAGTCTTGACGCGCAGAGAGAGGCGGAGGCTTG 240
Db      61 IleLeuSerGlnAspArgPheTyrLysValLeuThrAlaGluGlnLysAlaLysAlaLeu 80
QY      241 AAAGGACAGTACAATTTTGAACCATCCAGATGCTTGATATGATTTGATGCACAGACT 300
Db      81 LysGlyGlnTyrAsnHisPheAspHisProAspAlaPheAspAsnAspLeuMetHisArgThr 100
QY      301 CTGAAGAATCATGTGAGAGGCAAAACGGTGGAGTGGCGGACCTATGATTTTGACACAC 360
Db      101 LeuLysAsnIleValGlnGlyLysThrValGlnValProThrTyrAspPheValThrHis 120
QY      361 TCAGAGTTACAGAGACCAACGAGTGTCTACCTGCGGACGAGTGTCTGTTTGAAGGCATC 420
Db      121 SerArgLeuProGluThrThrValValTyrProAlaAspValValLeuPheGluGlyLe 140
QY      421 TTGGTGTTCCTACAGCGAGAGATCCGGGACATGTTCCACTGCGCTCTTCTGTGACACC 480
Db      141 LeuValPheTyrSerGlnGlnLysThrValGlnValProThrTyrAspPheValThrHis 160
QY      481 GACTCGACGTACAGGTGTCTCGAAGAGTTCTCCGGGACGTGGCGGAGGAGGACCTG 540

```

```

Db      161 AspSerAspValArgLeuSerArgValLeuArgAspValArgGlyArgAspLeu 180
QY      541 GAGCAATTTGACGACGATACACCTCTTGTAAGCGGCGCTTGGAGATTCTGCTG 600
Db      181 GluGlnIleLeuThrGlnTyrThrThrPheValLysProAlaPheGluGluPheCysLeu 200
QY      601 CCGAAGAAAGATGATCCGATGTGATCATCCGACGAGAGTGGACATATGATGTCATC 660
Db      201 ProThrLysTyrThrAlaAspValIleIleProArgGlyValAspAsnMetValAlaIle 220
QY      661 AACCTGATCGTGACAGACATCCAGACATTTGATATGATGATTCGAATGCGACCGA 720
Db      221 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlyAspIleCysIleStrpHisArg 240
QY      721 GGAGGTCCTCAATGGCGGAGCTACAGCGAAGCTTTTCTGAGCCAGGGAGACCTTGGG 780
Db      241 GlyGlySerAsnGlyAspSerTyrLysArgThrPheSerGluProGlyAspHisProGly 260

RESULT 4
US-09-536-647-3
; Sequence 3, Application US/09536647
; Patent No. 6579708
; GENERAL INFORMATION:
; APPLICANT: Ho, Yen Sen
; APPLICANT: Johnson, Randall
; TITLE OF INVENTION: No. 6579708e1 Human Uridine Kinase
; FILE REFERENCE: GP50020
; CURRENT APPLICATION NUMBER: US/09/536,647
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 277
; TYPE: PRF
; ORGANISM: Human
US-09-536-647-3

Alignment Scores:
Pred. No.: 2,33e-27 Length: 277
Score: 1325.00 Matches: 254
Percent Similarity: 95.67% Conservative: 11
Best Local Similarity: 91.70% Mismatches: 12
Query Match: 85.19% Indels: 0
Gaps: 0

us-09-896-522-3 (1-834) x US-09-536-647-3 (1-277)
QY      1 ATGGCTTCGGCGGAGCGGAGAACTGCGAGAGCCCGCGCGGAGCGGACCGTCCGCAC 60
Db      1 MetAlaSerAlaGlyGlyLysArgCysGluSerGluSerAlaAlaProGluAlaAspArgProGln 20
QY      61 CAGCGGCCCTTCTCTGTAAGGGGTGAGCGGCGGCACTGCCAGCGGAGAAAGTGCACCGTGTCT 120
Db      21 ProArgProPheLeuIleGlyValSerGlyThrAlaSerGlyLysSerThrValCys 40
QY      121 GAGAAATCATGAGTGTCTGGGAGAGAAAGAGTGGAGAGCGGCGAGCGGAGGTGTCT 180
Db      41 GlnLysIleMetCyluLeuLeuGlnGlnAsnGluValAspArgArgGlnArgLysValLeuVal 60
QY      181 ATCTTGAGCCAGAGAGGTTCTTCAAGAGTCTTGACGCGCAGAGAGAGGCGGAGGCTTG 240
Db      61 IleLeuSerGlnAspArgPheTyrLysValLeuThrAlaGluGlnLysAlaLysAlaLeu 80
QY      241 AAAGGACAGTACAATTTTGAACCATCCAGATGCTTGATATGATTTGATGCACAGACT 300
Db      81 LysGlyGlnTyrAsnHisPheAspHisProAspAlaPheAspAsnAspLeuMetHisArgThr 100
QY      301 CTGAAGAATCATGTGAGAGGCAAAACGGTGGAGTGGCGGACCTATGATTTTGACACAC 360
Db      101 LeuLysAsnIleValGlnGlyLysThrValGlnValProThrTyrAspPheValThrHis 120
QY      361 TCAGAGTTACAGAGACCAACGAGTGTCTACCTGCGGACGAGTGTCTGTTTGAAGGCATC 420

```

```

Db      121 SerArgLeuProGluThrValValValProAlaAspValValLeuPheGluGlyIle 140
Qy      421 TTGGTGTCTTACACCGAGATCCGGACATGTTCCACCTGCGCTCTTGAGACACC 480
Db      141 LeuValPheYrThrGlnGlnIleArgAspMetPheHisLeuArgLeuPheValAspThr 160
Qy      481 GACTCCGACGTCAGGCTGTCTCGAAGAGTTCTCCGGACCGCCCGAGGAGGAGACTG 540
Db      161 AspSerAspValArgLeuSerArgArgValLeuArgAspValGlnArgGlyArgAspLeu 180
Qy      541 GAGAGATTCTGACGACGATACACACCTTCGTAAGCCGCGCTTCGAGAGATTGCTGCTG 600
Db      181 GluGlnIleLeuThrGlnIleYrThrAlaPheValIleProAlaPheGluGlnPheCysLeu 200
Qy      601 CCGACAAAGAGTATGCCGATGTATCATCCACGAGAGTGAACAATATGTTGCCATC 660
Db      201 ProThrIysIysYrAlaAspValIleIleProArgGlyValAspAsnMetValAlaIle 220
Qy      661 AACCTGATCGTCGACGACATCCAGACATTTGTAATGTGACATCTGCMAATGGCACCGA 720
Db      221 AsnLeuIleValGlnHisIleGlnAspIleLeuAsnGlnAspLeuCysAlaArgHisArg 240
Qy      721 GGAGGTCCTCAATGGCGGAGCTACAGCGGACCTTTTCTGAGCCGAGGAGACACCTGGG 780
Db      241 GlyIysProAsnGlnArgAsnHisIleYrArgThrPheProGluProGlyAspHisProGly 260
Qy      781 ATGCTGACCTCTGCGAAACGGTCACTTTGGAGTTCAGACGACAGACCCAC 831
Db      261 ValLeuAlaThrGlyIysArgSerHisLeuGlnIleSerSerArgProHis 277

```

RESULT 5  
US-09-488-725A-1839  
Sequence 1839, Application US/09488725A

GENERAL INFORMATION:  
APPLICANT: Hyseq Inc  
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
FILE REFERENCE: 784FLPCT  
CURRENT APPLICATION NUMBER: US/09/488,725A  
CURRENT FILING DATE: 2000-12-22  
PRIOR APPLICATION NUMBER: US/09/488,725  
PRIOR FILING DATE: 2000-01-21  
PRIOR APPLICATION NUMBER: US09/552,317  
PRIOR FILING DATE: 2000-04-25  
PRIOR APPLICATION NUMBER: US09/598,042  
PRIOR FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: US09/620,312  
PRIOR FILING DATE: 2000-07-19  
PRIOR APPLICATION NUMBER: US09/653,450  
PRIOR FILING DATE: 2000-08-31  
PRIOR APPLICATION NUMBER: US09/662,191  
PRIOR FILING DATE: 2000-09-14  
PRIOR APPLICATION NUMBER: US09/693,036  
PRIOR FILING DATE: 2000-10-19  
PRIOR APPLICATION NUMBER: US09/727,344  
PRIOR FILING DATE: 2000-11-29  
NUMBER OF SEQ ID NOS: 7144  
SOFTWARE: pt\_fl\_genes\_b Versions 1.0  
SEQ ID NO 1839  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-488-725A-1839

Alignment Scores:  
Pred. No.: 8,06e-18 Length: 261  
Score: 957.80 Matches: 190  
Percent Similarity: 70.00% Conservative: 27  
Best Local Similarity: 61.29% Mismatches: 31  
Query Match: 61.58% Indels: 62  
DB: 1 Gaps: 1

us-09-896-522-3 (1-834) x US-09-488-725A-1839 (1-261)

```

Qy      27 CGAAGCCCCCGCGCGGACGACCGTCCGACACCGCGCCCTTCGTATAGGGGTAG 86
Db      13 GlnGlnProAsn--GlyGly-----GluProPheLeuIleGlyAlaSe 26
Qy      87 CGCGCGCACTCCGACGCGGAGAGTGCACCGTGTGTGAGAAAGATCATGAGTGTGGACA 146
Db      26 rGlyGlyThrAlaSerGlyIysSerSerValCysAlaIleValGlnLeuGlyGly 46
Qy      147 GAAAGAGGTGAAACAGCGCGACCGGAAAGGTGTTCATCTTCAGCCAGGACAGGTTTCMA 206
Db      46 nAsnGlnValAspTyrArgGlnIysGlnValIleLeuSerGlnAspSerPheYrAr 66
Qy      207 GGTCTCGACGCGACGAGAGAGGACCAAGGCTTGAAGAAGACATGATTTGACCATCC 266
Db      66 gValIleuThrSerGlnGlnIysAlaIysAlaLeuIysGlyGlnPheAsnPheAspHis 86
Qy      267 AGATGCTTGTATATGATTTGATGACACGACTGTGAGACATCGTGTGAGGGCAAAAC 326
Db      86 oAspAlaPheAspAsnGlnLeuIleLeuYsrThrLeuYsgIleThrGlnGlyYsr 106
Qy      327 GGTGAGAGTCCGACCTATGATTTTGTGACACTCAAGSTTACAGACACCGTGTGT 386
Db      106 rValGlnIleProValTyrAspPheValSerHisSerArgIysGlnGlnThrVal 126
Qy      387 CTACCCCTGCGGAGAGTGTGTGTTGAGGACATCTGTGTCTTACAGCCAGGAGATCCG 446
Db      126 IYrProAlaAspValValLeuPheGlnGlyIleLeuAlaPheYrSerGlnIleValAr 146
Qy      447 GGAATGTTCCACCTGCGCTCTTGTGTGACACGACTCCGAGTCAAGCTGTCTGAG 506
Db      146 gAspLeuPheGlnMetIysLeuPheValAspThrAspAlaAspThrArgLeuSerArgAr 166
Qy      507 AGTTCTCCGAGACTG---CGCGAGGAGGAGACTTGAACAATTTGACGACATAC 563
Db      166 gValIleArgAspIleSerGlnArgIysArgAspLeuGlnIleLeuSerGlnIyr 186
Qy      564 CACCTTGTGAGACCGGCGCTTGTGAGAGTCTGCTGCGGACAAAGAGTCCGAGTGT 623
Db      186 eThrPheValIysProAlaPheGlnGlnIysPheCysLeuProThrIysYsrAlaAspVa 206
Qy      624 GATCATCCACGAGAGTGTGACATATGTTGCCATCAACCTGATCGTGTGAGACATCCA 683
Db      206 IileIleProArgGlyAlaAspAsnLeuValAlaIleAsnLeuIleValGlnHisIleG 226
Qy      684 GACATTTGAAATGTGACATCTGCAAATGGACCGAGAGGTTCCATGTGGCGAGCTA 743
Db      226 nAspIleLeuAsnGly-----GlyProSerIysArgGlnTr 238
Qy      744 CAAGCGACCTTTTGTGAGCCAGGAGACACACCTGAGATGCTGACCTGTGCAACGGTGC 803
Db      238 hrAsnGly---CysLeuAsn-----GlyYrThrProSerArgIysArgG 252
Qy      804 ACATTTGAGTCCAGCAGACAGACCCAC 831
Db      252 nAlaSerGlnSerSerArgProHis 261

```

RESULT 6  
PCT-US00-05988-1160  
Sequence 1160, Application PC/TUS0005988  
GENERAL INFORMATION:  
APPLICANT: Craig Rosen,  
FILE REFERENCE: PA101PCT  
CURRENT APPLICATION NUMBER: PCT/US00/05988  
CURRENT FILING DATE: 2000-03-08  
EARLIER APPLICATION NUMBER: 60/124,270  
EARLIER FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1160  
LENGTH: 337

```

TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (38)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (46)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (155)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
FEATURE:
NAME/KEY: SITE
LOCATION: (169)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PCT-US00-05988-1160

Alignment Scores:
Pred. No.: 5.63e-17 Length: 337
Score: 934.80 Matches: 194
Percent Similarity: 64.60% Conservative: 25
Best Local Similarity: 57.23% Mismatches: 38
Query Match: 60.10% Indels: 82
DB: 3 Gaps: 2

us-09-896-522-3 (1-834) x PCT-US00-05988-1160 (1-337)
QY 4 GCTTCGCGGAGCGGAGCGGAGCTGCGA----- 29
Db 56 Alaglylaaglygylgylu-----ArglaaserValargThnrglySerGlyArgArglyg 74
QY 30 -----GAGCCCGCGCGGAGCGCGAC 51
Db 74 lvalaenhtsglyArgglylgnarGalaaPProalaglupro-----Proalagl 92
QY 52 CGTCCGCGAGCGGCGCTTCGATAGGGGTGAGCGCGCGGACCTGCGAGCGGGAAGTCG 111
Db 93 Arg-Arg---ArglaaleuProtyrArgArghts-GlyglyThralaSerGlyLysSer 110
QY 112 ACCGTGTGAGAAATCATGAGATTGCTGGGACAGACAGAGAGAGTGAACCGCGGACGCG 171
Db 111 SerValCysAlaAlaYstleValGlnleuDeuglyGlnmenGlnuValaPtyrArgGlnLys 130
QY 172 AAGGTGTCTCTGAGCGAGAGAGAGAGTCTTACAGAGTCTTGAACGCGAGAGAGAGCGC 231
Db 131 GlnValValilleuSerGlnaPserPheTyrrArgValleuThrSerGlnGlnLysAla 150
QY 232 AAGGCTTGAAGAGACATGATTTGACCATTCAGATGCTTGTATGATTTGATG 291
Db 151 lvalaaleuLys**GlnPheAsnPheAsPheAsPheAsPheAsPheAsPheAsPheAsPhe 170
QY 292 CACAGAGCTGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 351
Db 171 leuLysThrleuLysGlnleuThnrglyLysThrValGlnleuProvalTyrrAspPhe 190
QY 352 GTGACACACTCAAGATTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
Db 191 ValSerHisSerArgLysGlnGlnThValThValTyrrProalaaPValleuPhe 210
QY 412 GAGGAGATCTTGTGTCTTACAGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 471
Db 211 GlnGlylleuAlaPheTyrrSerGlnGlnuValArgAspLeuPheGlnMetLysleuPhe 230
QY 472 GTGAGACACGAGCTCGAGGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 528
Db 231 ValAspThrAspAlaAspThrArgLysSerArgArgValleuArgAspIleSerGlnArg 250
QY 529 GAGAGAGAGCTGAGAGAGATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 588
Db 251 GlyArgAspLeuGlnGlnleuSerGlnTyrrIleThrPheValLysProalaaPheGln 270

```

```

QY 589 GAGTTCGCTCGCGAGACAAAGATATCCGATGTGATCATCCAGAGAGTGCACAT 648
Db 271 GlnPheCysleuProtnrLysTyrrAlaAspValilleuProalaglAlaAspAsn 290
QY 649 ATGTTGCCATCAACTGATCTGTCAGACATCCAGAGAGAGAGAGAGAGAGAGAG 708
Db 291 leuValAlaIleuLeuIleValGlnIleIleGlnAspIleleuAsnGly----- 307
QY 709 AATGCGACGAGAGAGGTCATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768
Db 308 -----GlyProSerLysArgGlnThrAsnGly---CysleuAsn----- 319
QY 769 GACACCCGTGGAGATGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 828
Db 320 -----GlyTyrrThrProSerArgLysArgGlnAlaSerGlnSerSerArgPro 336
QY 829 CAC 831
Db 337 His 337

RESULT 7
US-09-488-725A-5411
Sequence 5411, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784PLCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
PRIORITY FILING DATE: 2000-12-22
PRIORITY FILING DATE: US/09/488, 725
PRIORITY FILING DATE: 2000-01-21
PRIORITY FILING DATE: US09/552, 317
PRIORITY FILING DATE: 2000-04-25
PRIORITY FILING DATE: US09/598, 042
PRIORITY FILING DATE: 2000-06-20
PRIORITY FILING DATE: US09/620, 312
PRIORITY FILING DATE: 2000-07-19
PRIORITY FILING DATE: US09/653, 450
PRIORITY FILING DATE: 2000-08-31
PRIORITY FILING DATE: US09/662, 191
PRIORITY FILING DATE: 2000-09-14
PRIORITY FILING DATE: US09/693, 036
PRIORITY FILING DATE: 2000-10-19
PRIORITY FILING DATE: US09/727, 344
PRIORITY FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pt_Pl_genes_b Versions 1.0
SEQ ID NO 5411
LENGTH: 342
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-5411

Alignment Scores:
Pred. No.: 1.13e-16 Length: 335
Score: 923.00 Matches: 200
Percent Similarity: 59.52% Conservative: 25
Best Local Similarity: 52.91% Mismatches: 37
Query Match: 59.35% Indels: 118
DB: 1 Gaps: 6

us-09-896-522-3 (1-834) x US-09-488-725A-5411 (1-335)
QY 4 GCTTCGCGGAGCGGAGAG----- 23
Db 4 AlaAlaAlagly--ArgArglyAlaLeuGlySerPheGlyLysProSerProvalThnrg 23
QY 24 --CTGCGAGAGCGCGCGCGCGAGAGC-----GAGCGTCTCGACACGAGCGG----- 66
Db 23 lyeu--ArgAlaAlaArgArgArgArgThrArgProSerAlaProAlaProSerVa 42
QY 66 ----- 66

```

```

Db      42  IGLYCYSGLYYSARGARGGLUSERASPALAGLYALAGLYGLUARGALASERVALAR 62
QY      66  -----
Db      62  gThrGlySerGlyARgARgGlyGlyArgThrMetAlaGlyAspSerGluInThrLeuG1 82
QY      67  -----
Db      82  nAsnHiGlnGlnProAenGlyGlyGluProPheLeuIleGlyAlaSerGlyGlyThrAl 102
QY      99  CAGCGGGAAGTCGACCGGTGTGAGAAAGATCATCATGTTGCGGACAGAAAGAGTGA 158
Db      102  aSerGlyYSerSerValCySAlaGlyIleValGlnLeuLeuGlnManGluValAs 122
QY      159  ACAGCGGACGAGGAAAGGTGTGATCTTGAGCCAGAGCAGGTTCACAGGTCTGACGCG 218
Db      122  pTYrArgGlnYpsGlnValIleLeuSerGlnAspSerPheTYrArgValIleuThrSe 142
QY      219  AGAGCAGAAAGCCAGGCGCTTGAAAGACATGACAAATTTTGACATCCAGATGCTTTGA 278
Db      142  rGlnGlnYsAlaYsAlaLeuYsGlyGlnPheAsnPheAspHisProAspAlaPheAs 162
QY      279  TAATGATTTGATGACGAGCATCTGAGAGACATCGTGGAGGCAAAACGCTGAGGTGCC 338
Db      162  pAsnGlnLeuIleLeuYsThrLeuYsGlnIleThrGlnGlyYsThrValGlnIlePr 182
QY      339  GACCTATGATTTTGTGACACACTCAAGGTTACACAGACCAAGGTGTCTACCTCGCGA 398
Db      182  oValTYrAspPheValSerHisSerArgIleGluInThrValThrValTYrProAlaAs 202
QY      399  CGTGTCTTGTTTGAGGCGATCTGTGTCTTCAAGCCAGAG--ATCCGGACATGTT 455
Db      202  pValValLeuPheGlnGlyIleLeuAlaPheTYrSerGlnGluArgIleArgAspLeuPh 222
QY      456  CCACCTGCGCTCTTCGTGACACCGCATCCGACGTGCTGCTCGAAGATGTTCTCG 515
Db      222  eGlnMetYsLeuPheValAspThrAspAlaAspThrArgLeuSerArgValLeuY 242
QY      516  GAGACGTG--CGCCGAGGAGGAGACCTGAGACATGTCAGCATGACAC--ACCTT 569
Db      242  sAspIleSerGlnArgGlyArgAspLeuGlnIleLeuSerSerSerThrLeuArgPh 262
QY      570  CGTGAAGCGGCGCTTCGAGAGATTTGCTGCGGCAAAAGATTTGCCATGTGATAT 629
Db      262  eValYsProAlaPheGlnGluPheCysLeuProYsYsYrAlaAspValIleI 282
QY      630  CCCACGAGAGTGAATATGTTGATCATCACTCACTGCGACATCGACATCGAGACAT 689
Db      282  eProArgGlyAlaAspAsnArgValProIleAsnLeuIleValGlnHisIleGlnAspI 302
QY      690  TCTGATGATGATCATCTGCAATGAGACCGAGAGAGGTCCAAATGGCGAGACTACAG 749
Db      302  eLeuAsnGly-----GlyProSerAsnArgInThrAenG 314
QY      750  GACCTTTTCTGAGCCAGGGGACCACTCGGATGCTGACCTTGCGAAACGTCACATT 809
Db      314  IY--CysLeuAsn-----GlyTYrThrProSerArgYsArgGlnAlaSe 328
QY      810  GGAGTCAGACAGACACCCAC 831
Db      328  rGlnSerSerSerArgProHis 335

```

```

PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pc FL_genes_b Versions 1.0
SEQ ID NO: 2188
LENGTH: 4619
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-2188

Alignment Scores:
Pred. No.: 231 Length: 4618
Score: 314.80 Matches: 121
Percent Similarity: 17.82% Conservative: 15
Best Local Similarity: 15.86% Mismatches: 75
Query Match: 20.21% Indels: 552
Gaps: 18
DB:

us-09-896-522-3 (1-834) x US-09-488-725A-2188 (1-4618)
QY      832  AGTGGGTCTGTGC----- 818
Db      121  ThrGlyGlyCysCysProAlaSerAlaGlnAlaGlyThrGlyGlnThrAspValArgThr 140
QY      817  -----TGACCTCCAAATGTGACCGTTTGC 794
Db      141  LeuCysSerLeuHisGlyValPheAspLeuSerArgCysThr-----CysSer-----Cys 157
QY      793  CAGAGTCAGATCCAGAGGTGTCCCTGCTCAGAAAGTCCGCTTGTAGCTCCGCC 734
Db      158  Glu-----ProGlyTYrGly-----Gly-----ProThrCysSerAsp--P 169
QY      733  CATTTGAC-----CCTCT----- 720
Db      169  rOThrAspAlaGlnIleProProSerSerProProSerAlaSerGlySerCysProAspA 189
QY      719  -----CGTGCCTATTGC----- 707
Db      189  sPCysAsnAspGlnGlyArgCysValArgGlyArgCys--ValCysPheProGlyTYrThr 208
QY      706  -----AGATGTCACCATTCAGATGCTCGA----- 680
Db      209  GlyProSerCysGlyTYrProSerCysPheProGlyAspCysGlnGlyArgGlyArgCysVal 228
QY      679  -----TGTGCTGACGATCAGT 662
Db      229  GlnGlyValCysValCysArgAlaGlyPheSerGlyProAspCysSerGlnArgSer--- 247
QY      661  TGAATGACACATATTGTCCACTCTGCTGGAGATGACATGCGCATCTTCTTGTG 602
Db      248  -----Cys-----ProArgGly-----CysSe 253
QY      601  GCAGCAGAACTCTTCAGAGCGCGCTTTCAGAGAGTGTGATCTGCGTCAATCTGCT 542
Db      253  rGln-----ArgGlyArgCys-----GlnGlyGly--ArgCysVal-----Cys 266
QY      541  CC-----AGTCCCTCCTCGGCGACGTCCCGA 512
Db      266  sProGlyTYrThrGlyAspAspCysGlyMetArgSerCysProArgGlyCysSerGlnA 286

```

```

RESULT 8
US-09-488-725A-2188
; Sequence 2188, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725

```



```

QY 511 GA-----ACTCTTCAGACAGCC 494
Db 286 rgglYargCySgluaSnglYargCySvalCySaenProglYrThrglYgluaSpcSg 306
QY 493 TGACGTGAGAGTGGTGTCCAGAGA-----467
Db 306 lYval-ArgSer---CysProarglYCySerSgluaRglYargCySlyAspRglYarg 324
QY 467 -----467
Db 325 CySvalCySaenProglYrThrglYgluaSpcSglYrThargSerCySProtrpAsp 344
QY 466 ---GGCGAGATGAGACATGT-----CCCGAGATCTCTGGC 434
Db 345 CySglYgluaRglYargCySvalAspRglYargCySvalCyStrpProglYrThrglY 364
QY 433 ---TGAGAACACCAAGATGCGCTCAACAGAACACAGTCGCGAGGTAGACACCG 380
Db 365 GluaSpcSerThrargThrcysProarg---AspCySarglYarglYarg-----C 382
QY 379 TGGTCTGTGTAACCTTGAGTGTCTC-----354
Db 382 YsgluaSrglY-----GlucylleCySaenRthrglYrSerSglYAspAspCySglYv 400
QY 354 -----354
Db 400 alargSerCySProglYAspCySaenRglYargCySgluaSrglYargCySvalC 420
QY 353 ---ACAAATCATAGGTGGGACCTTCACCGTTTGGCT-----317
Db 420 YstrpProglYrThrglYrThargSerArgala---CySProargAspCyS 438
QY 316 ---CCAGATGTCTTCAGAGTCTGTGCATCAATCATTTTCAAGGCATCTG 266
Db 439 ArgglYarglYarglYargCySgluaSnglYvalCySvalCySaen---Alagly--Tyr 455
QY 265 GATGTCATAATGTACTGTCTTCAAGGCT-----233
Db 456 SerSglYgluaSpcSglYargSerCySProglYAspCySarglYarglYargCyS 475
QY 232 ---TGGCTTCT-----GCT 221
Db 476 GluaSrglYargCySmetCyStrpProglYrThrglYrThargSerSglYrThargala 495
QY 220 CTGCGCTCAGACCTTGT-----203
Db 496 CySPro---GluaSpcSarglYarglYargCySvalAspRglYargCySvalCySaen 514
QY 203 -----203
Db 515 ProglYrThrglYgluaSpcSglYSerArgRglYargCySProglYAspCySarglYhls 534
QY 203 -----203
Db 535 GlYleuCySgluaSrglYvalCySvalCySaenRglYrThrglYgluaSpcSer 554
QY 202 ---AGAACTGTCTGTGCTGAGATGACCACTTCGCTCCGC-----162
Db 555 ThrargSerCySProglY---Gly-----CySarglYarglYgluaSyl 569
QY 162 -----162
Db 569 euAspRglYargCySvalCySgluaSrglYrThrglYgluaSpcSglYvalArglnc 589
QY 162 -----162
Db 589 YAspRglYargCySserSglYhlsGlyvalCySgluaSrglYvalCySleCyStrpSgluS 609
QY 161 -----TGTTCACCTCGTTCTGTCCAGAACCTCATGATCTTCTCAC 119
Db 609 lYrThrglYarglYargCySserlYargThrcysProSerAsn---Cy 624
QY 118 ACACGGGTGCA-----109

```

```

Db 624 SHSglYarglYargCySgluaRglYargCySleuCySaenProglYrThrglYpr 644
QY 108 -----CTCCCGCTGGAGTGGCGCGCTCACCCCTATCAGAGAG 68
Db 644 oThrcysAlaThrcysArgMetCySProala---AspCySArg-----G 657
QY 67 GCGCTGTGCTGAGACGCTGCGCTCCGCGCGGCGCTC-----30
Db 657 lYarg-----GlYargCySvalGlnGlyvalCySleuCyShlsvalGlyrGlyGlyG 675
QY 29 -----TCGAGTCTTCGCTCCGCGAGAGCC 3
Db 675 luaSpcSglYgluaRglYgluaRglYProProalaSerAla 686

RESULT 9
US-09-488-725A-3367
Sequence 3367, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US/09/488, 725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US09/552, 317
PRIORITY FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: US09/598, 042
PRIORITY FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: US09/620, 312
PRIORITY FILING DATE: 2000-07-19
PRIORITY APPLICATION NUMBER: US09/653, 450
PRIORITY FILING DATE: 2000-08-31
PRIORITY APPLICATION NUMBER: US09/662, 191
PRIORITY FILING DATE: 2000-09-14
PRIORITY APPLICATION NUMBER: US09/693, 036
PRIORITY FILING DATE: 2000-10-19
PRIORITY APPLICATION NUMBER: US09/727, 344
PRIORITY FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pc PL_genes_b Versions 1.0
SEQ ID NO 3367
LENGTH: 1455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-3367

Alignment Scores:
Pred. No.: 88.3 Length: 1454
Score: 291.40 Matches: 126
Percent Similarity: 16.60% Conservative: 33
Best Local Similarity: 13.15% Mismatches: 53
Query Match: 18.71% Indels: 746
DB: 1 Gaps: 18

us-09-896-522-3 (1-834) x us-09-488-725A-3367 (1-1454)
QY 825 TGTGCTGAGTCACTCAATGTGACCGTTTGGCCAGAGTCAAGATCCAGAGTGT-----770
Db 500 SerAla--Trp---ProglYleuLeuValProglYuaAlaAlaValSerSglYlYargA 518
QY 769 ---CCCTGTGCTCAGAAAAGGTGCTGTGAGCTCCGCCCATTTGAGACCTTCCTGGTGGCA 712
Db 518 rgProleu-----ProSerProAlaProPro-----ProProGln-LeuL 531
QY 711 TTTCGAGAGTCACTTCAGAA-----689
Db 531 euGlnAlaCySarglAProglYgluaRglYglYglYglYrTharglYvalAlaArgT 551
QY 688 -----T 688
Db 551 hrProProValAlgluMetSerSglYgluaRglYglYglYglYrThrc 571

```

```

QY 687 GTCTGATGTCGTCGACGATCAGTTGATGGCAACCATATTTCGACTCTCGTGGGAT 628
DB |||||
DB 571 yspProAlaValAlaAla-----GlySerArg-CysPro-GluArgGlyLeu 585
QY 627 GATCACAATCGGACATCTTCTTGTG----- 602
DB |||||
DB 585 uleuThr-----ThrThrValThrLeuGlnArgProValGluLeuAsnGlyGluArg 603
QY 601 -----GCAGGCGAGA- 593
DB 603 IuLeuValPheThrValValGluGluLeuSerLeuGlyAlaLeuAlaGlyAlaGlyArgP 623
QY 593 ----- 593
DB 623 roThrSerLeuAlaSerPheAspSerArgCysSerLeuArgAlaLeuAlaSerGlySerA 643
QY 592 -----ACTCTCGAAGGC 580
DB 643 rgProValSerIleIleSerSerIleAsnArgGluPheAspAlaIleThrSerGlnAlaP 663
QY 579 CGGCTTCAGAAGGTGTAAGTGGTCAGATCTGCT----- 542
DB 663 ro-----GluGlyGlyProLeu-----GluGlyAlaAlaIleArgAlaGlySerSerHisG 679
QY 542 ----- 542
DB 679 IySerSerIleSerSerIlePheSerGluValSerValCysThrAlaAspSerArgAsp 699
QY 542 ----- 542
DB 699 roThrProGlnProArgPheSerProAspSerIleAlaGlyLeuAspProGlyGlyProP 719
QY 542 ----- 542
DB 719 roAlaLeuAspGlySerLeuGlyAspGlySerSerGlyPheLeuGlyProAspArgProA 739
QY 541 -----CGAGTCCCTCCCTCGGC-----GCAC 520
DB 739 spSerProGlyProThrArgProCysProGlyGluValAlaAlaValAlaAspSerA 759
QY 519 GTCCCGAGAACTCTTCGAGACAGCGCTGACGTCGAGTGCACGAAAGCGCGAG 460
DB 759 rgProGly-----ArgGluProGlnAlaGly-----Pro-----SerA 770
QY 459 GTGAAACATGTCGCGATCTCTGCTGTAAACA-----CCAGATGCC 415
DB 770 gTrp-----AlaSerAlaAlaGlnThrIleHisSerSerLeuProArgLysP 786
QY 414 CTCAAACGAAACGACGTCGAGGGGTAGACACCGCTGCTCTGTAACTTGAAGTGT 355
DB 786 ro-----ArgThrAlaSerAla-----ThrThrArgVal-----Gly-----Cys 797
QY 354 CACAACATCATAGTGGCAGCTCCACCGTTTTCGCTTCA----- 314
DB 798 AlaArgLeu-----GlyGlnSer-----ProProGlyArgGlyGlyLeuPheG 812
QY 313 -----CGATGTTCTTCAGAG----- 299
DB 812 IuAspProTrpLeuLeuArgValGlyGlyCysAspThrGlnAlaAlaSerAlaGlyArgA 832
QY 298 -----TCCTGTG 292
DB 832 IaProSerProThrLeuGlySerProArgLeuProGlnAlaGlnValMetLeuAlaCysA 852
QY 291 CATCAATCATATTACAAAGCATCTGATGTCAAAATTTGACTGTC----- 245
DB 852 Ia-----GlnArgValValAspGly-----CysGluValAlaAlaArgAlaA 866
QY 245 ----- 245
DB 866 IaArgArgProGlnAlaValAlaArgIleProProLeuArgArgGlyAlaThrThrLeuG 886

```

```

QY 245 ----- 245
DB 886 IyValThrThrProAlaValSerTrpGlyAspAlaProThrGluValAlaCysSerG 906
QY 244 -----CTTT 241
DB 906 IySerLeuValaSerProThrSerIleValGlyLeuAlaProLysAlaGlyPheLeuP 926
QY 240 CAAGGCTTGCCCTTCGCTGCGTCCGACGACCTTGT-----A 202
DB 926 roArgProSerGlyAlaAlaProProAlaProProThrArgLysSerSerLeuGluAla 946
QY 201 GAACCTGTCTGCTGACGATGACCACT-----TCGCTG 166
DB 946 rgSerSerProAlaSerAla-----ProProHisValaValaAspProAlaArgValGlyAlaA 965
QY 165 CCGCTGTT----- 158
DB 965 IaAlaValLeuArgGlyGluGluProArgProSerSerArgAlaAspHisSerValP 985
QY 158 ----- 158
DB 985 roArgAlaThrSerSerLeuLysAlaArgAlaSerIleValGluAlaAlaHisArgLeuA 1005
QY 158 ----- 158
DB 1005 IaGlyHisAlaSerLeuGluArgTyrgLyuGlyLeuAlaHisSerSerIleGlyArgG 1025
QY 157 -----CCAGCTGCTTCTGTC-----CCAGCAACTTCAT 130
DB 1025 IuAlaProGlyArgProProArgAlaValaProLysLeuGlyValaProProSerSerPro- 1044
QY 129 GATCTTCTCACACGCTGCACCTCCCGCTGGACGTGCGC----- 89
DB 1045 -----ThrHisGlyProAlaProAla-----CysArgSerGlyAlaAlaLysAlaVal 1060
QY 89 ----- 89
DB 1060 aGlyAlaProLysProProValaGlyGlyGlyLysGlyArgGlyLeuValAlaGlyLys 1080
QY 88 -----CGCTCACCC- 80
DB 1080 eArgAlaLeuGlyProSerValIleLeuSerThrAlaSerValThrGlyArgSerProG 1100
QY 80 ----- 80
DB 1100 IyGlyProValaAlaGlyProArgAlaAlaProArgAlaGlyProSerValGlyAlaLysA 1120
QY 80 ----- 80
DB 1120 IaGlyArgGlyThrValMetGlyThrLysGlnAlaLeuArgAlaAlaHisSerArgValH 1140
QY 79 -----CTATCGAAGAGCGCGCTGTCGGAAGGTGCG----- 47
DB 1140 IsGluLeuSer-----AlaSerGlyAlaProGlyArgGlyGlySerSerTrpGlySerA 1158
QY 47 ----- 47
DB 1158 IaAspSerAspSerGlyHisAspSerGlyValaAsnValGlyGluGluArgProProThiG 1178
QY 47 ----- 47
DB 1178 IyProAlaLeuProSerProTySerIleValThrIaProArgArgProGlnArgTyS 1198
QY 46 -----CTTCGCGCGCGCG 34
DB 1198 eSerSerGlyHisGlySerAspAsnSerSerValLeuSerGlyGluLeuProProAlaMetG 1218
QY 33 GC----- 32
DB 1218 IyArgThrAlaLeuPheHisSerGlyGlySerSerGlyTyGlyLysLeuArgArgA 1238
QY 32 ----- 32

```





```

QY 382 -----CCGTGCTCTGGT----- 369
Db 560 LyeThrProAspPro--ValAsnGlyMetValHisValIleThrAspIleGlnValG 579
QY 368 -----AACCTTGAGTGTCTACAAATCATGCG----- 341
Db 579 LysArgIleAsnTyrSerCysThrThr-GlyHisArgLeuIleGlyHisSerSerAla 598
QY 340 -----TCGGCACCCTCCACCGCTTTGCG----- 320
Db 599 GluCysIleLeuSerGlyAsnAlaAlaHisIleTyrSerThrLysProProlIleCysGlnArg 618
QY 319 -----CCTCCA----- 314
Db 619 IleProCysGlyLeuProProThrIleAlaAsnGlyAspPheIleSerThrAsnArgGlu 638
QY 313 -----CGATGTTCTTCAAGATCC----- 296
Db 639 AsnPheHisTyrGlySerValIleThrTyrArgCysAsnProGlySerGlyArgLys 658
QY 295 -----TGTCATCAATCATCTTATCAA--GGC 271
Db 659 ValPheGluLeuValGlyGluProSerIleTyrCysThrSerAsnAspArgGlnValGly 678
QY 270 ATCTGG----- 265
Db 679 IleTyrSerGlyProAlaProGlnCysIleIleProAsnLysCysThrProProAsnVal 698
QY 265 ----- 265
Db 699 GluAsnGlyIleLeuValSerAspAsnArgSerLeuPheSerLeuAsnGlnValGlu 718
QY 264 -----ATGCTCAAAATTTGACTGCTCC 244
Db 719 PheArgCysGlnProGlyPheValMetLysGlyProArgArgValLys--CysGlnAlaL 738
QY 243 TTTCAGAGCCTTGAGCTTGTGCTGCGCTCAGAGACCTTGT--AGAAGCTGT-- 194
Db 738 euaAsnLys--TrrGluProGluLeuProSer-----CysSerArgValCysGlnProP 755
QY 193 -----CCTGGCT 187
Db 755 roProAspValLeuHisAlaGluArgThrGlnArgAspLysAspAsnPheSerProGly- 774
QY 186 CAGAGATGACCACTTCCGCTGCCGCG----- 162
Db 775 GlnGlu-ValPheTyrSerCysGluProGlyTyrAspLeuArgGlyAlaAlaSerMetAr 794
QY 162 ----- 162
Db 794 GlysThrProGlnGlyAspTyrSerProAlaAlaProThrCysGlnValLysSerCysAs 814
QY 162 ----- 162
Db 814 pAspPheMetGlyGlnLeuLeuAsnGlyArgValIleuPheProValAsnLeuGlnLeuG 834
QY 162 ----- 162
Db 834 yAlaLysValAspPheValCysAspGluGlyPheGlnLeuLysGlySerSerAlaSerTy 854
QY 161 -----TGTTCACCTTC 151
Db 854 rCysValIleuAlaGlyMetGluSerLeuThrPanserSerValProValCysGlnGlnI 874
QY 150 GTTCTGTCCAGACACTCATGATCTTTCACACACGGTGCAGTCTCCCGTGCAGTGGCC 91
Db 874 ePheCysProSer-----Pr 879
QY 90 GCGGCTCACCCCATCAGAAAGGCGGCTGTGCGAGCGTGGCT----- 44
Db 879 ofProValIlePro-AsnGlyArgHisIleThr-----GlyLysProLeuGlnValPheP 896
QY 43 -----CCGGGCGGCGGCTCT----- 29

```

```

Db 896 roPheGlyLysAlaValAsnTyrThrCysAspProHisProAspArgGlyThrSerPheA 916
QY 29 ----- 29
Db 916 sPheuIleGlyGluSerThrIleArgCysThrSerAspProGlnGlyAsnGlyValTrrs 936
QY 29 ----- 29
Db 936 erSerProAlaProArgCysGlyIleLeuGlnHisCysGlnAlaProAspHisPheLeuP 956
QY 29 ----- 29
Db 956 heAlaLysLeuLysThrGlnThrAsnAlaSerAspPheProIleGlyThrSerLeuLysT 976
QY 29 ----- 29
Db 976 yrrGluCysArgProGluTyrGlyArgProPheSerIleThrCysLeuAspAsnLeuV 996
QY 28 -----CGCAGTCTTGGCCTCCGCGCGAAGCCA 2
Db 996 aTrrPserSerProLysAspValCysLysArgLysSerCysLysThrProProAspPro 1015

RESULT 12
US-09-488-725A-5941
; Sequence 5941, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PL_FL_genes_b Versions 1.0
; SEQ ID NO 5941
; LENGTH: 2045
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5941

Alignment Scores:
Pred. No.: 336
Score: 280.10 Length: 2044
Percent Similarity: 13.58 Matches: 126
Best Local Similarity: 11.048 Conservative: 29
Query Match: 17.988 Mismatches: 69
DB: 1 Indels: 918
Gaps: 28

us-09-896-522-3 (1-834) x US-09-488-725A-5941 (1-2044)
QY 823 TGCTGC-----TGCACT 812
Db 27 CysCysGlyGlySerLeuLeuAlaValValIleuLeuAlaLeuProValAlaTrrp--G 46
QY 811 CCAATGTGACCGCTTGTGCAGAGAGTCCAGCANTCCAGGCTGCTCCCTGCTCAGAAAGG 752
Db 46 LysGlnCysAsn--AlaProGlu-----TrrPhe----- 54

```

```

QY      751 TCCGCTGTAGCTCCG-----CCCATTTGA----- 727
      |||
Db      55 -ProPheAlaArgProThrAsnLeuThrAspGluPheGluPheGlyThrTyrLe 74
QY      726 -----CCCTCCCGGTGGCCATTTC----- 707
      |||
Db      74 uAsnTyrGluCysArgProGlyTyrSerGlyArgProPheSerIle--IleCysLeuLys 93
QY      706 -----AGATGTCAACCATTCAGAAATG----- 686
      |||
Db      94 AsnSerValTrpThrGlyAlaLysAspArgCysArgArgLysSerCysArgAsnProPro 113
QY      686 ----- 686
Db      114 AspProValAsnGlyMetValHisValIleLysGlyIleGlnPheGlySerGlnIleLys 133
QY      686 ----- 686
Db      134 TyrSerCysThrLysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleSer 153
QY      686 ----- 686
Db      154 GlyAspThrValIleTrpAspAsnGluThrProIleCysAspArgIleProCysGlyLeu 173
QY      686 ----- 686
Db      174 ProProThrIleThrAsnGlyAspPheIleSerThrAsnArgGluAsnPheHisTyrGly 193
QY      685 -----CCTGATGTGTCGACAGATCA----- 665
      |||
Db      194 SerValValThrTyrArgCysAsnProGlySerGlyArgLysValPheGluLeuVal 213
QY      664 GGTGATGAGCAACA-----TATTGTCCACTCCTCGTGGATGATCAATCCAGCTACT 611
      |||
Db      214 Gly-----GluProSerIleTyrCys--ThrSerAsnAspArgGlnValGlyIleTr 230
QY      610 TCTTTGTCGACGC----- 596
      |||
Db      230 p-----SerGlyProAlaProGlnCysIleIleProAsnLysCysThrProProAsn 247
QY      596 ----- 596
Db      248 ValGluAsnGlyIleLeuValSerAspAsnArgSerLeuPheSerLeuAsnGluValVal 267
QY      595 -----AGAACTCCTCGAAGG-----CCGGCT 575
      |||
Db      268 GluPheArgCysGlnProGlyPheValMetLysGlyProArgArgValLysCysGlnAla 287
QY      574 TCACGAAGGTGG-----TGTACTGGGTGAGATCTGCTCCAGGTCC 533
      |||
Db      288 LeuAsnLysTrpGluProGluLeuProSerCysSer--ArgValCys--GlnProPr 305
QY      532 TCCCTCGGCG-----CACGTCCCGAGAACTCTTCGAGAC----- 498
      |||
Db      305 oProAspValLeuHis-AlaGluArgThrGlnArgAspLysAspAsnPheSerProGlyG 325
QY      497 -----AGCTGACGT 488
      |||
Db      325 InguValPheTyrSerCysGluProGlyTyrAspLeuArgGlyAlaAlaSerMet----- 343
QY      487 CGGAGTCCGCTGTCACGAAGAGCGCAGGTGGAATGCTCCGAGTCTCCGTGCTAGA 428
      |||
Db      344 -----ArgCysThrProGlnGly--AspTrpSer--ProAlaAlaProThrCysGlu 359
QY      428 ----- 428
Db      360 ValLysSerCysAspAspPheMetGlyGlnLeuLeuAsnGlyArgValLeuPheProVal 379
QY      428 ----- 428
Db      380 AsnLeuGlnLeuGlyAlaLysValAspPheValCysAspGluGlyPheGlnLeuLysGly 399

```

```

QY      428 ----- 428
Db      400 SerSerAlaSerTyrCysValLeuAlaGlyMetGluSerLeuTrpAsnSerSerValPro 419
QY      428 ----- 428
Db      420 ValCysGluGlnIlePheCysProSerProProValIleProAsnGlyArgHisThrGly 439
QY      428 ----- 428
Db      440 LysProLeuGluValPheProPheGlyLysAlaValAsnTyrThrCysAspProHisPro 459
QY      428 ----- 428
Db      460 AspArgGlyThrSerPheAspLeuIleGlyGluSerThrIleArgCysThrSerAspPro 479
QY      427 -----ACACCAAGATGC----- 416
      |||
Db      480 GlnGlyAsnGlyValTrpSerSerProAlaProArgCysGlyIleLeuGlnHisCysGln 499
QY      415 -----CCTCAACA----- 407
      |||
Db      500 AlaProAspHisPheLeuPheAlaLysLeuLysThrGlnThrAsnAlaSerAspPhePro 519
QY      406 -----GAACCAAGTCCGACG-----GGTAGACCA----- 383
      |||
Db      520 IleGlyThrSerLeuLysTyrGluCysArgProGluTyrTyrGlyArgProPheSerIle 539
QY      383 ----- 383
Db      540 ThrCysLeuAspAsnLeuValTrpSerSerProLysAspValCysLysArgLysSerCys 559
QY      382 -----CCGTGCTCTCGT----- 369
      |||
Db      560 LysThrProProAspPro--ValAsnGlyMetValHisValIleThrAspIleGlnValG 579
QY      368 -----AACCTTGAAGTGTGTCACAAATCATAG----- 341
      |||
Db      579 LysArgIleAsnTyrSerCysThrThr--GlyHisArgLeuIleGlyHisSerSerAla 598
QY      340 -----TCGGACCTTCACCGCTTTTC----- 320
      |||
Db      599 GluCysIleLeuSerGlyAsnAlaAlaHisTrpSerThrLysProProIleCysGlnArg 618
QY      319 -----CCTCGA----- 314
      |||
Db      619 IleProCysGlyLeuProProThrIleAlaAsnGlyAspPheIleSerThrAsnArgGlu 638
QY      313 -----CGATGTTCTTCAGAGTCC----- 296
      |||
Db      639 AsnPheHisTyrGlySerValValThrTyrArgCysAsnProGlySerGlyArgLys 658
QY      295 -----TGTCAATCAAAATCTTATTCAAA--GGC 271
      |||
Db      659 ValPheGluLeuValGlyGluProSerIleTyrCysThrSerAsnAspArgGlnValGly 678
QY      270 ATCTCG----- 265
      |||
Db      679 IleTrpSerGlyProAlaProGlnCysIleIleProAsnLysCysThrProProAsnVal 698
QY      265 ----- 265
Db      699 GluAsnGlyIleLeuValSerAspAsnArgSerLeuPheSerLeuAsnGluValValGlu 718
QY      264 -----ATGTCAAAATGTGACTGCTCC 244
      |||
Db      719 PheArgCysGlnProGlyPheValMetLysGlyProArgArgValLys--CysGlnAlaL 738
QY      243 TTTCAAGCCCTTGCCCTTGTGCTCTGCGCTCAGAGACTTGT--AGAACCGT----- 194
      |||
Db      738 euAsnLys--TrpGluProGluLeuProSer--CysSerArgValCysGlnProP 755
QY      193 -----CCTGCGT 187

```



```

QY 437 ----- 437
Db 240 GlyValAlaLeuGlyArgGlyLeuGlySerHisSerValAlaSerCysAlaProGlnLeu 259
QY 437 ----- 437
Db 260 LeuGlyAspArgGValAspAlaGlyHisThrAspGlnProValProSerGlySerVal 279
QY 437 ----- 437
Db 280 GlyGlyProAlaArgProAlaSerGlyProArgGlnAlaArgGlnAlaSerLeuValVal 299
QY 436 GCGTGTGAACA----- 425
Db 300 ThrCysArgHisLeuLysPheArgGlySerAsnSerTyrTyrValAlaAlaSerSerLys 319
QY 425 ----- 425
Db 320 SerProArgValAlaArgArgAlaLeuSerProArgValAlaAlaGluAsnValCysLys 339
QY 425 ----- 425
Db 340 AlaSerAlaGlyMetAlaAsnLysValGlyLysProGlnLeuLeuAlaAspProGlnPro 359
QY 424 ---CGAAGATGCGCTCAACAGACAGACCGAGCGGTAGACACCG----- 380
Db 360 LysProArgGlySProAlaThrSerSerLysPro--GlySerAlaProSerLysTyrLys 378
QY 379 ----- 377
Db 379 TrpLysAlaSerSerProSerAlaSerSerSerSerPheArgTyrGlnSerGlnAla 398
QY 377 ----- 377
Db 399 GlySerLysAspHisAlaSerGlnLeuSerProValLeuSerArgSerProSerGlyAsp 418
QY 377 ----- 377
Db 419 ArgProAlaValAlaGlyHisSerGlyLeuLysPheLeuSerGlyGlnThrProLeuSerAla 438
QY 377 ----- 377
Db 439 TyrLysValLysSerArgThrLysIleIleArgArgGlySerThrSerLeuProGly 458
QY 377 ----- 377
Db 459 AspLysLysSerGlyThrSerProAlaAlaThrAlaLysSerHisLeuSerLeuArgArg 478
QY 376 ----- 371
Db 479 ArgGlnAlaLeuArgGlyLysSerSerProValLeuLysLysThrProAsnLysGlyLeu 498
QY 370 GTAACCTTGAGTGTGCACAAATCATAG----- 341
Db 499 ValGln-----ValThrLys-HisArgGlyCysArgLeuProProSerArgAlaHis 515
QY 340 ----- 332
Db 516 LeuProThrLysGluAlaSerSerLeuHisAlaValArgThrAlaProThrSerLysVal 535
QY 331 ----- 326
Db 536 IleLysThrArgGlyArgGlyLeuValLysLysThrProAlaSerProLeuSerAlaProPro 555
QY 325 TTT----- 323
Db 556 PheProLeuSerLeuProSerTrpArgAlaArgGluSerLeuSerArgSerLeuVal 575
QY 323 ----- 323
Db 576 LeuAsnArgLeuArgProValAlaSerGlyGlyLysAlaGlnProGlySerProTrp 595
QY 323 ----- 323

```

```

Db 596 TrpArgSerLysGlyTyrArgCysIleGlyGlyValLeuTyrLysValSerAlaAsnLys 615
QY 323 ----- 323
Db 616 LeuSerLysThrSerGlyGlnProSerAspAlaGlySerArgProLeuLeuArgThrGly 635
QY 323 ----- 323
Db 636 ArgLeuAspProAlaGlySerCysSerArgSerLeuHisAlaSerArgAlaValGlnArgSer 655
QY 323 ----- 323
Db 656 LeuAlaIleIleArgGlnAlaArgGlnArgGlyLysArgGlyLysGlyLysTyrCysMetTyr 675
QY 322 ----- 317
Db 676 TyrAsnArgPheGlyArgCysAsnArgGlyGluArgCysPheTyrHisAspProGlu 695
QY 317 ----- 317
Db 696 LysValAlaValCysThrArgPheValArgGlyThrCysLysLysThrAspGlyThrCys 715
QY 316 ----- 305
Db 716 ProPheSerHisHisValSerLysGlyLysMetProValCysSerTyrPheLeuLysGly 735
QY 304 ----- 296
Db 736 IleCysSerAsnSerAsnLysCysProTyrSerHisValTyrValSerArgGlyValGluVal 755
QY 295 TGTGCATCAATGATCTTATCAAGGACATCTGATGTCGTAATGTTACTGCTTCAAG 236
Db 756 CysSerAsp-----PheLeuLysGly-----TyrCysPro----- 765
QY 235 CTTTGGC-----CTTCTGCTCTGC-----CGTCA 212
Db 766 -LeuGlyAlaLysCysLysLysLysHisThrLeuLeuCysProAspPheAlaArgArg-- 784
QY 211 GAACTTGT----- 203
Db 785 GlyAlaCysProArgGlyAlaGlnCysGlnLeuLeuHisArgThrGlnLysArgHisSer 804
QY 202 ----- 176
Db 805 ArgArgAlaAlaThrSerProAlaProGly--ProSerAspAlaThrAlaArgSerArg 823
QY 176 ----- 176
Db 824 ValSerAlaSerHisGlyProArgLysProSerAlaSerGlnArgProThrArgGlnThr 843
QY 175 CTTTCCGCTGCGCTGTTCCACTGCTGTTGTCGCCAGAACTCATATGTTCTTCACACA 116
Db 844 ProSerAlaAlaLeuThrAlaAlaAlaValAlaAlaIaIaProPro-----His 859
QY 115 CGGTGCACTTCCGCTGCGAGTGGCGGCGCTCAACCTTATCAGGAAGCGCGTGTGG 56
Db 859 S-----CysProGlyGlySerAla-----SerProSerSerSerLysAla----- 872
QY 55 GACGTCGCGCTCCGCGCGGCGCTTCGCAAGTCTTCGCTCCGCC 9
Db 873 -----SerSerSerSerSer-----SerSerSerSerProProAla 884

```

```

RESULT 14
US-09-488-725A-6091
; Sequence 6091, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725

```





```

Db      565 SerLeuProSerTrpArgAlaArgArgLeuSerLeuSerArgSerLeuValLeuAsnArg 584
Qy      323 -----
Db      585 LeuArgProValAlaSerGlyGlyLysAlaGlnProGlySerProTrpTrpArgSer 604
Qy      323 -----
Db      605 LysGlyTyrArgCysIleGlyGlyValLeuTyrLysValSerAlaAsnLysLeuSerLys 624
Qy      323 -----
Db      625 ThrSerGlyGlnProSerAspAlaGlySerArgProLeuLeuArgThrGlyArgLeuAsp 644
Qy      323 -----
Db      645 ProAlaGlySerCysSerArgSerLeuAlaSerArgAlaValGlnArgSerLeuAlaIle 664
Qy      323 -----
Db      665 IleArgGlnAlaArgGlnArgArgGlyLysArgLysGlyLysCysMetTyrTyrAsnArg 684
Qy      322 -----
Db      685 PheGlyArgCysAsnArgGlyGlyLysArgCysProTyrIleHisAspProGlyLysValAla 704
Qy      317 -----
Db      705 ValCysThrArgPheValArgGlyThrCysLysLysThrArgGlyThrCysProPheSer 724
Qy      316 -----
Db      725 HisHisValSerLysGlyLysMetProValCysSerTyrPheLysLysGlyIleCysSer 744
Qy      304 -----
Db      745 AsnSerAsnCysProTyrSerHisValTyrValSerArgLysAlaGlnValCysSerAsp 764
Qy      286 AATGATTATCAAGGCACTGGATGGTCAGAAATTGACTGCTTTCAGAGGCTTGCC-- 229
Db      765 -----PheLeuLysGly-----TyrCysPro-----LeuGlyAl 774
Qy      228 -----CTTCTGCTCTGC-----GCTCAGAGCTTGT 203
Db      774 aLysCysLysLysLysHisThrLeuLeuCysProAspPheAlaArgArg--GlyAlaCys 793
Qy      203 -----
Db      794 ProArgGlyAlaGlnCysGlnLeuLeuHisArgThrGlnLysArgHisSerArgArgAla 813
Qy      202 AGAAGCTGTCTGGCTCAGATGACCA----- 176
Db      814 AlaThrSerProAlaProGly--ProSerAspAlaThrAlaArgSerArgValSerAla 832
Qy      175 -----CCTTCGGCT 167
Db      833 SerHisGlyProArgLysProSerAlaSerGlnArgProThrArgGlnThrProSerSer 852
Qy      166 GCGCGTGTTCACCTGCTTGTGCTCCAGCACTGCATGATCTTCCACACAGCGTGCAGT 107
Db      853 AlaAlaLeuThrAlaAlaAlaValAlaAlaProPro-----His-----Cys 866
Qy      106 TCCCGCTGGCAGTCCCGCGCTCACCCTATCAGAAAGGCGGTGTCGGAGCGTCCG 47
Db      866 sPrGlyGlySerAla-----SerProSerSerSerLysAla-----Sers 880
Qy      46 CTTCCGGCGGCGGCTCTCGCAGTCTTCCGCTCCCGCC 9
Db      880 erserSerSer-----SerSerSerSerProAla 890

```

```

: Sequence 6797, Application US/09488725A
: GENERAL INFORMATION:
: APPLICANT: Hyseq, Inc
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
: FILE REFERENCE: 784FLPCT
: CURRENT APPLICATION NUMBER: US/09/488,725A
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US/09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: US09/620,312
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: US09/653,450
: PRIOR FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: US09/662,191
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: US09/693,036
: PRIOR FILING DATE: 2000-10-19
: PRIOR APPLICATION NUMBER: US09/727,344
: PRIOR FILING DATE: 2000-11-29
: NUMBER OF SEQ ID NOS: 7144
: SOFTWARE: pt FL_genes_b Versions 1.0
: SEQ ID NO 6797
: LENGTH: 472
: TYPE: PRT
: ORGANISM: Homo sapiens
: NAME/KEY: misc feature
: LOCATION: (1)...(469)
: OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-6797

Alignment Scores:
Pred. No.: 19.7 Length: 469
Score: 275.50 Matches: 107
Percent Similarity: 22.20% Conservative: 32
Best Local Similarity: 17.09% Mismatches: 72
Query Match: 17.69% Indels: 415
DB: 1 Gaps: 10

us-09-896-522-3 (1-834) x US-09-488-725A-6797 (1-469)
Qy      830 TGGGATCTGTCTGTGACTCCAAATGACCGCTTTCAGAGGTCAGACATCCAGGCTG 771
Db      34 TTP-----AlaGlyMetArgMet-----SerValValGlyValThrLeu-----Gl 47
Qy      770 TCCCGTGTCTCAGAAAGGTCGCTGTGACT----- 739
Db      47 yProMetAlaGln-----GlyLeuLeuSerAlaSerGlyThrThrThrGlnAlaThrTrp 66
Qy      739 ----- 739
Db      66 hArgProThrThrHisLeuThrLeuIleArgTrpTrpLeuLeuThrAlaSerArgVala 86
Qy      738 -----CGGCCATTGACCTCTCGTGGTCCATTTCAGATGTCACCATT-- 634
Db      86 sPrProGlnArgProPro-----ProPro-----ProSerAspAspLeuThrLeuL 102
Qy      693 -----CAGATGTCGTGAGT 678
Db      102 euGlnSerSerSerSerTyrLysAsnLeuAspAlaGlnIleProGlnAsp-----TrpSer 120
Qy      677 TGTGACAGATCAGGTGATGAGCAACCATATTGCACTCTCGTGGAGATCAGATCG 618
Db      121 --MetSerProSerThrSerGly***Arg-----ProLeu-----ThrSerAr 134
Qy      617 GCATPACTTCTTTGCGGAGGAGCAACT----- 590
Db      134 galaserSerIleMetArgSerArgThrAlaIleProSerAlaSer***SerArgLeuTh 154
Qy      589 -----CTCGAAGCGCGGCTTCAG 570

```

```

Db      154 rThrLysHisThrValGlyGlySerProSerAlaThrArgPro---ArgProThrSerAr 173
Qy      569 AAGG-----
Db      173 gSerValSerThrProValSerSerSerThrGluThrThrAlaSerGlySerCysLeuTh 193
Qy      565 -----TGGTGTACTGCTGCAGAACTGCTCCAGTCCCTCCGCGGAGACTCCCGGAGA 510
Db      193 rTPrTriP-----SerSerSerProAlaProCysProSerSerSerAla---ProAlaHi 210
Qy      509 ACTCTTGAGACAGACCTGACGTCCGAGTCGAGTCGTCACAGAGAGCCGAGGTGAGACATG 450
Db      210 sSerPheGluAlaSer-----CysCylLysThrSerLeuTriPglySerCy 225
Qy      449 TCCCGGA-----
Db      225 sGlyGlySerGlyAspGlySerSerAlaCysGlySerGlyTriPasnLeuSerMetalagl 245
Qy      442 -----TCTCCGCGGTGTAACACCAAGATGCCCTCA 411
Db      245 yThrSerCysSerSerProAlaMetCysSerPro-----SerArgAlaProSer 261
Qy      410 AACAGAACCAAGTCGCGAGGGTAGACCA-----
Db      262 ***ArgSerAlaSer-----ArgProArgThrTriPArgAlaThrThrSerAlaAlaSe 279
Qy      382 -----CCGTGGTC 375
Db      279 rSerTriPAlaProArgArgCysTriPcysGlyTriPAla***SerAlaThr***ProSerSe 299
Qy      374 TCTGTAACTGTAGTGTGTCACAAATCATAGTCGGACCTCCACCGTTTGCCCTCC 315
Db      299 rThrThrThrThrLeuSer---SerSerProHisCysGlyTriPPro-----CysPro-- 314
Qy      314 ACAGATGTTCTTCAGAGCTCTGTCATCATATCATTAACAAGCGATGATGTCATAAA 255
Db      315 -----AlaSerCysAlaSer-----AlaAlaAlaAlaTriP----- 323
Qy      254 TTGTACTGTCTCTTCAAGGCTTGCGCTTCTGCTCTCCGTCAGACCTGTG----- 203
Db      324 -----LeuSerSerThrTriPAlaThrAlaSerValAlaGlySerCysTriPglyPr 340
Qy      203 -----
Db      340 oLleMet***SerSerAlaHisSerProTriPcysLeuSerAlaCysSerArgSerSerMe 360
Qy      202 -----AGAACCTGTCTGCTCAGATGATGACCACTTCGCGTCCGCT----- 161
Db      360 tGlyThrThrCys-Leu***ArgSer--ProProSerGlyAlaSerArgAlaAlaAla 379
Qy      161 -----
Db      379 aTriPcysGlySerSerProSerSerThrPheThrProSerSerAlaSerSerSerThrTr 399
Qy      160 -----GTTCACCTGCTTCTGTCGACG 138
Db      399 pCysSerAlaSerSerSerArgSerSerProAlaProThrThrProSerSerIleProAl 419
Qy      137 AACT-----CCATGATCTTTCACACAGGTCACTTC 105
Db      419 aAlaGlnAlaGlnArgArgAlaSerCysArgPro---ThrSerHisSerAlaArgThrAl 438
Qy      104 CCGCTGAGTGCCTGCGCGCTCAACCCCTATACAGAGAGCGGTGTCGAGCGGCC 45
Db      438 a-----ProPro-----ProAlaSerSer--AlaAlaGlyVala---AlaArgPr 451
Qy      44 TCCGCGCGGCGGCTCTCG-----CAGTCTTCGCGCTCCGCGGACG 4
Db      451 o-----AlaAlaPheSerAlaAlaAlaGlnGlyThrPro--ArgArgSer 465

```

```

; Sequence 5699, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 5699
; LENGTH: 490
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)---(483)
; OTHER INFORMATION: xaa = any amino acid or nothing
US-09-488-725A-5699

Alignment Scores:
Pred. No.: 21
Score: 275.50
Percent Similarity: 22.50%
Best Local Similarity: 18.45%
Query Match: 17.69%
DB: 1
Gaps: 11

us-09-896-522-3 (1-834) x US-09-488-725A-5699 (1-483)
Qy      834 TCACTGGGGTCTGCTGCTGAGCTTCAAAATGTGACCGTTGCGAGGTGACATCCAGG 775
Db      136 SerLysGlySerGly--TriPgluThrProVal-ProTriSer**AlaGln---Progl 153
Qy      774 GTGG-----TCCCGTGGCTCA----- 759
Db      153 yTriPValSerGlyLeuLeuLeuLeuGlyAspProSerGlyProGlySerLeu**ArgSe 173
Qy      758 -----GAAAGTCCGCTTGTAGCTCCG 736
Db      173 rThrTriPLeuValGlyGlyAlaArgGlyProGluGlySerGlyValArg-----Glys 191
Qy      735 CCATTTGACCTCTCTGCGTCCATTTGCAATGATGACCATTCAGATGTCTCGATG 676
Db      191 erGlyTriP-ProSerGly-Cys-----SerAspIle-----GlyTriP----- 202
Qy      675 CTGCAGATCAGGTGATGACCAACCATATTGTCCAC----- 640
Db      203 --AlaLeuAlaGly--TriP-AsnHisSer**HisLeuAspProAsnThrTriPThrGln 220
Qy      640 ----- 640
Db      221 LysTriPThrGlyGluSerProAlaProGlyGluGluGlyValAlaAlaProAlaProArgGly 240
Qy      639 -----TCTCTGCGGATGATCAATC 619
Db      241 ProThrAlaGluHisGlyHisCysGlyLeuThrThrGluSerGlyLeuThrSerSerAsnVal 260
Qy      618 GGCATCTTCTTGTGTGCGAGGAGCAACTCTCGAAGCGCGCTTACAGAAAGTGTGTGA 559

```



```

Db      282  erValIleLeuThrProAsnCyserProCysSerLeuAlaGlyGln***ProProGlyL 302
Qy      589  -----CTCGAAGCGCGCTTACGAAAGGTGTACTGCTCGTCAAGATCTGCTCCAGGTC 535
Db      302  eUTYrProLysThrProLysGlnArgTrp-----ArgArgProLeuLeuLeu--GlyP 320
Qy      534  CCTCCCTCGGGGCGACGTCGGGAGAACTCTTCGAGACG----- 496
Db      320  roser-----Gln***GlySerArgGlnSerThrCys***GlnValGly 334
Qy      495  -----CCTGACGTC----- 487
Db      335  AlaleuGlyGluProValArgIleProGlyLeu***ProAspLeuSerCysIleLeuSer 354
Qy      486  -----GGAGTCGGGTGC 475
Db      355  AsnGlySerIlySerIlySerArgGlyGlyLeuSerPheProArgSerLeuGlyProGly--- 373
Qy      474  CACGAAGAGCGGCGAGTGGAAATGTCGGGATCTCGTGGCTGTAGAAACACCAAGATGCC 415
Db      374  --ArgArgGlyProAlaGlyLeu-----GlnSerLeuGlyCys----- 385
Qy      414  CTCAAACAGAACCACTCCGACG----- 392
Db      386  -----SerProThrProLysAsnThrAlaCysHisSerSerGlyHisValAlaLeuG 403
Qy      392  ----- 392
Db      403  lnaIaGlyHisAspSerAlaArgAspValGlySerGlyHisValAlaLeuGlnAlaGlyH 423
Qy      391  -----GTTAGACCAACCGTGTCTGTCTGTGTAACCTTGAGTGTGCAC 352
Db      423  iAspSerThrGlnAspValGlyArgProValIleParg--IleIlePro----- 438
Qy      351  AAATCATAGAGTGGGACACTCCACCGTTTGCCCTCCACAGATGTTCTTCAGAGTCTGTG 292
Db      439  -----LeuGln**LeuGlyLeu-----SerArgGlyThr--- 448
Qy      291  CATCAAAATCATTTCAAAAGC--ATGTGATGTGTCAAAATTTGACTGCTCTTCAAGC 235
Db      449  GlyGlnAlaThrArgArgGlyLeuValIlePle-----SerProGlyArgAl 464
Qy      234  CTGGCCTTGTGCTGCTGCC----- 216
Db      464  aaIaAlaAlaCysValAlaCysAlaGlnAlaLeuGlnGlyProLeuArgLeuProG 484
Qy      215  -----GTGAGACCTGTAGAACTGTGCTGGC-----TCAGATGACAC 175
Db      484  yGlnAspArgGlyAlaGln--ProCysSerHisCysProGlyArgAlaAlaGlyGlnProG 504
Qy      174  CTTCCGCTGCGCGCTGTTCACTGT-----TCG 145
Db      504  lnrProGlyAlaGlyAlaProCysArgGlyGlyGly**AspProThrGlyLeuThrGlyV 524
Qy      144  TCCGAGAACTCATGATCTTTCACACAGGTGCACTTCCC----- 103
Db      524  alProGlyThr--AspProLysArgGlyGlyArgIlyArgIlyArgIlyGlnSerGlyGlnG 542
Qy      102  -----GCTGCGAGTGGCGCGCTCACCCCTCA----- 77
Db      543  ThrGlnGlyProThrValIlePserGly---Pro-GluSerProLeuGlnProLysPro* 561
Qy      76  -----TCAGAAAGGCGCGCTGTGTGGAGCGGTGGCGCTCCGCGC 37
Db      561  *GluArgGlnGlyValGlyAlaGlyAlaSerSerGly-----ValGlyLeuSerArg 578
Qy      36  GGGGCTCTCGCACTCTTCGCTCCGCGCAAGCC 3
Db      579  Gly-----ArgAlaGlyGlyProSerSerAla 587

```

```

: Sequence 2174, Application US/09488725A
: GENERAL INFORMATION:
: APPLICANT: Hyseq Inc
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
: FILE REFERENCE: 784PLPCT
: CURRENT APPLICATION NUMBER: US/09/488,725A
: CURRENT FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US/09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: US09/620,312
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: US09/653,450
: PRIOR FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: US09/662,191
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: US09/693,036
: PRIOR FILING DATE: 2000-10-19
: PRIOR APPLICATION NUMBER: US09/727,344
: PRIOR FILING DATE: 2000-11-29
: NUMBER OF SEQ ID NOS: 7144
: SOFTWARE: PL_FL_genes_b Versions 1.0
: SEQ ID NO 2174
: LENGTH: 723
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-488-725A-2174

Alignment Scores:
Pred. No.: 55.7 Length: 722
Score: 273.80 Matches: 103
Percent Similarity: 17.46% Conservative: 33
Best Local Similarity: 13.22% Mismatches: 71
Query Match: 17.58% Indels: 572
DB: 1 Gaps: 12

us-09-896-522-3 (1-834) x US-09-488-725A-2174 (1-722)
Qy      825  TCGTGTGCTGAGTCCAAATGTGACCGTTTGCCAGAGTCCAGGAGTGTCC 766
Db      139  SerSerGlyGlyMetGlnAlaThrPro-----AlaThrGlyGly----- 151
Qy      765  TGGCTGAGAAAGTCCGCTTGTAGCTCCGCCATTGACCTCTCGTGCATTGCA 706
Db      152  -----LeuAlaArgProGlnAlaProSerSer----- 160
Qy      705  GATGTACCACTTGAATGTCTGATGTGCTGCACAGATCAGGTGATGGCAAC----- 652
Db      161  ---SerAlaPheArg-CysProTyrCys-----LysGlyLysPheArg 173
Qy      651  -----CATATTGCCACTCCGCGG----- 631
Db      174  ThrSerAlaGlyArgGlyArgHisLeuHisIleLeuHisArgProIlePlyCysGlyLeu 193
Qy      630  -----GATGATCACATCGAGCACTCTTTGTCCGACGCA 595
Db      194  CysSerPheGlySerSerGlnGlnGlnGlnLeuLeu--HisHisSerLeuThrAlaHisG 213
Qy      594  GAACTCTCGAAGCGCG----- 578
Db      213  lValaProGlyArgProLeuAlaAlaThrSerAlaAlaProProGlnProGlnProG 233
Qy      578  ----- 578
Db      233  lnrProProGlnProGlnProArgSerValProGlnProGlnProGlnProG 253
Qy      578  ----- 578
Db      253  lnrArgGlnAlaThrProThrProAlaProAlaAlaProGlnGlnProProAlaProProG 273

```

```

QY 578 ----- 578
Db 273 IupheargCysglInValCysglYglInserPheThrInserTrpPheLeuYsgLYHSM 293
QY 578 ----- 578
Db 293 eLarGlySHleYAlaserPheAerPHIsAlaCySProValCyglYArgCySPhelysG 313
QY 577 ----- 577
Db 313 IuproTrpPheLeuYsAerPHIsMeLYsValHIsAlaSerLYsLeu-GlyProLeuArg 332
QY 552 CAGATCTGCTCCAGATCTCCCTCGGCGACGCTCCGCGAAGTCTTCCAGACAGCT 493
Db 333 -----AlaProGlyProAlaSerGly-----ProAlaArgAlaProGlnProPro 347
QY 492 GACGTCGAGTGGGTGTCCAGAAAGGCGACGAGTGGAACATGTCCTCCGATCTCTGCT 433
Db 348 AspLeuGlyLeuAlaYrGlnProLeu-Gly-----ProAlaLeuLeuLeu 363
QY 432 GTAGAACCCAGATGCGCTCAACAGAACGACGCTCGG----- 395
Db 364 Ala-----ProAla-----ProThrProAlaGlnArgGlnProPro 377
QY 394 -----CAGGTAGACCA----- 383
Db 377 erLeuLeuGlyTYrLeuSerLeuArgAlaGlyGlnGlyArgProAlaGlnGlyGlnGly 397
QY 382 -----CGGTGCTCTCTGTAACTTGAGTG 358
Db 397 IuproGlyProGlyArgSerPheGlyGlyPheArgProLeuSerSerAlaLeuProAla 417
QY 357 TGTCAAAAATCATAGTCGCGACCTCCA----- 329
Db 417 rGAlaArgArgHIsArgAlaGlnGlnProGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 437
QY 329 ----- 329
Db 437 IugIuThrTrpAlaArgGlyArgSerLeuGlySerLeuAlaSerLeuHIsProArgProG 457
QY 329 ----- 329
Db 457 IygluGlyProGlyHIsSerAlaSerAlaAlaGlyAlaGlnAlaArgSerThrAlaThrG 477
QY 329 ----- 329
Db 477 IugIuGlnAerGlyLeuLeuValGlyGlyThrArgProGlnGlyGlyArgGlyAlaThrG 497
QY 328 -----CCGTTTGCCCT----- 317
Db 497 IylySArCySArProPheCySglYySerSerPheArgSerAlaHIsHIsleuYsValHIsL 517
QY 316 -----CCACGATGTTCTTCAGAGTCTGCTG 292
Db 517 euArGValHIsThrGlyGlnArgProTYrLYsCySProHIsCySArYrGAlaGlyThrG 537
QY 291 CATGAAT-----CATTAACAAGGCAT----- 269
Db 537 InSerGlySerLeuYrHIsleuGlnArgHIsHIsArgGlnGlnArgSerGlyAlaG 557
QY 269 ----- 269
Db 557 IyProGlyProProProGlnProProProProSerGlnArgGlySerAlaProGlnSerG 577
QY 268 -----CTGATGTCGAAATTTGACTGCTCTT 241
Db 577 IyAlaYrProSerProGlnProAlaThrTrpValGlnGlyAlaSer-----SerPro-- 594
QY 240 CAAGGCTTGCGCTCT----- 224
Db 595 --ArgPro--ProSerSerGlyAlaGlyProGlySerArgArgGlySerProAlaSerProG 613
QY 223 -----GCTCTGCGCT 214

```

```

Db 613 IyArgThrLeuArgAerGlnGlyArgGlyGlyGlnAlaGlnIuproLeuAerPheLeuSerLeuArgA 633
QY 213 CAGACCT-----TGTAGAACCTGTCT- 191
Db 633 IagIyProGlyGlyGlnAlaGlyProGlyGlyAlaLeuHIsArgCySleuPheCySArPro 653
QY 191 ----- 191
Db 653 heAlaThrGlyAlaProGlnIuLeuMetaAlaLeuHIsleuGlnValHIsSerArgArgA 673
QY 190 -----GGCTCAGATGACACCTTCCGCTGCGCTGTCCACTCTGTCGACGAA 136
Db 673 IaaArgGly-ArgArg-ProProGlnAlaAerPheAlaSerProPro----- 686
QY 135 CTCATGATCTTCTTCACACACGAGTGCACCTCCGCTGCGAGTGCAGCCGCTAT 76
Db 687 -----TYrAlaArgValProSerLYsIuThrProProSerProSer 700
QY 75 CAGAAAGGCGCGTGTGTGCGACGCTCGGCGCGGAGCTTCGACATCTTCGCC 16
Db 701 GlnGlnGly-----GlnGlnGlySerGlyLeuSerArg----- 711
QY 15 TCCCGCCGAGCC 3
Db 712 -ProGlyGlnAla 715

```

## RESULT 19

```

US-09-488-725A-7031
: Sequence 7031, Application US/09488725A
: GENERAL INFORMATION:
: APPLICANT: Hyseng Inc
: TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
: FILE REFERENCE: 784F.PCT
: CURRENT APPLICATION NUMBER: US/09/488,725A
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: US/09/488,725
: PRIOR FILING DATE: 2000-01-21
: PRIOR APPLICATION NUMBER: US/09/552,317
: PRIOR FILING DATE: 2000-04-25
: PRIOR APPLICATION NUMBER: US/09/598,042
: PRIOR FILING DATE: 2000-06-20
: PRIOR APPLICATION NUMBER: US/09/620,312
: PRIOR FILING DATE: 2000-07-19
: PRIOR APPLICATION NUMBER: US/09/653,450
: PRIOR FILING DATE: 2000-08-31
: PRIOR APPLICATION NUMBER: US/09/662,191
: PRIOR FILING DATE: 2000-09-14
: PRIOR APPLICATION NUMBER: US/09/693,036
: PRIOR FILING DATE: 2000-10-19
: PRIOR APPLICATION NUMBER: US/09/727,344
: PRIOR FILING DATE: 2000-11-29
: NUMBER OF SEQ ID NOS: 714
: SOFTWARE: P1 FL_genes_b Versions 1.0
: SEQ ID NO 7031
: LENGTH: 304
: TYPE: PRT
: ORGANISM: Homo sapiens
: NAME/KEY: misc_feature
: LOCATION: (1)...(301)
: OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-7031

```

## Alignment Scores:

```

Pred. No.: 8.77 Length: 301
Score: 272.80 Matches: 109
Percent Similarity: 23.45% Conservative: 16
Best Local Similarity: 20.45% Mismatches: 56
Query Match: 17.51% Indels: 352
DB: 1 Gaps: 9

```

```

us-09-896-522-3 (1-834) x US-09-488-725A-7031 (1-301)

```

```

QY 796 TCCAGAGGTGACATCCAGAGGTGTCCTGCTGAGAAAGTCCG----- 748
Db 2 Cys-----SerValProGly--AlaGluTrpProArgLysProProAlaGlnIleCy 18
QY 747 -----CTGTACTCCGCCCA-----TTGACCTCTCTCGCT 716
Db 18 sProGlnLeuThrSer-ArgProHisLeuSerSerProArgSerLeuSerPro---Gly 36
QY 715 GCCATTGACAGATGTCAAGATTGCTGGATGTGTCGACGATGAGTTGATG 656
Db 37 -----CysGlyHisSerProGlyProGlyCys----- 45
QY 655 CAACCATATTGTCCATCTCTGCGATGATCAGATCGCATCTTCTTGTCCGAGGC 596
Db 46 LysPro-----SerArgHis-----CysArgGlu-- 53
QY 595 AGAATCTCTGAGAGCGCGCTTCAAGAGTGGTGTACTGCTGAGAACTGCTCCAGGT 536
Db 54 -----LeuHisGluGly-----ProSerArgThrAla-----A 63
QY 535 CCTCCTCGGCGCAGCGTCCGAGAACTTTGAGACAGCTGACGTCGAGTCCGCTG 476
Db 63 LalaLeuPro-CysGlyLysPro-----GlnProLysHisGlyVal----- 75
QY 475 CCAGAAAGAGCGCGAGGTGGAACATGTCCCGATCTCTGCTGATAGAACACAGATGC 416
Db 76 -----GluGlyLys-----GlyProCysPro-----CysLeuAlaProArg-Ar 88
QY 415 CTTCAACAGAACCA-----GTCGCGAGGTGATGACACCGTGTCTGTG 371
Db 88 glnLeu--ThrGlnProAlaLeuThrValSerProValGlyArg--AlaAlaProSerG 107
QY 370 GTAACCTT-----GAGTGTGTCACAAATCATAGGTCCGCA 335
Db 107 LysAlaLeu***ProSerGlyArgAlaCysSerAlaCys-----SerHisArgLeuAla 124
QY 334 CTTCCACCGTTTTCCTCCAGATGTTCTTCAAGATCTGTGTCATCAAACTATCA 275
Db 125 Pro-----GluAlaAlaLeuSerAlaAlaAlaProArgPro-----SerLeu--- 138
QY 274 AGGATGTGATGTCAAAATGTACTGTCTTTCAGAGCTTGGCTTGTCT----- 221
Db 139 -Gly-----SerGlyGlnMetAlaSer-----GlyLeu--ProAlaAlaSerLeu 152
QY 220 -----CTGCGTCAGAGCCTTGTAGAACCTGT 194
Db 153 ProProGlnAspSerSerGlnProHisLysThrValProSer---ProAlaArgSerVal 171
QY 193 CTTGCTCAGATGACCACTTCGCTGCGCTGCTTTCACCTCGT----- 149
Db 172 ProProLeuGly-----AlaGlnAlaArgAlaAlaProProArgLeuTrpCysProArg 189
QY 148 -----TCT 146
Db 190 AlaLeuValSerGly**GluAlaSerProGluAlaValSerValAlaAlaGlyProPro 209
QY 145 GTCCGACGACATCTCCAGATTTTTCACACAGGTTCATCCCGCTGGAGCGCGCCG 86
Db 210 ValProGly--Pro-----ThrProSerThrSer--GlySerThrAla 223
QY 85 TCACCCCTTACAGAAAGCGCTGTGTC----- 57
Db 223 rHisSer--ArgArgGly-----Cys***SerProArg***ThrProAlaProPro 240
QY 56 -----GACGCTCGGCC----- 45
Db 240 rGhrGhrpHisGlyArgSerAlaAlaPheGluValLeuThrAlaAlaAlaSerAlaGlnP 260
QY 44 -----TCCGCGCGCGGCGCTCGGAGCTCT----- 21
Db 260 rOCyAlaSerGlnGlyGlyProArgProThrGlyAlaGlyArgThrProSerProLeuG 280
QY 20 -----TCGCTCTCCGCC 9

```

```

Db 280 LysLeuProPheSerArgGlyProProAla 289
RESULT 20
US-09-488-725A-6951
Sequence 6951, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784PLPCT
CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488, 725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pc_Fl_genes_b Versions 1.0
SEQ ID NO 6951
LENGTH: 573
TYPE: PRT
ORGANISM: Homo sapiens
NAME/KEY: misc feature
LOCATION: (1)...(566)
OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-6951

Alignment Scores:
Pred. No.: 35,6 Length: 566
Score: 272.50 Matches: 107
Percent Similarity: 18.46% Conservative: 15
Best Local Similarity: 16.19% Mismatches: 75
Query Match: 17.49% Indels: 465
DB: 1 Gaps: 10

us-09-896-522-3 (1-834) x US-09-488-725A-6951 (1-566)
QY 814 ACTCCAAATGTACCGCTTGTCCAGAGTCAAGATCCAGAGGTGTC-----CCCTG 764
Db 89 ThrProThr-----ProArgAlaGluGly--HisProProThrThrProSerProPro 106
QY 763 GCTCAGAAAGGTGCGCTTGTAGCTCGGCCATT-----GACCTCTCTCGGTGCATT 710
Db 106 rLeuArgGln***Pro-----ProProLeuLeuLysAlaProSerSerThrGly-- 122
QY 709 TGCAGATGTCAACATTCAGAAATGCTGTGATGTGTGACGATCAGATTGATGCAAC 650
Db 123 -----ProAlaProAlaAla-----MetAlaThrT 131
QY 649 TATTGTCACTCTGCTGCGATGATGATCAATCCGATACTTCTTGTCCGCA----- 599
Db 131 hSerSerLysProGluGly-----ArgProArgGlyGlnAlaAlaProThrIle 147
QY 599 ----- 599
Db 148 LeuLeuThrLysProProGlyAlaThrSerArgProThrThrAlaProProArgThrThr 167
QY 598 -----GGCAGAACTCTCGAAGCGCGCTTCAAGAGTGTGTACTGCTCAGAAATCTGCT 542
Db 168 ThrArgArgProProArgProProGlySerSerArgGlyAlaGlyLysSerSerArg 187

```

```

QY 541 CCAAGTCCCTCCGCGGACACGTCGCGAGAACTCTTCGAGACAGCGCTGACGTCGAGT 482
Db 188 Pro-ValProProLa-----ProGly-GlyHisSerArgSer----- 199
QY 481 CGGTGTCCAGGAGAGCGGAGTGAACATGTCGCCGATCT----- 440
Db 200 -----LysGluGlyGlnArgGlyArgAsnProSerSerThrProLeuGlyGlnLys 216
QY 440 ----- 440
Db 217 ArgProLeuGlyLysIlePheGlnIleTyrLysGlyAsnPheThrGlySerValGluPro 236
QY 439 ---CCTGGCTGTAAACACCAAGATGCCCT-----CAACAGCAACCAAGTCGCG 395
Db 237 GluProSerThrLeuThrProArgThrProLeuTyrGlySerSerSerProGlnPro 256
QY 394 CAG----- 392
Db 257 GlnThrValAlaIaIaThrThrValProSerAsnThrSerTrpAlaProThrThrThrSer 276
QY 392 ----- 392
Db 277 LeuGlyProAlaLysAspLysProGlyLeuArgArgAlaIaGlnGlyGlySerThr 296
QY 391 -----GGTAGACCAACCGTGCT 374
Db 297 PheThrSerGlnGlyGlyThrProAspAlaThrAlaIaSerGlyAlaPro-----ValS 315
QY 373 CTGTGAACCTTGAGTGTGTGACAAATATCATGATGCGGACCTGCACCG----- 326
Db 315 er-----ProProSerCysProSerAlaPhe-SerAlaProProProArg***ProThr 332
QY 325 -----TTTTCGCCCTCCACATGTTCTTCGAGTCC 296
Db 333 GlyTyrProGlnPro***LeuLeuAlaTyrCysTyrPro---CysThrSerArg-Pr 351
QY 295 TGTGCATCAATCATTTATCAAGGATCTGGA----- 264
Db 351 o-----LeuSerThrSerSerGlyValPheThrAlaIaThrGlyProThrP 367
QY 264 ----- 264
Db 367 roAlaIaPheAspThrSerValSerAlaProSerGlnGlyIleProGlnGlyAlaSer 387
QY 264 ----- 264
Db 387 hrThrProGlnAlaProThrHisProSerArgValSerGluSerThrIleSerGlyAla 407
QY 264 ----- 264
Db 407 ysgIuGluThrValAlaProSerPro***ProThrGlyCysProValLeuSerProGln 427
QY 263 -----TGTCGCAAAATGTTACTGCTCTTCA 239
Db 427 rPyTyrProGlnProGlnAlaIleSerSerThrAlaIaTrpSer-----Pro----- 441
QY 238 AGGCGCT----- 233
Db 442 ---ProGlyProGlySerLeuGlyGlnGlnGlyThrSerProMetTrpProArgGlyThr 460
QY 232 -----TGG 230
Db 461 AsnArgSerThrGluProProSerAla***AlaArgTrpIleSerProGly***SerTrp 480
QY 229 CTTCTGTCTGCGGTGAGACCTTGTAGAACCTGTCTGCTGAGATG----- 180
Db 481 ProSerAlaCysProSerProPro-----LeuCysProAlaAspGlyValLeuHisGlu 498
QY 180 ----- 180
Db 499 GluGluGluAspArgGluProGlyGluGlnProGlnAlaIaTyrGlyAsnAsnThrHis 518
QY 179 -----ACCACTTCGCGCTGCGCTGTTCACACTGTTCTGTCCAGACAACTCCATG 129

```

```

Db 519 HisProGlyThrThrPheGlnGlnAlaCys-----ArgGly-----AlaIaPro-- 533
QY 128 ATCTTCTCACACACGCTGCACTTCCGCTGCGAGTCGCCCGCTGCACCCCTATCAGAA 69
Db 534 -----GlyGluIleProVal-----ProLeuLysProLeuArgThr 545
QY 68 GCGCGCTGCGGAGCGGTGCGCTCCGCGCGCGGCG 32
Db 546 --GlnLeu-SerGluProArgSerProAlaAsnGly 556

RESULT 21
US-09-488-725A-1897
Sequence 1897, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyscg Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pc FL_genes_b Versions 1.0
SEQ ID NO 1897
LENGTH: 826
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-1897

Alignment Scores:
Pred. No.: 90.6 Length: 825
Score: 270.50 Matches: 110
Percent Similarity: 21.57% Conservative: 36
Best Local Similarity: 16.25% Mismatches: 68
Query Match: 17.37% Indels: 464
DB: 1 Gaps: 15

us-09-896-522-3 (1-834) x US-09-488-725A-1897 (1-825)
QY 833 CAGTGGGTGCTGCTGCTGACCTCAATATGACCGTTGCGAGAGTCAGCA----- 782
Db 261 GlnTyr-----Trp-----AspGlnIlePro-AsnProAlaArgSerAr 273
QY 781 -----TCCGAGGGTGTCCCTGCTCAGAAAAGTCC-- 749
Db 273 glauValAlaIleIleIleGlnAspAlaGlnGlySer-GlnTyr-GluLysArgSerAr 292
QY 748 -----GCTGTAGCTCCGCCATTTG-----ACCTCTCTCGG 717
Db 292 gGlyGlnGluProAlaLysCys---Pro-HisTrpLysAsnGlySerThrLysLeu-L 310
QY 716 TGCATTGTGAGATGTCACCATTCAGAAATG----- 687
Db 310 euPro-CysPheLeuGluHisAsn-MetLysArgAspGluAspProHisLysAlaAla 328
QY 686 -----TCCGATGTGCTGTCAGATCAGGTTG 660
Db 329 LysGluMetProPheGlnGlySerGlyLysSerAlaTrp-----CysProValGluIle 346

```



```

QY 659 ATGGCAACATATATGTCACCTCTGGAGATGATCATCGGACATCTTGTGGC 600
Db 347 SerIleThrValIleu-----TrpProGluSerIleSerValValArgCys--- 361
QY 599 AGGCAGAACTCTTCGAA----- 583
Db 362 --ValGluLeuPheGluAlaProValGluCysGluGluGluValGluGluL 381
QY 583 ----- 583
Db 381 yseGlySerPheCysAlaSerProGluSerSerArgAspPheGluGluYArgGlu 401
QY 582 -----GGCCGGCTTCAGAA-----GGTG 564
Db 401 LylLeValAlaArgLeuThrGluSerLeuPheLeuAspLeuGlyGluGluAsnGly 421
QY 563 GTGTACTGCGTCAGAAAT-----CTGCTCCAGGTCCTCC----- 529
Db 421 LyrPheCysGlnGlnAspMetGlyGluSerCysLeuLeu-----ProProSerGlySer 439
QY 528 --TCGGCGCACTCCG----- 514
Db 439 hrSerAlaHisMetProTrpAspIleuPheProSerAlaGlyProLysGluAlaProPro 459
QY 514 ----- 514
Db 459 rpGlyLysGluGlnProLeuHisLeuGluProSerProProAlaSerProThrGlnSer 479
QY 514 ----- 514
Db 479 roAspAsnLeuThrCysThrGluThrProLeuValIleAlaGlyAsnProAlaTyrArg 499
QY 513 -----GAGAACTCTTCAGACAGCCTGACGTCGAGTCGCTCCAGAAAGCGCAG 459
Db 499 erPheSerAsnSerLeuSerGln-----SerProCysProArg----- 511
QY 458 TGGAACTGTCCTGGATCTCTGCTGTAGAACACCAAGCCCTCAACAGAACAGC 399
Db 512 --GluLeuGlyProAspProLeuLeuAlaArgHisLeuGlu---GluValGluProG 529
QY 398 T-----CCGACAGGCTAGACCAACCGTG 378
Db 529 umetProCysValProGluLeuSerGluProThrValProGluProGluProGlu 548
QY 377 GTCTCTGTACTCTGAGTGTGCACAAATCATAGGTGGACCTCCACCGTTTGGCC 318
Db 549 --ThrTrp-----GluGlnIleLeuArgArgAsn-----ValLeuGln 560
QY 317 TCACAGATGTTCTTCAGAGTCTGTGCATCAATCATATCAAAAGCATCTGATGCTCA 258
Db 561 --HisGlyAlaAlaAlaAlaProValSer-----AlaProThrSerGlyTyrGln 576
QY 257 AAATTG----- 252
Db 577 GluPheValHisAlaValGluGlnGlyGlyThrGlnAlaSerAlaValGlyLeuGly 596
QY 252 ----- 252
Db 597 ProProGlyGluAlaGlyTyrLysAlaPheSerSerLeuLeuAlaSerAlaValSer 616
QY 251 -----TACTGTCTTTCAAGGCC 234
Db 617 ProGluLysCysGlyPheGlyAlaSerSerGlyGluGluGlyTyrLysProPheGlnAsp 636
QY 233 TTGGACCTTCTGTCTGCTGCGCTCAGGACCTTGTAGAACCTGCTGCTCAGAGATGAC 174
Db 637 Leu-----IlePro---Gly-----CysProGly-----AspPro 646
QY 173 TTCGCGTCCGCTGTTTCA-----CTTCGTTCTGTCTCCAGCAACTCC 132
Db 646 laProValPro--ValProLeuPheThrPheGlyLeuAspArgIleProProArgSerPr 665

```

```

QY 131 ATGATCTTCTACACACAGGTGCACTTCCCGCTGACAGT----- 93
Db 665 ogInSerSerHis-----LeuProSerSerSerProGluHisLeuGlyLeuGluP 682
QY 92 -----CCGCGCTTCACCCCTATCAGAAAGG----- 67
Db 682 roGlyGluLysValGluAspMetProLysProProLeu--ProGlnGluGlnAlaThrAs 701
QY 66 --CCGCTGTGCGGACCGGTGCGCTCCGCG----- 39
Db 701 pProLeuValAspSerLeuGly--SerGlyTyrSerAlaLeuThrCysHisLeuG 721
QY 39 ----- 39
Db 721 yseGlyHisLeuLysGlnCysHisGlyGlnAlaAspGlyGlnThrProValMetAla 741
QY 38 -----GGCGGCGCTTCGAGTCTTGGCCTCC 12
Db 741 erProCysGlyGlyCysCysGlyGly---AspArgSerSerProPro 755

RESULT 22
US-09-488-725A-7029
; Sequence 7029, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hysag Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FIPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 7029
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(434)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-7029

Alignment Scores:
Pred. No.: 23
Score: 270.10
Percent Similarity: 22.63%
Best Local Similarity: 17.64%
Query Match: 17.34%
DB: 1
Gaps: 10

us-09-896-522-3 (1-834) x US-09-488-725A-7029 (1-434)
QY 830 TGGGGTCTGCTGTGACATCCAAATGTGACCGTTTSCCAGAGGTGAG----- 784
Db 43 TrpGly-----Pro--Cys--ProHisAla---GlyArgGluThrGlyProA 56
QY 783 -----CATCCAGGCTGTGCTCCCTGAGCTCAGAA 756
Db 56 rGAlaSerAlaProIleProGlySer***GlyHis---GlyTrpHis--Trp***ArgL 74

```

```

Qy 755 AA-----GGTCGGCTTGTAGCTCCGCCATTGGACCCCTCT 720
Db 74 ysapglYarglygluYargsergluYproserAlaLeuserProHisserProserL 94
Qy 719 CGGTGACATTTGACATGTACCATTCAGATGT---CTTGATGTCTGCACCATGAG 663
Db 94 euleu-AmetGlnGlnAlaPro-ThrHisValGlyProGlyMetGlyserGln--Arg 112
Qy 662 TTGATGGCAACCATATTTGTCACCTCTCGTGGATGATACATGGCACTTCTTTGTC 603
Db 113 ProArserSerValVal-----Pro-----GlnGlnValGly-----Val 124
Qy 602 GCGAGGAGCAACTCTCGAAGCGCGGCTTCAGAAAGTGATCTGTGTCAGATCTGC 543
Db 125 GlyserGlnLeuserArgGln-----ArgTrp-----Arg--Ala 135
Qy 542 TCCAGTCCCTCCCTCGCGCAGCTCCGAGAACTTTCCAGACAGCTGACCTCGAG 483
Db 136 ***ArgserLeuPro-GlyAlaAlaAlaSerGlu-----ArgThrGlnMetThrLysGlu 153
Qy 482 TCGGTGTCCAGAAAGCGCAGGTGAAACATGTCGGA-----443
Db 154 -ArgserProArg-----ProCysGlnGlyTyraPserSerAenTrpPh 168
Qy 442 ----TCTCCGTGGCTGTAGAACCAAGATGCCCTCAACAGACAGCTCGCGGTAG 387
Db 168 ethGlnProGlyLysLysThr--Arg-----LysArgAAsenSer--ArgArg-- 182
Qy 386 ACCACCGGTGTCTCT-----372
Db 183 AsnThrMetValSerArglyGlyGlyCysLeuLeuTrpProLeuGlnInsrLleMetPro 202
Qy 371 ----GTTACCTTGAGTGTGTACAAATATAGTGGCACTCC 330
Db 203 Glu***GlnLeuArg***Gly-----AlaHis-----AlaSerProPr 215
Qy 329 A-----CGTTTTGCCCTCCAGATGTTTCAGATC 297
Db 215 oThGlnGlnArg***GlyLysGlyGlyPro-----ArgserP 228
Qy 296 CTGTGATCAATATATATCAAGGATGTGATGTCMAATGTACTGCTTTCAG 237
Db 228 ro-----LeuThrLysAlaSerGlyThrThrHisLleProThrProPhe--- 242
Qy 236 GCGTTGGCTTGTCTGCTGCGG-----215
Db 243 --PheGly-----SerLleProArgProThrArgApsSerGlyProGlyThrApsAsnSe 260
Qy 214 -----TCAGAGACCTTGTAGACCTG 195
Db 260 rAlaAlaProGlyLysArgLysArgLysArgLysAla***GlnGlyPro---GlnProV 279
Qy 194 TCTGTGCTCAGATGACCATCTCGCTCGCTGCTGTTCCACCTGTTCTGTCCAGCAAC 135
Db 279 al-TripGlyArgValThrThr-----HisLeu-----287
Qy 134 TCCATGATCTTCTCACACAGGTGACTTCCCGCTGCGAGTCCGCGCTACCCCTTA-- 77
Db 288 -----GlnGly-----ProAlaGly***Thr-----LysProLeuGln 298
Qy 76 -----TCAGAAAGCGCGGTGTGTCGGA 54
Db 298 ySerArgAenTrpValProGlyProAlaGlnGlyGlnGlnGlnGlnGlnGlnGln 318
Qy 53 CGGTGAGCT--CCGCGCGCGGCTCTCGAGT-----23
Db 318 uGlyArgArgPro***ProLeuLysGlyCysArgSerThrLeuThrPheSerProGlnLeuSe 338
Qy 23 -----23
Db 338 rIleProMetValGlyLysLysProProGlnGlyThrThrAlaSerPhePheProArgSe 358

```

```

Qy 23 -----23
Db 358 rCyHisSerGln***ArgLysProProProserCysProHisAlaProAlaLeuserL 378
Qy 22 -----CTTCGCTTCCCGCGGAGCCA 2
Db 378 uProHisProLeuProLeuProLeuProProLeuPro 390

RESULT 23
US-09-488-725A-5717
; Sequence 5717, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784PLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_pl_genes_b Versions 1.0
; SEQ ID NO 5717
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5717

Alignment Scores:
Pred. No.: 29 Length: 481
Score: 270.00 Matches: 109
Percent Similarity: 22.92% Conservative: 23
Best Local Similarity: 18.92% Mismatches: 75
Query Match: 17.33% Indels: 370
DB: Gaps: 14

us-09-896-522-3 (1-834) x US-09-488-725A-5717 (1-481)
Qy 834 TCAGTGGGCTGTCTGTGTGATCCCAATGTGACCGTTT-----796
Db 91 SerLeuGlyAlaArgProGlyLeu-----ProTrpGlyLeuSerApsArgGlnSer 107
Qy 796 -----796
Db 108 GlyGlyGlyArgAlaLeuserAlaGlnSerGlnValGlnGlnProAlaArgGlyProGly 127
Qy 795 -----GCCAGAGTACGATCCAG-----GTTGTCCTGCTGCTGAG 758
Db 128 GlnAlaArgGlyGlnArgProGlyProAlaCysGlnLeuCysGlyGlyProThrGlnGln 147
Qy 757 AAAAGTCCGCTGTAGCTCCGCCATTTGACCTCTCTCGGTGCTTGTGCAATGTGAC 638
Db 148 ----GlyPro--CysCysGlyAlaGly-GlyProGlyGlyGlyPro-----LeuLeuP 163
Qy 697 CATTCAAGATGCTCTGATGAGC-----TGACGATCAGATTGATGAGCAACATATTGT 644
Db 163 roProArgLeuLeuTrpSerCysArgLeuCysThrPhe-----ValSe 177
Qy 643 CCACTCTCGTGGAGTATGACAT-----CGCATACTTCTTTGCGGAGGCAAGACT 590

```

```

Db      177 rHISlySer-----SerHisLeuIyArGHisMetGlnThrHisSerGlyIuLys 194
QY      589 CCTGAGAGCGCGGCTTACAGAGGTGGTGTACTGCGGCAAAATCTGTCCAGG----- 537
Db      195 ProPheArg-----CysGlyArgCysProT 203
QY      536 -----TCCCTCCCTCGGCGCAGTCCCGAGAACTCTTCGAGACA 497
Db      203 yAlaSerAlaGlnLeuValAsnLeuThrArgHisThr-----ArgThr-----HisThr 219
QY      496 GCGTGAAGTCGTGGAGTGGTGTCCAGAGAGCGCGCAGGTGAACATGTCCC----- 446
Db      220 GlyIuLysProTyrArgCysProHis-----CysProPheAlaCys 233
QY      445 -----GGATCTCCTGGGTGAGA 428
Db      234 SerSerLeuGlyAsnLeuArgHisGlnArgThrHisAlaGlyProPro----- 250
QY      427 ACAACAAGATGCCCTCAACA-----GAAACAAGTCCGACAGGTAGA 386
Db      251 ThrProCysPro-----ThrCysGlyPheArgCysCysThrProArgPro-----AlaArg 268
QY      385 CCAACCGTGTCT----- 374
Db      269 ProPro-----SerProThrGlnGlnGlyAlaValProArgArgProGlnAspAlaLeu 287
QY      373 -----CTGGTAACCTTGTAGTGTGCAAAATCATAGTGGCAGCTTCA----- 329
Db      288 LeuLeuProAspLeuSerLeu-----His-----ValProProGlyAlaAlaSer 302
QY      328 -----CCGTTTTCCTCCACAGATGTTCTTCAGAGTCCGTGCATCA----- 287
Db      303 PheLeuProAspCys-----GlyGlnCysGlyValIyLeuValArgHisAlaGlyLeuAsp 321
QY      286 -----AATCATATATCAAGGATCTGATGTGCAAAATTTGATCTCTTCAGAGCCTTGG 230
Db      322 GlnAsnHisCysGln-----SerSerLeuPhe-----ProTyr 332
QY      230 ----- 230
Db      333 ThrCysArgGlyCysGlyGlnGlnLeuGlnGlyGlyIySerArgLeuGlyAlaAla 352
QY      229 -----CCTTCGTGCTGCCGTGAGA 209
Db      353 MetCysGlyArgCysMetArgGlyGlyAlaGlyGlyAlaSerGlyIyProGlnGly 372
QY      208 CCT-----TGTAGAACCTGTCT----- 191
Db      373 ProSerAspIySerGlyPheAlaCysSerLeuCysProPheAlaThrHisTyrProAsnHis 392
QY      190 -----GGTCAAGATGACCACTTCCTCCGCTGC-----CGCT 161
Db      393 LeuAlaArgHisMetIySerThrHisSerGlyIuLys-----Pro-----PheArgCysAlaArgC 411
QY      160 GTTCCACATCGTGTCTGTCCAGCACTCCATGATCTTTCACACAGGTGATCCCGC 101
Db      411 yS-----ProTyrAla-----SerAlaHisIySerAspAsnLeuIyValArgHisGlnArgValHis 429
QY      100 TGGCAGATGCCCGCGCTCAACCTTCATGAGAGAGCGCGTGGTGCAGAGGTCCGCGC 41
Db      429 rGlyIuLys-----LysProTyr-----LysCysProLeu-----ProTyr 441
QY      40 GCGCGGCGCTCTGCAAGTCTTCCCTCCGCGCGAAGCCAT 1
Db      442 AlaCysGlyAsn-----LeuAlaAsnLeuIySerArgHis 452

RESULT 24
US-09-488-725A-5469
; Sequence 5469, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT

```

```

CURRENT APPLICATION NUMBER: US/09/488, 725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488, 725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pt FL_genes_b Versions 1.0
SEQ ID NO 5469
LENGTH: 839
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-5469

Alignment Scores:
Pred. No.: 99.7 Length: 839
Score: 269.50 Matches: 108
Percent Similarity: 20.57% Conservative: 36
Best Local Similarity: 15.43% Mismatches: 71
Query Match: 17.30% Indels: 485
DB: 1 Gaps: 14

us-09-896-522-3 (1-834) x US-09-488-725A-5469 (1-839)
QY      833 CAGTGGGAGTGTGTGTGACTCCAAATGTGACCGTTTCCAGAGTCCAGCA----- 782
Db      275 GlutTrp-----Trp-----AspGlnIlePro-AsnProAlaArgSerAr 287
QY      781 -----TCCCAAGGAGTGTCCCTCGGTCCAGAAAAGTCC-- 749
Db      287 GlnValAlaIleIleIleGlnAspAlaGlnIySer-GlnTrp-GlnIySerArgSerAr 306
QY      748 -----GTTTGTAGCTCCGCCCATTTG-----ACCTCTCTCGG 717
Db      306 gGlyGlnGlnProAlaIyCys-----Pro-HisTrpIyAsnCysLeuThrIySerLeu-L 324
QY      716 TGGCATTTGCAATGTGACCACTTCAGATG----- 687
Db      324 euPro--CysPheLeuGlnHisAsn--MetIyAsArgAspGlnAspProHisIyValAlaAla 342
QY      686 -----TCCGTGATGTGTGACAGATCAAGTTG 660
Db      343 IySGlnMetProPheGlnIySerGlyIySerAlaTrp-----CysProValGlnIle 360
QY      659 ATGGCAACATATGTGTCACTCTCGTGGAGATGACATCGGCATATCTTTGTTCGCGC 600
Db      361 SerIyThrValIeu-----TrpProGlnSerIleSerValIyArgCys----- 375
QY      599 AGGCAAGAACTCCTCGAA----- 583
Db      376 --ValGlnLeuPheGlnAlaProValGlnCysGlnGlnGlnGlnValGlnGlnIuL 395
QY      583 ----- 583
Db      395 yGlySerPheCysAlaSerProGlnIySerSerArgAspAspPheGlnGlnGlnIyArgGln 415
QY      582 -----GGCGGCTTCAAGAA-----GGTG 564
Db      415 IyIleValAlaIyArgLeuThrGlnIySerLeuPheLeuAspLeuGlnGlnIyGlnIyAsnGlyG 435
QY      563 GTGTACTGTGTGAGAA-----CTGTCTCAGGTCCCTCCC----- 529

```

```

Db      435  lypheCysgInglInAspMetClygluSerCysLeuLeu-----ProProSerClysert 453
Qy      528  --TCGGCGCAGCTCCG-----
Db      453  hrSerAlaHisMetProTrrpAspGluPheProSerAlaGlyProLygluAlaProProtr 473
Qy      514  -----
Db      473  rpgLyysgIngluProLeuHisLeuGluProSerProProAlaSerProThrGlnSerp 493
Qy      514  -----
Db      493  roAspAenLeuThrCysThrGluThrProLeuValIleAlaGlyAsnProAlaIrrArgS 513
Qy      513  ----GAGAACTCTTCAGACAGCCTGACGTGGAGTGGTGCACGAGAGGCGCAGG 459
Db      513  erPheSerAsnSerLeuSerGln-----SerProCysProArgGlu--LeuG1 528
Qy      458  TGGAAcATGTCcCGGATCTCTGGCTGTAGAAcACCAAGATCCCTCAACAGAACAGCAG 399
Db      528  y-----ProAspProLeuLeuAlaArgHisLeuGlu-----GluValGluProG1 543
Qy      398  T-----CCGAGGGTAGACACCGCTG 378
Db      543  uMeProCysValProGlnLeuSerGluProThrThyAlProGlnProGluProGlu-- 562
Qy      377  GTCTGTGTAACTTGAGTGTGTCAAAATCATAGTGGCAGCTCCACGGTTTGGCCC 318
Db      563  --Thrrp-----GluGlnIleLeuArgArgAsn-----ValLeuGln 574
Qy      317  TCCAGCATGTTCTCAGAGTCCTGTCGATCAATCATATCAAGAGCATGTGATGCA 258
Db      575  --HisGlyAlaAlaAlaAlaProAlaSer-----AlaProThrSerGlyTyrGln 590
Qy      257  AAATTG----- 252
Db      591  GluPheValHisAlaValGluGlnGlyGlyThrGlnAlaSerAlaValGlyLeuGly 610
Qy      252  ----- 252
Db      611  ProProGlyGluAlaGlyTyrTyrAlaPheSerSerLeuLeuAlaSerSerAlaValSer 630
Qy      251  -----TACTGCTCTTCAAGCC 234
Db      631  ProGluLysCysGlyPheGlyAlaSerSerGlyGluGlnGlyTyrLysProPheGlnAsp 650
Qy      233  TTGGCTTCTGCTGCGCCGACAGCTTGAGAACTGCTGCGCTCAGATGACCAACC 174
Db      651  Leu-----IlePro--Gly-----CysProGly-----AspProA 660
Qy      173  TTCGCGTGCcCGCTGTTCa-----CCTCGTCTGTCTCCAGCAACTCC 132
Db      660  laProValPro--ValProLeuPheThrPheGlyLeuAspArgGluProProAlaGSerPr 679
Qy      131  ATGATCTTCTACACACAGCTGACTCC----- 104
Db      679  oGlnSerSerHisLeuProSerSerProGlnHisLeuGlyLeuGluProGlyGly 699
Qy      104  ----- 104
Db      699  sValGluAspMetProLysProProLeuProGlnGlnAlaThrAspProLeuValAs 719
Qy      104  ----- 104
Db      719  pSerLeuGlySerGlyIleValTyrSerAlaLeuThrCysHisLeuCysGlyHisLeuLy 739
Qy      104  ----- 104
Db      739  sGlnCysHisGlyGlnGluAspGlyGlyGlnThrProValMetAlaSerProCysCysG1 759
Qy      103  -----CGCTGGCAGTGGCGCGCGCTCACCCCATCAGAGAGCGCG----- 64

```

```

Db      759  yCysCysCysGlyAspArg--AlaSerProProThrThrProLeuArg--AlaProAsp 778
Qy      63  -----CTGATGGGAGAGCGGCGCTCGGGCGG 36
Db      778  roSerProGlyGlyValProLeuGlnAlaSerLeu--CysProAlaSerLeuAlaProSer 797
Qy      35  GGGCTCTCGCAGCTTCG 18
Db      798  GlyIleSerGluLysSer 803

RESULT 25
US-09-488-725A-2346
; Sequence 2346, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt FL_genes_b Versions 1.0
; SEQ ID NO 2346
; LENGTH: 566
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2346

Alignment Scores:
Pred. No.: 53.1 Length: 565
Score: 265.80 Matches: 110
Percent Similarity: 23.14% Conservative: 24
Best Local Similarity: 19.00% Mismatches: 73
Query Match: 17.09% Indels: 372
DB: 1 Gaps: 11

us-09-896-522-3 (1-834) x US-09-488-725A-2346 (1-565)
Qy      9  GCGCGAGGCGGAGAG-----CTGCGAGAGCGCGC----- 38
Db      186  GlyGlyArgAlaArgAlaGserAlaCysLeuArgGluProGlnLeuArgGlyArgArg 205
Qy      39  ---GCCGAGGCGCA----- 59
Db      206  GlyArgGlyGlyArgArgAspGlyArgLeuArgCysArgThrCysAlaLeuProAlaAla 225
Qy      60  CCA-----GGCGCCCTTCTGATGAGGGGTAGCGCGGCGCACTGCGCAG 101
Db      226  AlaThrProArgArgValGlyAlaAlaAlaPro-----GlyCysAlaG1 240
Qy      102  CCGGAGATCGAC-----GTGTG 119
Db      240  nGlyArgAlaThrAspGlyAlaArgArgAlaGluLeuArgArgGluProAlaValAla 260
Qy      120  TGAAGATCATGAGTTCCTGGGACAGAACAGGTGGAACAGCGGCGGAGAGGTGCT 179
Db      260  anIleArg--HisGlyHisAlaGlyAlaHisGlnGlyGlyAlaGlnAlaAla----- 276

```

```

QY 180 CATCTGAGCCAGGACGATTCTCAAGAGTCTTCAGCGAGAGGAGCGGACGCTT 239
Db 277 ---AlaGlnProHisArgLeuGlnValProGlnAlaGlnAla---GlyAlaHisLeu 294
QY 240 GAAAGACAGTACATTTTGGACATCCAGATGCTTGGATTAATGATTGATGACAGAC 299
Db 295 Ala-----ProGlyArg-----GluSerGlu---AspProGlnGlu 305
QY 300 TCTGAAGACATCTGAGGCGCAAAACGCT-----GGAGGTGCCGAC 341
Db 306 Ser---GlnHisGlyAlaGlyValHisGlyGluProAlaAlaArgAlaGlyValAla--- 323
QY 342 CTATGATTTTGTGACACACTCAA----- 364
Db 324 -----AlaGlnAlaGluSerProGlnProArgGlnArgLeuProA 338
QY 365 -----GGTTACGAGAGACAC 380
Db 338 LaaAlaAlaProAlaProGlyAlaAlaArgValLeuSerProArgAlaGlyArgMetArg--- 356
QY 381 GGTGCTTACCTCCGAGCGAGCGGTCTGTTGAGGCGCATCTGTTCTTACAGCCAGGA 440
Db 357 GlyHisProProGlnGlyAlaGlySer---ArgGly---GlyValAla-----Gly 371
QY 441 GATCCGGAGCATGTTCCAGCTGCGCTCTTCGTGAGACACGACCTCCGACGTCAGGCTGC 500
Db 372 AlaPro-AspLeuGlnArgValArg---ProTyrGlyProProProArgValCys- 389
QY 501 TCGAAGAGTTCTCCGAGCGTCCGCGAGG----- 530
Db 390 ProGlyThrGlnArgGlyArgGlyProArgGlyPheProProGlnGlyAlaGlnAspSer 409
QY 531 GAGGGA-----CCTGAGAGCATTCGAGCGCA 557
Db 410 GlnGlyAlaProArgThrArgGlnAlaGlyProProAlaProGlyGlyGlu--Argm 429
QY 558 GTACACACCTCTCGTGAAGCCGCGCTTCGAGAGATTCTGCTGCGGCAAAAGAGTAGTC 617
Db 429 ethrProPro-----ProSerArg-----CysLeu-----PheP 439
QY 618 CGATGTGATCATCCGAGAGAGTGAACAATATGTTGCCATCAACCTGATCGTGACGA 677
Db 439 ro-----ProArgGlyArgProValLeu---HisLysProAlaArgLeuGly 453
QY 678 CATCCGAGCATTTCTGATGTGATCATCTGCATAATGCGACCGA-----GGAGGCTC 728
Db 454 CysPro-----PheVal-----HisArgAlaAlaGlnGlyGlySe 465
QY 729 CAATGGCGGAGCTACAAGCGGACCT----- 754
Db 465 rGlnGly-----AlaGlnProGlnThrLeuProPheLeuTyrPheTyrPhePheP 482
QY 754 ----- 754
Db 482 hePhePheLeuTyrPheArgGlnGlnSerValArgPheCysProIleTyrValSerT 502
QY 754 ----- 754
Db 502 hrArgGlnGlnThrLeuValValCysValPheLeuCysTrpPhePheLeuGln 522
QY 755 -----TTTC 758
Db 522 etGlyArgGlyValHisSerProProLeuSerSerIleSerLeuProProSerVal 542
QY 759 TGAAGCAGGAGGACACCTCGGATGCTGACCTCTGCGCAACGCTCATATTGGAGTCCAG 818
Db 542 euser-ThrGlyProPro-----SerLeuPheCysSerValLeuPheCysPhe-Al 558
QY 819 CAGCAGACCCAC 831
Db 558 atmSerProHis 562

```

```

US-09-488-725A-3157
Sequence 3157, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784PLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US/09/488,725
PRIORITY FILING DATE: 2000-01-21
PRIORITY APPLICATION NUMBER: US/09/552,317
PRIORITY FILING DATE: 2000-04-25
PRIORITY APPLICATION NUMBER: US/09/598,042
PRIORITY FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: US/09/620,312
PRIORITY FILING DATE: 2000-07-19
PRIORITY APPLICATION NUMBER: US/09/653,450
PRIORITY FILING DATE: 2000-08-31
PRIORITY APPLICATION NUMBER: US/09/662,191
PRIORITY FILING DATE: 2000-09-14
PRIORITY APPLICATION NUMBER: US/09/693,036
PRIORITY FILING DATE: 2000-10-19
PRIORITY APPLICATION NUMBER: US/09/727,344
PRIORITY FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: pt FL_genes_b Versions 1.0
SEQ ID NO 3157
LENGTH: 1079
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-3157

Alignment Scores:
Pred. No.: 212 Length: 1078
Score: 265.70 Matches: 111
Percent Similarity: 17.79% Conservative: 26
Best Local Similarity: 14.42% Mismatches: 70
Query Match: 17.08% Indels: 563
DB: 1 Gaps: 14

US-09-896-522-3 (1-834) x US-09-488-725A-3157 (1-1078)
QY 13 GAGAGGAGAGACATGCGAG-----AGC 33
Db 43 GlyGlyArgAspGlySerGlyGlyCysGlnCysTyrProGlnLysGlyArgGlyGln 62
QY 34 CCGGCGCGGAGCGGACGCGTCCGACACGAGCGGCGCTTCTCT----- 74
Db 63 ProGlyProValGlyProGlnGlyTyr-AsnGlyPro-ProGlyLeuGlnGlyPheProG 82
QY 75 -----GATAGGGGTGAGCGGCGGACATGCGAGCGGAAATCGACC 114
Db 82 LysLeuGlnGlyArgGlyValAspLysGlyGlnArg-----GlyValAla--Pr 96
QY 115 GTGTGTGAGAAGATCATGAGTGTGCTGGACAGACAGAGTGAACAGCGGCGGAG 174
Db 96 o-----GlyValThrGlyProLys-----GlyAspValGlyValArgG 109
QY 175 GT-----GATCATCTGAGCGGACAGGTTTC 201
Db 109 LysValSerGlyPheProGlyAlaAspGlyIleProLys-----ProGlyGln----- 125
QY 202 TACAGGTCTGAGCGGACGAG----- 221
Db 126 --GlyGlyProArgGlyArgProGlyTyrAspGlyCysAsnGlyThrGlnGlyAspSerG 145
QY 222 -----CGAGAGGC-----CAAGGCTTG 240
Db 145 LysProGlnGlyProProGlySerGlnGlyPheThrGlyProProGlyProGlnGly-Pro 164
QY 241 AAGAGCAGTACATTTTGGACATCCAGATGCTTGGATTAATGATTGATGACAGACT 300
Db 165 LysGlyGlnLysGly-----GlnProTyrAlaLeuProLys-----GlnGlnAla 179

```

```

QY 301 CTGAAGACATCTGAGAGGCAAAACGTGAGGTCCGACCTATGATTTGTGACACAC 360
Db 179 rgaaparglyrarg---glylnProgly-----GlnProglyLeuval----- 192
QY 361 TCAGAGTTACCAAGACAGCAGGTGATCTACCCCTGCGACGTGTCTTCTTGAGGAGCATC 420
Db 193 ---GlyPheGlnGlyPro-----Pro---GlyArgPro-----GlyHisv 204
QY 421 TTGGTGTCTA-----CAGCCAGAGATCCGGACATCTTCAC 459
Db 204 aGlyGlnMetGlyProValGlyAlaProGlyArgProGlyProProGly-----Prof 222
QY 460 CTGGGCGCT----- 467
Db 222 roGlyProLyseGlyGlnGlnGlyAsnArgGlyLeuGlyPheTyrglyVallyseGlyLul 242
QY 467 ----- 467
Db 242 ysglyAspValGlyGlnProGlyProAsnGlyIleProSerAspThrLeuHisProIleI 262
QY 467 ----- 467
Db 262 leaIaProThrGlyValThrPheHisProAspGlnTyrglyGlyLulysGlyserGlyug 282
QY 467 ----- 467
Db 282 lyGlnProGlyIleArgGlyIleSerLeuLyseGlyGlnGlyIleMetGlyPheProG 302
QY 468 ---CTTCGAGACAGCAGCAGCTCCGACGTCTCGAAGAGTTCTCCGGA----- 518
Db 302 lyLeuArgGlyTyrr---ProGlyLeuSerGly-----GlnLyseGlySerProGlyGlnlysg 320
QY 519 ----- 536
Db 320 lySerArgGlyLeuAspGlyTyrglnGlyProAspGlyProArgGlyProlys---Glyg 339
QY 536 ----- 536
Db 339 lualaglyAspProGlyProProGlyLeuProAlaTyrrSerProHisProSerLeuAla 359
QY 536 ----- 536
Db 359 ysglyAlaArgGlyAspProGlyPheProGlyAlaGlnGlyGlnProGlySerGlnGlyg 379
QY 536 ----- 536
Db 379 luproGlyAspProGlyLeuProGlyProProGlyLeuSerIleGlyAspGlyAspGlna 399
QY 536 ----- 536
Db 399 rgarGlyLeuProGlyGlnMetGlyProLyseGlyPheIleGlyAspProGlyIleProa 419
QY 537 ----- 579
Db 419 laleuTyrglyGlyProProGlyProAspGly--LyseArgGlyProProGly--ProProG 438
QY 580 GCCTTCAGAGAGTCTGCTT----- 599
Db 438 lyLeuProGly-----ProProGlyProAspGlyPheLeuPheGlyLeuLyseGlyAla 456
QY 599 ----- 599
Db 456 ysglyArgAlaGlyPheProGlyLeuProGlySerProGlyAlaProGlyProLyseGly 476
QY 600 -----GCCGACAAAGATATGCCGATGT----- 623
Db 476 rplysglyAspAlaGlyGlnCySarGlyCyrtnGlnGlyAspGlnAlaIleLyseGlyLeu 496
QY 624 -----GATCANTCCAGAGAGACTGCAC 645
Db 496 roGlyLeuProGlyProLyseGlyPheAlaGlyIleAsnGlyGlnProGlyArgGlysgly 516

```

```

QY 646 AATATGTTGCCATCAACTGATCTGCAGACAT----- 680
Db 516 splysgly-----AspProGlyGlnHisGlyLeuProGlyPheProGlyLeuL 532
QY 680 ----- 680
Db 532 ysglyValProGlyAsnIleGlyAlaProGlyProLyseGlyAlaLyseGlyAspSerArgT 552
QY 681 -----CCAGACATTTCTG 693
Db 552 hrllethrThrLyseGlyGlnArgGlyGlnProGlyValProGlyValProGly-----Met 570
QY 694 AATGTGACATCTGCAATGACACCGAG----- 721
Db 571 lyseGlyAsp-----AspGlySerProGlyArgAspGlyLeuAspGlyPheProGlyLe 588
QY 722 -GAGGTTCAATGGCGGAGCTACAGCGGACCTTTCTGACGAGGAGC-----CAC 774
Db 588 uproGlyProProGlyAspGlyIleLyseGlyPro-----ProGlyAspProGlyTyrr 605
QY 775 CTGGGATGCTGACCTCTGCGCAACGTCACATTTGGAGTCCAGACAGACCCCA 830
Db 606 ProGlyIle---Pro-----Gly-ThrlyseGly-----ThrPro 615

```

## RESULT 27

```

US-09-488-725A-3367
Sequence 3367, Application US/09488725A
GENERAL INFORMATION:
APPLICANT: Hyseq Inc
TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
FILE REFERENCE: 784FLPCT
CURRENT APPLICATION NUMBER: US/09/488,725A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US/09/488,725
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
PRIOR FILING DATE: 2000-11-29
NUMBER OF SEQ ID NOS: 7144
SOFTWARE: PC FL_gene_b Versions 1.0
SEQ ID NO 3367
LENGTH: 1455
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-3367

```

## Alignment Scores:

```

Pred. No.: 389 Length: 1454
Score: 265.60 Matches: 118
Percent Similarity: 16.41% Conservative: 32
Best Local Similarity: 12.91% Mismatches: 92
Query Match: 17.08% Indels: 673
DB: Gaps: 17

```

us-09-896-522-3 (1-834) x US-09-488-725A-3367 (1-1454)

```

QY 4 GCTTCGGCGGAGGCGGAA---GACTGAGAGAGCCCGCGGAGCCGACCTGCGGAC 60
Db 307 SerSerSerGlyGlyGlnSerSerCyseGlnGln-GlyArgAlaArg-ArgPro-ProHis 325
QY 61 CAGCGGCGCTTC----- 72

```

```

Db      326 LeuArgProPheHisProArgThrValAlaLeuAspProAspArgThrProProCysLeu 345
QY      72 -----
Db      346 ProGlyAspProAspTyrSerSerSerSerGlnSerCysAspThrValIleTyrVal 365
QY      72 -----
Db      366 GlyProGlyGlyAlaAlaLeuSerAspArgGlnLeuThrAspAsnGlnGlyProProAsp 385
QY      73 -----CTGATA-----
Db      386 PheValProIleIleProAlaLeuSerArgHisArgProSerTyrGlyProArgAspAla 405
QY      78 -----
Db      406 AspHisPheArgCysSerThrPheAlaGlnLeuGlnIleuArgLeuGlnCysMetAspGly 425
QY      79 -----GGGGTGAAGCGCGCGCACTGCCAGCGGAAAGT-----
Db      426 AsnGlnGlyProSerGlyGly-----ProGlyGlyThrAspGlyAlaGlnAlaSerProAl 444
QY      109 -----
Db      444 ArgGlyGlyArgGlySerSerProProGlyAlaAlaAspSerProArgLysAlaValGlyTh 464
QY      109 -----
Db      464 rPromeAlaAlaSerThrProArgGlySerSerGlyProAspThrHisGlnGlyThrPr 484
QY      110 -----CGACCGTGTGTGAGAGATCATGAGTTGCTGGAGACAGACGAGTGGAAACA-----
Db      484 ogLuproCyluValAlaIleValTrp-----GlyAspGlnArgGlnAspSerSerAlaTr 502
QY      162 -----GGCGGACGCGGAAAGTGGTCAT-----
Db      502 rPProGlnLeuLeuValProGlnLysAlaAlaValSerGlyGlyArgArgProLeuProS 522
QY      183 -----CCTGAGCCGACGACAGTCTTACAA-----
Db      522 erProAlaProProProGlnLeuLeuGlnAlaCysArgAlaProGlnGlnProGlyG 542
QY      207 -----GGTCCCTGACGCG-----
Db      542 LysGlyGlyThrAspGlyValAlaArgThrProProValGlyMetSerGlyGlnValAlaG 562
QY      219 -----AGACGACAGAG 228
Db      562 LysSerPromeCLeuProGlyAlaThrCysProArgLeuAlaAlaGlySerArgCysProG 582
QY      229 GCCAAGGCTTGAAGAGACAGTACATTTTGAACCATCCAGATGCTTTGATATATGA--- 284
Db      582 LuArgGlyLeuLeu-----ThrThrThrValThrLeuGlnArgProValGlnLeuAsnG 600
QY      284 -----
Db      600 yGluAspGlnLeuValPheThrValValGlnGlnLeuSerLeuGlyAlaLeuAlaGlyAl 620
QY      284 -----
Db      620 aglyArgProThrSerLeuAlaSerPheAspSerAspCysSerLeuArgAlaLeuAlaSe 640
QY      285 -----TTTGATGCACAGACTC 301
Db      640 rGlySerArgProValSerIleLeuSerSerIleAsnAspGlnPheAspAlaTyrThrSe 660
QY      302 TGAAGAACATCGTGAAGCGCAAAACGGTGAAGGTC----- 338
Db      660 rGlnAlaProGlnGlyGlyProLeuGlnGlnGlyAlaAlaIleTrpAlaGlySerSerHisGlySe 680
QY      339 -----GACCTATGATTTTGT----- 353
Db      680 rSerIleSerSerTrpLeuSerGlnValSerValCysThrAlaAspSerArgAspProTh 700

```

```

QY      354 -----GACACACTCAAGGTTACACAGACACGCGGTGCTAC 391
Db      700 rProGlnProArgPheSerSerProAspSerLeu-----AlaGlyLeuAspProGlyGlyProPr 719
QY      392 CTGC-----GGACGTGGTCTGTTTGAAGGCGCATCTTGTTGTTCTACAGCC 436
Db      719 AlaLeuAspGlySerLeuGlyAspGlySerSer-----GlyPheLeuGlyProAspArgPr 738
QY      437 AGAGATCCGGACATGTTCCACCTGCGCTCTTCTGAGACCCGACTCG-----ACG 490
Db      738 AspSerProGly-----Pro--ThrTrpGlyProCysProGlyGlnVal 752
QY      491 TCAGCTGCTCTCAAGACTCTCCGGACGCTGGCGGAGGAGGAGCT----- 539
Db      753 Ala-AlaValAlaProSerArgProGlyArgGlnProGlnAlaGlyProSerArgTrpAl 772
QY      539 -----
Db      772 AserAlaAlaGlnThrIleHisSerSerLeuProArgLysProArgThrAlaSerAlaTh 792
QY      539 -----
Db      792 rThrArgValGlyCysAlaArgLeuGlnSerProProGlyArgGlyLysLeuPheG 812
QY      539 -----
Db      812 uAspProTrpLeuLeuArgValGlyGlnCysAspThrGlnAlaAlaSerAlaGlyArgAl 832
QY      539 -----
Db      832 arProSerProThrLeuGlySerProArgLeuProGlnAlaGlnValMetLeuAlaCysAl 852
QY      539 -----
Db      852 agLArgValAlaAspGlyCysGlnValAlaAlaArgAlaAlaArgArgProGlnAlaVa 872
QY      539 -----
Db      872 lAlaArgIleProProLeuArgArgGlyAlaThrThrLeuGlyValThrThrProAlaVa 892
QY      539 -----
Db      892 lSerTrpGlyAspAlaProThrGlnValValAlaCysSerGlySerLeuLysAlaSerPr 912
QY      540 -----GGACGACA 547
Db      912 oThrSerLysGlyLeuAlaProLysAlaGlyPheLeuProArgProSerGlyAla-- 931
QY      548 TTCTGACGACATACACACACTTGTGTAAGCGCGCTTCGAGAGGTTCTGCTGCCGACAA 607
Db      932 -----AlaProProAla-----Pro--ProThrArgLysSerSerLeuGlnG 945
QY      608 AGAAGTATGCCGATG----- 623
Db      946 ArgSerSerPro-AlaSerAlaProProHisAlaValaAsnProAlaArgValAlaAl 965
QY      624 -----GATCAT----- 629
Db      965 AlaValaLeuArgGlyGlnGlnGlnProArgProSerSerArgAlaAspHisSerValPr 985
QY      629 -----
Db      985 oArgAlaThrSerSerLeuLysAlaArgAlaSerLysValGlnAlaAlaHisArgLeuAl 1005
QY      629 -----
Db      1005 acGlyHisAlaSerLeuGlnArgTrpGlnGlyLeuAlaHisSerSerSerLysGlyArgG 1025
QY      630 -----CCGAC 634
Db      1025 uAlaProGlyArgProProArgAlaValaProLysLeuGlyValProProSerSerSerProTh 1045

```

```

Qy 635 GAGAGTGCACATATGTTGCCATCAACCTGATGTCAGACATCCAGACATTCTGCA 694
Db 1045 r-----HisGlyProAlaProAlaCysArgSerGly----- 1055
Qy 695 ATGTGCATCTGCATAATGGACCGAGAGGGGTCCAAATGGCGAGCTACAG----- 747
Db 1056 ---AlaAlaIysAlaValGlyAlaProIysProProValGlyGly--LysGlyArgG 1074
Qy 748 -----CGAACCTTTCTG 760
Db 1074 LyleValAlaIaGlyIysSerArgAlaLeuGlyProSerValIysLeuSerThrAlaSerV 1094
Qy 761 AGCCAGGGGAGCCACCTCGGATGCTGACCTCGGCAACGGTCAATTGGAGTCCAGCA 820
Db 1094 alThrGlyArgSerProGlyIysProValAlaGlyProArgAla-----AlaProArg 1111
Qy 821 GCAGACCCCACT 832
Db 1112 AlaGlyProSer 1115

RESULT 28
US-09-488-725A-2418
; Sequence 2418, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc FL_genes_b Versions 1.0
; SEQ ID NO 2418
; LENGTH: 1503
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2418

Alignment Scores:
Pred. No.: 418 Length: 1502
Score: 265.40 Matches: 108
Percent Similarity: 19.91% Conservative: 28
Best Local Similarity: 15.81% Mismatches: 81
Query Match: 17.04% Indels: 466
DB: 1 Gaps: 13

us-09-896-522-3 (1-834) x US-09-488-725A-2418 (1-1502)
Qy 822 GCTGCTGACTTCGAATGTGACCGTTTGCAGAGGTGACATCCAGGGGTGTCCTCGG 763
Db 721 AlaGlyGlyLeuGlyMetProPro-----SerLeuPro----- 731
Qy 762 CTCAGAAAAGGCTCGCTGTAGCTCCGCCATTGACACCTCTCTCGGTGCCATTGGACAT 703
Db 732 -----Pro-----ProProLeuGlnProProSerLeuPro-LeuSerMe 744
Qy 702 GTCACCATTC-----AGAAATGCTCGATGTC-- 675

```

```

Db 744 tGlyProValLeuProAspProPheThrHisIstYrAlaProLeuProSerTrpProCysTrp 764
Qy 675 ----- 675
Db 764 rProHisValSerProSerGlyTrpProCysLeuProProProProThrValProLeuVa 784
Qy 674 -----TGCACGATCAGGTTGATGCCMAC 652
Db 784 lSerGlyThrProGlyAlaIstYrAlaValProProThrCysSerValPro-----TrpAlaP 803
Qy 651 CA-----TATTGTCACCTCTGCTG 631
Db 803 roProProAlaProValSerProTrpYserSerThrCysThrTrpGlyProLeu-GlyTrp 822
Qy 630 GATGATCAATCGGCATACTTCTTTGTCGCGAGGACGAATCCTCGAAGCGCGCTTCAC 571
Db 823 -----Gly-----ProGlyProGlnHis-----AlaProPhe-- 831
Qy 570 GAAGTGTGTACTGCGTCAGAAATCTGCTCCAGGTCCCTCCGCGCAGTCCCGAG 511
Db 832 -----TrpSerThr-----ValProProProProProProAla 843
Qy 510 AACTTTGAGA-----CAGCTGACGTGAGTGGTGTCCAGAGAGCGCAG 460
Db 844 SerIleGlyArgAlaValProGlnProIysMet-GluserArgGlyThrPro-----AlaG 862
Qy 459 GTGGAACATGTCCC-----G 445
Db 862 lY-----ProProGlnAsnValLeuProLeuSerMetAlaProProLeuSerLeuG 879
Qy 444 GATCTCGGCTGTAGAACACCAAGATGCCCTGAACAGAACCA----- 401
Db 879 lYleuProGly-----His--GlyAlaProGlnThrGluProThrIysValGluVal 896
Qy 401 ----- 401
Db 896 ysProValProAlaSerProHisProIysHisIysValSerAlaLeuValGlnSerProG 916
Qy 401 ----- 401
Db 916 lMetIysAlaLeuAlaCysValSerAlaGluGlyValThrValGluGlnProAlaSerG 936
Qy 400 -----CGTCCGACGGGTAGACCAACCGGTGCTCTGG 370
Db 936 lIuArgLeuysProGluThrGlnGluThrArgProArgGluIysProProLeuPro---A 955
Qy 369 TAACTTGAAGTGTGCACAAATCATAGTGGCACCCTCA-----CGGTTTGGCCCTC 316
Db 955 lAthrIysAlaIaValProThrProArgGlnSerThrValProIysLeuPro---AlaVal 973
Qy 315 CAC----- 313
Db 974 HisProAlaArgLeuArgIysLeuSerPheLeuProThrProArgThrGlnGlySerGlu 993
Qy 312 GATGTTCTCAGAGTCTGTGCATCAATCATATTATCAAGGCACTCGATGTCATAAATT 253
Db 994 AspValValGlnAlaPheIleSerGluIleGlyLe-GluAlaSerAspLeuSerSerIe 1013
Qy 252 GTAC-----TGTCCTTTCAGGCTTTGGCTT 226
Db 1013 lUeuGluGlnPheGluIysSerGluAlaIysIysGluCysPro-----ProP 1029
Qy 225 CTGCTTCGCCGTCA----- 212
Db 1029 roAla-----ProAlaAspSerIleuAlaValGlyAsnSerGlyGlyValAspIleProGln 1048
Qy 212 ----- 212
Db 1048 lIuIysArgProLeuAspArgLeuGlnAlaProGluIleuAlaAsnValAlaGlyLeuThrP 1068
Qy 212 ----- 212
Db 1068 roProAlaThrProProHisGlnIleuTrpIysProLeuAlaIaValSerLeuLeuAlaI 1088

```



QY	212	-----	212
Db	1088	ysalalysSerProlyserThrlaGlnGluGlyThlLeuLysProGluGlyValThrG	1108
QY	211	-----	GGACCTTGAGAACTT 196
Db	1108	luAlaLysHisProAlaAlaValaArgLeuGlnGluGlyValHisGlyProSerArgValH	1128
QY	195	GTCTGGGTGAGATGACCAC-----CTTCCGCGCCGCGCTTTCCACTCGTGGTTG	145
Db	1128	tsValGlySerGlyAspHisAspTyrCysValArgSerArg-ThirProGlyLysW	1147
QY	144	TCCGAGCAATCCATGATCTTTCTGACACACGAGTCGACTTCCGCTGGCAGTCCGC	89
Db	1147	etProAla--LeuValIleProGluVal--GlySerArgTyrAsnValLysArgH	1164
QY	89	-----	89
Db	1164	isGlnAspIleThrlLeuLysProValLeuSerLeuGlyProAlaAlaLProProProC	1184
QY	88	-----CGTCACTCCCTATCAGAGAGGCGCTGTCGTCGCGACCGAGCT-44	
Db	1184	ysIleAlaLaserArgGluProLeuAspHisArgThrSerSerGlnAlaAspProS	1204
QY	43	-----	CCGCGCGCGGGCT 31
Db	1204	eraLProCybLeuAlaProSerSerLeuLeuSerProGluAlaSerProCybArgAsnA	1224
QY	30	CTGCAGCTCTCGCTCCCGCGAAGCA 2	
Db	1224	spMetAsnThrArgThrProProGluPro 1233	

```

RESULT 29
US-09-488-725A-5990
; Sequence 5990, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_Fl_genes_b Versions 1.0
; SEQ ID NO 5990
; LENGTH: 1567
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5990

Alignment Scores:
Pred. No.:          473
Score:              264.50
Percent Similarity: 18.36%
Best Local Similarity: 14.72%
Query Match:        16.98%
I:                   1
Gaps:                14
Length:              1565
Matches:             117
Conservative:        29
Mismatch:            64
Indels:              585

```

us-09-896-522-3 (1-834)	x	us-09-488-725A-5990 (1-1565)
QY 832 AGTGGGCTCTGCTGCTGACTCCAAATGTGACGTT		797
Db 833 SerGlyThrProCysLeuProProProProThrValProLeuValSerGlyThrProGly		852
QY 796		777
Db 853 AlaThrAlaValProProThrCys		870
QY 776		758
Db 870 roValSerProTyrSerSerThrCysThrTyrGlyProLeuGlyTyrGlyPro		887
QY 757 AAAAGTCCGCTGTAGCT		722
Db 888		906
QY 721 CTGGGTG		715
Db 906 aSerIleGlyArgAlaValProGlnProTyrProMetCysSerArgGlyThrProAlaGlyPr		926
QY 714		683
Db 926 oProGluAsnValLeuPro-LeuSerMetAlaPro		942
QY 683		683
Db 943 LeuProGlyHisGlyAlaProGlnThrGluProThrTyrValGluValLysProValPro		962
QY 683		683
Db 963 AlaSerProHisProLysHisLysValSerAlaLeuValGlnSerProGlnMetLysAla		982
QY 682		648
Db 983 LeuAlaCysValSerAlaGluGly		1001
QY 648		648
Db 1001 euLysProGluThrGlnGluThrArgProArgGluLysProProLeuProAlaThrLysA		1021
QY 648		648
Db 1021 IaaValProThrProAlaGlnSerThrValProLysLeuProAlaValHisProAlaArgL		1041
QY 647		611
Db 1041 euArgLysLeuSerPheLeuProThrProArg		1054
QY 611		611
Db 1055 SerGluAspArgValAlaGlnAlaPheIleSerGluIleGlyIleGluAlaSerAspLeuSer		1074
QY 611		611
Db 1075 SerLeuLeuGluGlnPheGlyLysSerGluAlaLysLysGluCysProProProAlaPro		1094
QY 610		580
Db 1095 AlaAspSerLeuAlaValGly		1113
QY 580		580
Db 1113 gProLeuAspArgLeuGlnAlaProGluLeuAlaAsnValAlaGlyLeuThrProProAl		1133
QY 580		580
Db 1133 aThrProGlnIleGlnLeuTyrLysProLeuAlaAlaValSerLeuLeuAlaLysAlaLys		1153
QY 580		580



```

Db      317 AlaAlaArgAlaGlyAlaAlaGlnAlaGlu-----SerProGlnProArgG 333
Qy      426 CACCAAGATGCCCTCAACAGAACACAGCTCCG----- 395
Db      333 lnglnArgLeuProAlaAlaAlaProAlaProGlyAlaArgValLeuSerProArgAlaG 353
Qy      394 -----CAGGGTAGACCGCTGCTCTGCT----- 369
Db      353 lYargMetArgGlyHisProPro-----GlnGlyAlaGlySerArgGlyValAlaG 371
Qy      368 -----AACCTTGAAGTGTGCACAAATCATATCATATCAAGGCATCTGAGTGTCAA 256
Db      371 yAlaProAspLeuGlnArgVal-----ArgProTropGlyProPro-----ProP 386
Qy      315 CACGATGTTCTTCAGAGTCCCTGTGCATCAATCATATCAAGGCATCTGAGTGTCAA 256
Db      386 roArgVal-----CysProGlyThr-----GlnArg-----GlyArgG 397
Qy      255 ATGTACTGTCTTCAGAGCTTCAAGGCTTGTCTGTCTGCTGCGTCAAGA----- 209
Db      397 lY-----Pro-----ArgGlyPhePro-----ProGlnGlyAlaGlnAspSerG 410
Qy      208 -----CCTTGTAAC-----TGCTCTGCTCAAGA----- 182
Db      410 lnglYAlaPro-----ArgThrArgGlnAlaGlyProProAlaProGlyGlyGlyLurGm 429
Qy      181 -----TCACCACTTCGCGCTGCGCTGTTCACCTGCTGTCTCCGACCACTTCATGAT 127
Db      429 eUrThrProProProSerArgCysLeuPheProAlaGlyArgProAla-LeuHis--- 447
Qy      126 CTTCACACACAGGTCGACTTCCCGCTGCGAGTGCAGCCGCTCAACCCCTATCAGGAAGG 67
Db      448 -----LysProAlaAlaGlu-----GlyCysProPheValHisArgAlaAlaGlnGly 463
Qy      66 CCGCTGTGCGGACGGT----- 50
Db      464 -----GlySerGlnGlyAlaGlnProGlnThrLeuProPheLeuTyPheTyPhePheP 482
Qy      50 ----- 50
Db      482 hePhePheLeuTyPheArgGlnGlnSerValArgPheCysProIleTyValSerT 502
Qy      50 ----- 50
Db      502 hrArgGlnGlnThrLeuValValCysValCysValPheLeuCySTPPhPheLysGln 522
Qy      49 -----CGGCTTCGCGCGCGCGCTCTCGCAGTCTTCGCTCCGCG 10
Db      522 ecGlyArgArgLysLysAsnSerProPro-----LeuSer-SerIleSerLeuProP 539
Qy      9 CG 8
Db      539 ro 539

```

```

; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PC FL_genes_b Versions 1.0
; SEQ ID NO 5728
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-5728

Alignment Scores:
Pred. No.: 15.5 Length: 293
Score: 262.40 Matches: 104
Percent Similarity: 24.17% Conservative: 19
Best Local Similarity: 20.43% Mismatches: 73
Query Match: 16.85% Indels: 315
DB: Gaps: 6

us-09-488-522-3 (1-834) x US-09-488-725A-5728 (1-293)
Qy      828 GGGTCTGCTGCTGAGTCTCCAAATGTGACCGTTTGCCAGAGTCAAGCATCCAGGTGTC 769
Db      17 GlySerAlaGlyGlyLeu-----ArgAlaPro-----GlyAlaAlaAlaGlyGlyP 32
Qy      768 CCTGTGCTCAAGAAAGAGTCCGCTT-----GTAGCTG 728
Db      32 roGlyValGlnProAlaGlyGlySerGlyLeuProGlyAsnAlaIleAlaGlyAlaAsp 52
Qy      737 CGCCCATGTGACCCCTCTGCGTCCATTTGACAGATGTCAACATTCAGATGCTCGATG 678
Db      52 roGlyArgGlyProAlaSer-----ProPheThrAspLeuSer-----LeuProTrp--- 67
Qy      677 TGCTGCACGATCAGGTGATGACCAACCATATTCCTCTCTGAGATGATCAC----- 622
Db      68 -----Asp-----Leu-TripProPro-----Pro-----ThrAspHisAlaP 78
Qy      621 -----ATCGGCATATCTTCTTGTG 603
Db      78 roGlyAlaProAspPheProAlaAlaValGlnGlyArgProTrpAlaGly----- 93
Qy      602 GGCAGCAGAACTCTTCGAAGCGCGCTTCACGAGAGGTGTATCTGCTCAGAAATCTGC 543
Db      94 -----GlyArgProPro-----TripProAlaSer-----Gly-ValLeuGlySerArgValCys 109
Qy      542 TCCAGGTCCC-----TCCCTCGGCGCAGCTCCCGAGAACTTTGAGACAGCTTG 492
Db      110 -----GlyProLeuTyPheThrSerProAlaGlyProGly-SerGlyGlyLeuSerProS 128
Qy      491 AGGTGAGTCCGCTGTCCAGAAAGCGCAGGTGGAACATGTCGCCGATTCCTGCTG 432
Db      128 ecGlnGly--Gly--Pro--AlaGlyAlaGlyGlyAspAla--GlyLeuProGly-- 143
Qy      431 TAGAACACCAAGATGCTCAAAACAGAACACAGACGTCGCGAGGTAGACACCGTGTCTCT 372
Db      144 -----ArgCysPro-----SerAla-----ProTrp----- 150
Qy      371 GGTAACTTGAGTGTGTCAAAATCATATGATGTCGAGCACTCCACCGTTTGGCTTCACG 312
Db      151 -----ArgAlaGlySerArgProAlaAlaSerCysPro-----A 162
Qy      311 ATGTCTTCAGATCCTGTGATCAATATCATATTAAGAGCATCTGAGTGTCAAAATTTG 252
Db      162 sPTripLeProGlyPro-----GlnGlyLeuTrpLeuHisArg----- 174
Qy      251 TACTGTCTTCAGAGCCTTGAGCTTGTGCTGCGCTGAGCA----- 209
Db      175 -AsnProThrSerGlyPro-----ProSerGlnIleGlyGlnGlyAlaGlnGlyAspG 193

```

```

QY 208 -----CCTTGAGAACCTGTCTGCTCAGGATGACACC 174
Db 193 uGIyValAlaAspAlaProGlnIleGlnCyblyAsnGly----AlaGlnAsp--ProPr 211
QY 173 TTCGCGTCCGCGCTGTTCCACCTCGTTCCTCCAGCAATCCATGATCTTCTCAGACAG 114
Db 211 o-----AlaGlnAspIuProProGlnI--ValPro----- 220
QY 113 GTCGACTCCGCGCTGCGAGAGTCCGCCCTCACCCTTATCAGAGAGGCCGCT----- 62
Db 221 -----GluAlaGlyGlnGlnAspAlaValProAlaGlnGlnGlyProGlyGlyThrp 238
QY 61 -----GTTG 58
Db 238 roGIuThrGlnAlaAspGlnValArgGlnArgProGlnAlaHisLeuAlaGlnGlyAla 258
QY 57 CGGACGGTCCGCGCT-----CGGCGCGGGGCTTCGCA 25
Db 258 lAlYsGlySerProArgArgLeuAlaAspProGlnAspLeuProAla---GlyGlnMetS 277
QY 24 GTCTTCGCTCCCGCCGCGAGCCA 2
Db 277 erLeu---AlaProProPhePro 283

```

# RESULT 32

```

US-09-488-725A-2188
; Sequence 2188, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLEPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/01-21
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: Pf_Fl_genes_b Versions 1.0
; SEQ ID NO 2188
; LENGTH: 4619
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2188

```

```

Alignment Scores:
Pred. No.: 740 Length: 4618
Score: 262.40 Matches: 120
Percent Similarity: 19.36% Conservative: 25
Best Local Similarity: 16.02% Mismatches: 68
Query Match: 16.87% Indels: 536
DB: 1 Gaps: 15

```

us-09-896-522-3 (1-834) x US-09-488-725A-2188 (1-4618)

```

QY 3 GCGTTCGCGGAGGCGGAAGACTGCGAGAGCCCGCGCGGAGCGCGACGTCGCGACCA 62
Db 671 G1YTYr---G1Yg1Yg1uAspCyS-----G1Yg1nGlnGlnProPro 683
QY 63 GCGGCGCTT----- 71

```

```

Db 684 AlaSerAlaCySProGlyGlyCySg1YProArgGlnLeuCySArgAlaGlyGlnCySVal 703
QY 72 -----CCTGAT----- 77
Db 704 CySValGlnGlyPheArgGlyProAspCySAlaIleGlnThrCySProGlyAspCySArg 723
QY 78 -----AGGGGTGAGCGCGGCACTGCCAGCGGAAAGTCAGCCGTGTGTGAGAAATCATGGA 134
Db 724 G1YArgG1Yg1u-----CySHis-AspGlySerCySValCyS--LysAsp---Gly 738
QY 135 GTTCTGGGACAGACGAGT----- 155
Db 739 TyrAlaGlyG1uAspCySg1Yg1nGlnValProThrIleGlnGlyMetArgMetHisLeu 758
QY 156 -----GSAACAGCGCGAGCGGAAAGGTGTCATCTCTGAGCAGACAGT----- 200
Db 759 LeuGlnGlnThrThrValArgThrGln--TrpThr--ProAlaProGlyProValaProAla 777
QY 200 ----- 200
Db 778 TyrGlnIleGlnPheIleProThrThrGlnGlyAlaSerProProPheThrAlaArgVal 797
QY 200 ----- 200
Db 798 ProSerSerAlaSerAlaTyrAspGlnArgGlyLeuAlaProGlyGlnGlyVal 817
QY 200 ----- 200
Db 818 ThrValArgAlaLeuArgGlyThrSerTrpGlyLeuProAlaSerThrIleThrThr 837
QY 201 -----CTACAGAGTCTGTGACGCGACAGCAGAGG----- 229
Db 838 MetIleAspGlyPro-----GlnAspLeuArgValAlaValThrProThrThrLeuG 856
QY 229 ----- 229
Db 856 IuLeuGlyTrpLeuArgProGlnAlaGlnValAspArgPheValIleSerTyrValSerA 876
QY 230 -----CCAGGCGCTTAAAGACAGTACATTTTGA 260
Db 876 laGlyAsnGlnArgValArgLeuGlnValPro--ProGlnAlaAspGlyThrLeuLeuT 895
QY 261 CCATCCAGAGTCTGTGATGATGATTTGATG----- 291
Db 895 hr-----AspLeuMetProGlyValG1uTyrValValThrValTh 908
QY 292 -----CACAG 236
Db 908 rAlaGlnArgGlyArgAlaValaSerTyrProAlaSerValArgAlaAsnThrGlyHisG 928
QY 297 GACTGTGAAAGAACATCGTGGAGGGCAAAACGGTGGAGGTCCGACCTATGATTTTGTGAC 356
Db 928 nGlnTrp---TrpAlaTrpArgGlyMet-GlyGly--LeuArg-----Asp 941
QY 357 ACACTCAGGTTCACAGGACCAACGAGTGTCTACCTCGGAGCGTGTCTGTTTGAAGG 416
Db 942 Thr-AspArgPhePro-----SerValLeuPheProAlaPro-----Gly 954
QY 417 CATCTTGTTGTTCACAGCCAGAGATCCGGAGACATTTCCACTCTGG----- 464
Db 955 HisTyrSer---Tyr--Pro-GluValArg-----ProProAlaProProProLys 969
QY 465 -----CCTCTTCGNG----- 475
Db 970 SerArgProArgProAlaProAlaProArgProProProPro--TrpProSerA 988
QY 476 -----ACACCGACTCCGACGTCAGCTGTCTCGAAG 506
Db 988 rGProAlaGlnGlnArgGlnGlnGlnSerProProArgPro-----SerLeu 1003
QY 507 AGTTCTCCGGAGCGTCCGCGAGGAGGACCTGG-----AGCA 545
Db 1004 SerGlnProProArgArgPro-----TrpGlyAsnLeuThrAlaGlnLeuSerA 1020

```

```

QY 546 GATTCTGACGACAGTACA----- 562
DB 1020 rghhe---ArgGlyThrValGlnAspLeuGlnArgHisLeuArgAlaHisGlyTyrProL 1039
QY 562 ----- 562
DB 1039 euArgAlaAsnGlnThrTyrThrSerValAlaArgHisLeuHisGlyTyrLeuGlnArg 1059
QY 563 ----- 563
DB 1059 rglLeuLeuAlaAlaAlaProAlaGlySerProAlaProProAlaArgHisSerProArgProT 1079
QY 585 CGAGAGTTCGCTGCGCG-----ACAAAGAG-----TA 614
DB 1079 hrAlaSer-----ProAspProGlyThrArgValArgAspSerAsnGlnGlyLeu 1096
QY 615 TGCAGATGATGATCCACAGAGAGTGAACAATATGTTGCCATCAACCTGATCGTGA 674
DB 1096 rglY-----LeuSerProGluGlyValAspArgValAlaAla-----SerArgHis 1111
QY 675 GCACATCCAGACATCTGTAATGTGACATCTGCAATGCGACC----- 718
DB 1112 ProLysPro-GluValLeu---Gly-SerSerAlaAspGlyAlaLeuLeuValSerLeu 1130
QY 719 -----GAGG 722
DB 1130 spGlyLeuArgGlyGlnPheGlnArgValValLeuArgTyrArgProGlnProAlaG 1150
QY 723 AGGCTCAATGGGC-----GGAGCTCAAGCGAGCCTTTCTGAGCAGG 767
DB 1150 luGlyProGlyGlyGlnLeuThrValProGlyThrThr-ArgThrValSerLeuProAs 1169
QY 768 GACCAACCTGGG----- 780
DB 1169 pleuArgProGlyThrThrThrThrHisValGlnValHisGlyValArgAlaGlyGlnThrSe 1189
QY 780 ----- 780
DB 1189 rlySerTyrAlaPheIleThrThrThrGlySerSerProLeuGlyLeuLeuGlyThrTh 1209
QY 781 -----ATGCTGACCTCTGGCAACGGTCACTTTGAGATC 815
DB 1209 rAspGluProProSerGlyProSerThrThrGlnGlyAlaGlnAlaProLeu--Leu 1228
QY 816 CAGCAGACAGACC 828
DB 1229 GlnGln-ArgPro 1232

RESULT 33
US-09-488-725A-7033
; Sequence 7033, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344

```

```

; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: PL_FL_genes_b Versions 1.0
; SEQ ID NO 7033
; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)-(292)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-7033

Alignment Scores:
Pred. No.: 15.4 Length: 292
Score: 262.30 Matches: 104
Percent Similarity: 23.488 Conservative: 20
Best Local Similarity: 19.704 Mismatches: 67
Query Match: 16.844 Indels: 337
DB: 1 Gaps: 8

us-09-896-522-3 (1-834) x US-09-488-725A-7033 (1-292)

QY 831 GTGGGGTCTGCTGCTGACTCCAAATGTGACCGTTTGACAGAGTCAGATCCAGGT- 773
DB 6 LeuSerSerSerAla--ThrSerAsn-----Arg-AlaArgArgSerLysCysSerGlyP 23
QY 772 -----GRTCCCTGGCTCAGAAAGTCCGCTTGTAAGT 739
DB 23 rlySerArgAlaThrProLeuAspSerGlyPro-----GlyPro-----Ala 37
QY 738 CCGCCCATGAGACCCCTCGGTGGCATTTGACATGTCACCATTCAGATGTCGAT 679
DB 38 ProPro--GlyProSerSer-AlaLeu---MetMetPro-SerSerCysProTrp- 53
QY 678 GTGCTCAGACATCAGGTTGATGCAACATATTTGTCACCTCTCGTGAGATGTCAT- 620
DB 54 -----ArgThrGlyAlaLeuGlyPro-----SerProAlaGly--SerArg 67
QY 619 -----CGCATCTCTTTGTCGCGCAGGAGAACTCTCGAAGCGGCTTGAGAA 568
DB 67 lAlaGlyArgCysThrSer--SerAlGly-----ProGlySer---A 80
QY 567 GGTGTGTACTGCGTGA----- 551
DB 80 rgrTrpLeuThrThrThrThrSerSerProGlyCysAlaThrArgThrTyrArgThrMetArgM 100
QY 550 -----GAATCTGCTCCAGGTCCTCCCTCGGCG 523
DB 100 etGluProArgProLeuArgSerArgMetGlyGluSerAlaProGly--IlePro--Ala 118
QY 522 CAGCTCCGAGAACTCTTCGAGACAGCTGACGTGAGTGGGTGCCAGAGAGCGG 463
DB 119 GluLeuPro-----SerAlaAlaPro-----S 126
QY 462 CAGGTGGAACATGTCCCGGATCTCTCGGTGAGAACACCAAGATCCCTCAACAGAAC 403
DB 126 etGly-----ProSerAlaProSerAlaAlaAlaProSerAlaProThrThr--Pr 142
QY 402 CAGCTCGCAGAGGTAGACACCGGTGCTCTGTGTAACCTTGAGTGTGTCAAAATCAT 343
DB 142 oAlaAlaAlaGlyProAsnThrLeu***Ser-----ArgAl 154
QY 342 GGTGCGACCTCCACCGTTTGC---CTTCCAGATGTTCTTCAGAGTCCGTGCAATCA 286
DB 154 rGThrAla-----GluTrpCysTrpProProSerCysSer-----Cys----- 166
QY 285 ATCATATTAAAGCATCTGTGATGTGCAAAATTTACTCTCTTCAAGCCTTGG----- 230
DB 167 -----CysTrpGlyTrp-----Cys***SerTrpSer--AlaTrpAspTr 179
QY 229 -----CCTTGTGCTCTGCGGTCAAGACCTTGTAAG----- 200
DB 179 rPArgArgProProLeuGlnValSerProAla-----ProSerSerSerCysArgAlaS 197

```

```

QY 200 ----- 200
Db 197 erCyStrpCyLeuGlusertleThr**SerSerSerThralaArgSerArgAlat 217
QY 199 ----- ACCTGCTCTGCTCAGATGACACCTTCGCGCCGCTG 160
Db 217 hrdglAlaserSerSerSerThrcySerProthrSerArgSerAspArgGlyAlaAlatPrp 237
QY 159 TTCCA---CCTGCTGCTGCCAGCAACTCCATGATCTTTCACACACGCTGCATTC 103
Db 237 hrProSerProMetGlyAlaPro-----LeuLeu-----Pr 247
QY 102 GCTGCGAGTCCG-----CGCTCAC 82
Db 247 oCySerValProLeuLeuSerArgGluGluAlaLeuGlnAspProArgAsnPro-Serp 267
QY 81 CCTATCAGAGAGGCGCTGCTGTCGAGACGCTCCGCGCGGCGCTTCGCGAGTC 22
Db 267 ro---**GlyValCySerSerGlySerSerGlyHis-----AlaGlyLeuAlaLeuG 283
QY 21 TTGCGCTCCC 12
Db 283 yLysProPro 286

RESULT 34
PCT-US00-05988-1601
; Sequence 1601, Application PC/TUS0005988
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Human Prostate Cancer Associated Gene Sequences and Polypeptides
; FILE REFERENCE: P101PCT
; CURRENT APPLICATION NUMBER: PCT/US00/05988
; CURRENT FILING DATE: 2000-03-08
; EARLIER APPLICATION NUMBER: 60/124,270
; EARLIER FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentm Ver. 2.0
; SEQ ID NO 1601
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US00-05988-1601

Alignment Scores:
Pred. No.: 12.4 Length: 253
Score: 260.70 Matches: 99
Percent Similarity: 25.89% Conservat: 24
Best Local Similarity: 20.84% Mismatches: 59
Query Match: 16.76% Indels: 293
Gaps: 6

us-09-896-522-3 (1-834) x PCT-US00-05988-1601 (1-253)
QY 2 TGGCTTGGCGGGAGGCGAAGCTGCCAGACCCCGCGCGGAGCCGACCTCCGAC 61
Db 21 Trp--AlaAlaAlaGly-----ProArgArgArg--AlaValArgMet 33
QY 62 AGCGGCGCTCTCTGATAGGGGTGAGCGCGGCGACTGCCAGGGGAGATGCACCTGTGTG 121
Db 34 SerGly----- 35
QY 122 AGAAGATCATGAGTGTCTGGACAGAGACGAGTGGACACGCGGACGAGAGGTGTCA 181
Db 36 -----TrpAla-----Asp-GluArgGlyGly--GluGlyAspGlyArg--IleT 49
QY 182 TCTCGAGC-----CAGACAGGTTCTTACAG 208
Db 49 yrValGlyAsnLeuProThrAspValArgGlyAspLeuGluAspLeuAspLeuTherlyST 69
QY 209 TCTGACGCGAGAGAGGCGAAGGCTTGAAGAAGACAGTACAAATTTGACCATCCAG 268

```

```

Db 69 yr-----GlyArgGle-ArgGluIleGluLeuLysAsnArgHisGly-LeuVal--Pro 86
QY 269 ATGCCCTTGAATATATGATT---GATCACAGACCTCTGAAGAATCATGTCGAGGCAAA 325
Db 86 heAlaheValArg--PheGluAspProArgAspAlaGluAspAlaIleTyGlyArgAs 105
QY 326 CGGTGAGAGTCCGACCTATGATTGTGTGACACACTCAAGGTTTACAGAGA----- 376
Db 105 nGly-----TyrAspTyr-----GlyGlnCyAspArgLeuArgVal 116
QY 377 -----CAACGCTGCTACCTCGGACGCTGCTGTCTTTGAGGCACTTCGTGTTCT 430
Db 117 GluPheProArg--ThrTyGly--GlyArgGly-----GlyTrp--Pro 129
QY 431 ACAGCAGAGAGATCCGCGACATGTTCCACCTGCGCTCTTCGAGACACCGACTCCGAG 490
Db 130 ArgGlyGlyArgAsnGly-----ProProThr-----ArgArg--SerAsp 143
QY 491 TCAGGCTGTCTCGAAGATTCTCCGGAAGCTGCGCGGAGGAGGACCTGACAGATTC 550
Db 143 heArg--ValLeuValSer-----GlyLeuProPro--SerGlySerTrp-----G 157
QY 551 TGAAGCAGTACACCACTTCGTGAGACCGGCTTCGAGAGATTCTGCTGCCAGAAAGA 610
Db 157 nAspLeuLysAspHisMetArgGluAlaGly-----AspValCys----- 170
QY 611 AGTATGCCGATGTGATCA----- 628
Db 171 --TyrAlaAspVal-GlnLysAspGlyValGlyMetValGluTyrLeuArgLysGluAsp 189
QY 629 -----TCCACAGAGAGTGGACA 646
Db 190 MetGluTyrAlaLeuArgLysLeuAspAspThrLysPheArgSerHisGlu--GlyG 208
QY 647 A-----TATGTTGCCATCAACTGATCTGTCAGACATCATCAGACA 688
Db 208 uThrSerTyrlArgValTyr-----ProGluArgSerThSerTyrlTy 224
QY 689 TTCTGATGTGACATCTGCAATGGCACCGAGAGAGTTCATGGCGGAGTACAGC 748
Db 224 rSerArg-----SerArgSerGlySerArgGlyArg--Asp 235
QY 749 GACCTTTCTGAGCGGAGGACCACTCGTAGATGTCACCTCTGCAAAAGCTGCACATT 808
Db 236 SerProTyrlGlnSer-ArgGlySerPro-----HisTyr 246
QY 809 TGAAGTCCAGCAGACAGCCCCAC 831
Db 247 PheSerPro--PheArgProTyr 253

RESULT 35
US-09-488-725A-3201
; Sequence 3201, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hysed Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19

```

```

; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pt_Fl_genes_b Versions 1.0
; SEQ ID NO 3201
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3201

Alignment Scores:
Pred. No.: 88.8      Length: 615
Score: 260.20      Matches: 123
Percent Similarity: 23.24%      Conservative: 32
Best Local Similarity: 18.44%      Mismatches: 74
Query Match: 16.71%      Indels: 438
DB: 1      Gaps: 21

us-09-488-522-3 (1-834) x US-09-488-725A-3201 (1-615)
QY 830 TGGGCTGTGCTGCTGCAATGACCGCTTGGCAGAGTCAGATCCAGGCTG 771
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 72 TTP---CysAlaThrThrProAsn-----PheAspGlnAspGlnArg---TTP 85
QY 770 -----TCCCTGGCTCA 759
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 G1YTYCYsLeuGlnProlYsValYsValAspHisCYsSerYsHisSerPro-CysG1 105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 758 GAAAGAGTCGCTGTG---AGCTCCGCCATGAGACCTCTCGGTGCAATTCG 707
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 105 nLYsG1Yg1YThrCYsValAsnMet-ProSerG1Y---ProHisCYs-LeuCYsProG1 123
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 707 ----- 707
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 123 nHisLeuThrG1YAsnHisCYsGlnYsG1YsCYsPheGlnProlnLeuArgPh 143
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 706 -----AGATGTACCA 696
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 143 ePheHisLYsAsnGlnIleTrrTYrArgThrGlnGlnAlaValAlaArgCYs---- 161
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 695 TTCGAATGTCTCGA----- 680
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 162 ---GlnCYsLeuG1YProAspAlaHisCYsGlnArgLeuAlaSerGlnAlaCYsArgTh 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 679 -----TGTGCTGCACGAT-----CAGGTGATGCGACCAATTTCTCAC- 640
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 180 rAsnProCYs-LeuHisG1Yg1YArgCYsLeuGlnValGlnGlnHisArgLeuCYsHisC 200
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 639 -----T 639
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 200 ySProValG1YTYrThrG1YProPheCYsAspValAspThrLYsAlaSerCYsTYrAspG 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 638 CCGTGGAGATGATACATCGG-----CATACTCTTTGTCGACGACGACGATCC 588
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 220 LY-ArgG1YLeu-SerTYrArgG1YLeuAlaArgThrThrLeuSer---Gly---AlaPr 237
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 587 TCGAAGCCG---GCTTCA----- 572
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 237 oCYsGlnProTrrAlaSerGlnAlaThrTYrArgAsnValThrAlaGlnGlnAlaArgAs 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 571 -----CGAAGTGGTG 561
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 nTrrG1YLeuG1Yg1YHisAlaPheCYsValArgAsnProAspAsnAspIleArgProTrrCY 277
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 560 T-----AC 558
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 sPheValLeuAsnArgAspArgLeuSerTrrG1YTYrCYsAspLeuAlaGlnCYsGlnTh 297
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 557 TGGCTGAGATTCGCTCCAGGCTCT-----CCCTGGCGGCACGTC----- 517
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 297 rProThrGlnAlaAlaArg-----ProThrProValSerProArgLeuHisValProleum 316
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 516 -----CCGAGAGAACTTCTGAGACGACCTCGAGCTCGGAG 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

Db 316 eTrProAlaGlnProAlaProProLYsProGlnProThrThrArgThnProPro---GlnSe 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 482 TCGGTGTCCACGAAAGGCCCA----- 461
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 335 rGlnThrPro-----GlyAlaLeuProAlaLYsArgGlnGlnProProSerLeuThrAr 353
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 461 ----- 461
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 353 gAsnG1YProLeuSerCYsG1YnArgLeuArgLYsSerLeuSerSerMetThrArgVa 373
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 460 ---GGTGAACA----- 452
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 373 lValG1Yg1YLeuValAlaLeuArgG1YAlaHisProTYrIleAlaAlaLeuTYrTrrG1 393
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 451 -----TGTCCCGAGATCTCTCG-----GCTGTAGACACC 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 393 yHisSerPheCYsAlaG1YSer-LeuIleAlaProCYsTrrValLeuThrAlaAlaHis- 412
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 422 AAGATGCCCTGAACAGAACACAGTCGCGAGGAGTAACACCGGTGCTGTGTAACCTT 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 413 ---CYsLeuGlnAspArgProAlaProGlnAsp-LeuThrValValLeuG1Yg1n--- 429
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 362 GAGTGTGTCAAAATCAT-----AGTCTGCGACCC 333
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 430 G1U---ArgArgAsnHisSerCYsGlnProlProCYsGlnThrLeuAlaValArgSer----- 446
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 332 TCCACGCTTTTGCTCCACGATGTTCTTCAGATCCTGTGCATCAATCATTAACAAG 273
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 447 ---TYrArgLeuHisG1YAla-Phe-SerProVal-----SerTYrGlnHis 460
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 272 GCATCTG-----GATGTCAAATGTACTGCTCTTC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 sAspLeuAlaLeuLeuArgLeuGlnGlnuAspAlaAspG1Y---SerCYsAlaLeuLeuSe 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 239 AAGGCTTTG-----CCTTGTGCTGTGCGCTGACGACCTTGTAGAACCTGTGCGCTC 186
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 479 r---ProTYrValGlnProValCYsLeuProSerG1YAlaAlaArg-----ProSerG1 496
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 185 AGATGACACACCTTCGCTGC----- 165
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 496 u---ThrThrLeu---CYsGlnValAlaG1YtrG1YHisGlnPheGlnG1YAlaG1u 513
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 164 -----CGCTGTCC 156
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 514 G1UTYrAlaSerPheLeuGlnGlnAlaGlnValProPheLeuSerLeuGlnuArgCYsSer 533
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 155 -----ACCTGTTCTGTGCCAGAACATCCATGATCTTCTCACACAGC 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 534 AlAProAspValHisG1YSerSerIleLeuProG1Y-----MetLeuCYsAlaArg 550
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 113 GTCGACTTCCCGCTGACAGTCGCGCGCTCACCCCTATCAGAAAGGCGCGTGTGCGG- 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 550 lYrPheLeuGlnG1Yg1YThrAspAlaCYsGlnG1YAspSerG1Yg1YProLeuValCYsG 570
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 54 -----ACGTCGCGCTCCGCC 39
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 570 lAspGlnAlaAlaG1uArgArgLeuThrLeuGlnG1YIleIleSerTrrG1Y-SerG1Y 589
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 38 GCGGAGCTCTCGCAGTCTCGCTCCCGCCGACGCA 2
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 590 CYs-G1YAspArgAsn-----LYsPro 596
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 36
US-09-488-725A-3206
; Sequence 3206, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725

```

```

PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: US09/598,042
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US09/653,450
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: US09/662,191
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: US09/693,036
PRIOR FILING DATE: 2000-10-19
PRIOR APPLICATION NUMBER: US09/727,344
NUMBER OF SEQ ID NOS: 714
SOFTWARE: pc FL_versions 1.0
SEQ ID NO 3206
LENGTH: 1156
TYPE: PRT
ORGANISM: Homo sapiens
US-09-488-725A-3206

```

## Alignment Scores:

```

Pred. No.: 361 Length: 1155
Score: 258.90 Matches: 95
Percent Similarity: 17.32% Conservative: 47
Best Local Similarity: 11.59% Mismatches: 67
Query Match: 16.62% Indels: 611
DB: 1 Gaps: 10

```

```

us-09-896-522-3 (1-834) x US-09-488-725A-3206 (1-1155)

```

```

QY 830 TGGGCTCTGCTGCTGACTCCAAATGTGACCGTTTGCAGAGTCAGATC----- 780
DB 536 TrrAlaLeuLeuLeu-----ThrAlaCys-----GluileGlyileLeuileAla 552
QY 780 ----- 780
DB 553 SerLeuAspGluValAlaProileuSerMetPhePheLeuMetCysTrpMetPheVal 572
QY 779 -----CCAGGCTGCTCCCTGCTGCTCAGAA 756
DB 573 AsnLeuAlaCysAlaValAlaGlnThrLeuLeuArgThrProAsnTrpArgPro----- 589
QY 755 AAGGTCGCTTGAAGCTCCGCCCATTTGACCTCTCGTGCCATTGGACATGTACCA 696
DB 590 ArgPheArgTyr-----TyrHisTrpThrLeu-----SerPheLeuGlyMetSerL 605
QY 695 TT----- 694
DB 605 euCysLeuAlaLeuMetPheileCysSerTrpTyrTyrAlaLeuValAlaMetLeuileA 625
QY 694 ----- 694
DB 625 laeGlyLeuileTyrIlySerTyrileGluTyrArgGlyAlaGluLeuGluTrpGlyAspGlyI 645
QY 694 ----- 694
DB 645 leArgGlyLeuSerLeuSerAlaAlaArgTyrAlaLeuLeuArgLeuGluGluProp 665
QY 693 -----CAGA 690
DB 665 roHisTrpHisAsnTrpArgProGlnLeuLeuValArgValAspGlnAspGlnA 685
QY 689 ATGTCTGTGATGTGCTGACGATCAGTT----- 661
DB 685 sn-----ValValHisProGlnLeuLeuSerLeuThrSerGlnLeuLeuYsAlaGlyL 702
QY 661 ----- 661
DB 702 ysGlyLeuThrIleValGlySerValLeuGluGlyThrPheLeuGluuAsnHisProGlnA 722

```

```

QY 661 ----- 661
DB 722 laeGlnArgAlaGluGluSerIleArgArgLeuMetGluAlaGluLeuValIlyeGlyPheC 742
QY 660 -----GATGGC---AACCATATTGTC----- 643
DB 742 ysGlnValValIleSerSerAsnLeuArgAspGlyAlaSerHisLeuileGlnSerGlyG 762
QY 643 ----- 643
DB 762 IyLeuGlyLeuGlnHisAsnThrValLeuValGlyTrpProArgAsnTrpArgGlnL 782
QY 642 -----CACTCTGCTGGATGAT-----C 624
DB 782 ysGlnAspHisGlnThrTrpArgAsnPheileGluLeuValArgGluThrTrAlaGlyH 802
QY 623 ACATCGGCATACTCTTTTGTGCGCAGGCAGAACTCTCGAAGCCGG----- 577
DB 802 lseuAlaLeuLeuValThrIlyAsnValSerMetPheProGlyAsnProGluArgPheS 822
QY 576 -----CTTCACGAAGGCTGCTGA----- 559
DB 822 eArgGlySerIleAspValTrpTrpIleValHisAspGlyLeuMetLeuLeuP 842
QY 559 ----- 559
DB 842 roPheLeuLeuArgHisIleIlyValTrpArgIlyCysIlyMetArgIlePheThrValA 862
QY 559 ----- 559
DB 862 laeGlnMetAspAsnSerIleGlnMetIlyAspLeuThrThrPheLeuTyrHisL 882
QY 559 ----- 559
DB 882 euArgIleThrAlaGluValGluValValGluMetHisGluSerAspIleSerAlaTyrT 902
QY 559 ----- 559
DB 902 hTrpGlyIlySerThrLeuValMetGluGlnArgSerGlnileuLeuYsGlnMetHisLeuT 922
QY 559 ----- 559
DB 922 hTrpAsnGluArgGluArgGluileGlnSerIleThrAspGluSerArgIlySerIleA 942
QY 558 -----CTGGCTCAGAAATGCTGCTCAGAGTCCTCCCTCCG 525
DB 942 rGArgIlyAsnProAlaAsnThrArgLeuArgLeuAsn-----ValProGlu 957
QY 524 CGCAGCTCCCGAGAACTTTCGAGACAGCCTGACGTCGAGTCCGTGTCACAGAGAGG 465
DB 958 GluThrAla-GlyAsp-SerGluGluIlySerProGlu-----GluGluV 971
QY 464 CGCAGCTGGAACATGTCGCCGATCTCTGCTGTAGAACACCAAGATCCCTCAACAGA 405
DB 971 alGlnLeuileHis-----AspGlnSerAla-----ProSerCysProSerSerSe 986
QY 404 ACCACGTCGCCAGGT----- 389
DB 986 rProSerPro--GlyGluGluProGluGlyGluThrAspProGluYsValH 1005
QY 389 ----- 389
DB 1005 sLeuThrTrpThrIlyAspIlySerValAlaGluIlyAsnIlyGlyProSerProValSe 1025
QY 388 -----AGACCAACCGTGTCTCTGTGAACCTTGAG 360
DB 1025 rSerGluGlyIleIlyAspPhePheSerMetIlySProGluTrpGlu-----AsnLeu--- 1042
QY 359 TGTGTCAAAATCATATGCGGACCTCCACCGTTTGCCCTCCACGATGTTCTTGAGA 300
DB 1043 ---AsnGlnHis-----AsnValArgArg---MetHisTrpAlaValArg- 1055
QY 299 GTCTGTGATCAAAATCATATGAAAGCATGTGATGTCAAAATGTGATGCTTTC 240

```





TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides  
 FILE REFERENCE: 784FLEPCT  
 CURRENT APPLICATION NUMBER: US/09/488,725A  
 PRIOR FILING DATE: 2000-12-22  
 PRIOR APPLICATION NUMBER: US/09/488,725  
 PRIOR FILING DATE: 2000-01-21  
 PRIOR APPLICATION NUMBER: US09/552,317  
 PRIOR FILING DATE: 2000-04-25  
 PRIOR APPLICATION NUMBER: US09/598,042  
 PRIOR FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: US09/620,312  
 PRIOR FILING DATE: 2000-07-19  
 PRIOR APPLICATION NUMBER: US09/653,450  
 PRIOR FILING DATE: 2000-08-31  
 PRIOR APPLICATION NUMBER: US09/662,191  
 PRIOR FILING DATE: 2000-09-14  
 PRIOR APPLICATION NUMBER: US09/693,036  
 PRIOR FILING DATE: 2000-10-19  
 PRIOR APPLICATION NUMBER: US09/727,344  
 PRIOR FILING DATE: 2000-11-29  
 NUMBER OF SEQ ID NOS: 7144  
 SOFTWARE: pc\_fl\_genes\_b Versions 1.0  
 SEQ ID NO 5699  
 LENGTH: 490  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(483)  
 OTHER INFORMATION: Xaa = any amino acid or nothing  
 US-09-488-725A-5699

## Alignment Scores:

Pred. No.: 58 Length: 483  
 Score: 258.60 Matches: 99  
 Percent Similarity: 17.84% Conservative: 25  
 Best Local Similarity: 14.24% Mismatches: 77  
 Query Match: 16.63% Indels: 494  
 DB: 1 Gaps: 10

us-09-896-522-3 (1-834) x US-09-488-725A-5699 (1-483)

QY 2 TGGCTTCGCGGAGAGCG----- 19  
 Db 9 TrpValArgArgThrValProAlaMetClnCysProAlaGlyLeuSerArgValProGly 28  
 QY 19 ----- 19  
 Db 29 ValAlaGlyAspProSerLeuProSerPheArgGlyProArgAspGluAlaAlaHisArg 48  
 QY 20 -----AGACTGGGAGAGCGCGCGCGCG----- 43  
 Db 49 GlyThrIleGlnThrAlaArgHisThrArgIleuLeuTyValGlnGlyProAlaSerGly 68  
 QY 44 -----AGG 46  
 Db 69 ProProLeuProArgValSerThrGlnValAlaIle\*\*\*AspGluIlyProLeuAlaArg 88  
 QY 47 CCGACCGTCCGACCGAGCGCGCTTCTGATAGGGGTGAGCGCGGCACTGCCAGCGGGA 106  
 Db 89 ProSerGlyArgThrAsnAlaPro-----PheProGlnGly 100  
 QY 107 AGTGCACCGTGTGAGAGATCATGAGTGTGGACAGACAGAGGTGAAACAGCGGC 166  
 Db 101 GlnIlySPro-----AlaGlyIlySalAlaAlaProGlyProAlaAl 113  
 QY 167 AGCGGAAGT-----GTCATCCT----- 185  
 Db 113 aala---GlyArgValAlaMetArgProGlyHisProGlyLeuLeuAlaSerAspSerG 132  
 QY 186 -----GAGCC 190  
 Db 132 nargSerSerSerIlySerGlyTyPrpGluThrProValProTrpSer\*\*\*AlaGlnPr 152

QY 191 AGGACAGGTT----- 200  
 Db 152 ogIlyTrpValSerGlyLeuLeuLeuGlyAspProSerGlyProGlySerIleu\*\*\*Ar 172  
 QY 201 -----CTACAGGTTCTTACGCGAGGACAGAGCGCAAGGCT 238  
 Db 172 gserThrTrpLeuValGlyIlyAlaArgGlyPro-----GlnGlySerGly-V 188  
 QY 239 TGAAGACAGTACATTTTGACATCCAGATGCCCTTGTATATGATTTATGACACAGA 298  
 Db 188 alArgIlySer---GlyTrp--ProSerGlyCys-----SerAspIle----- 200  
 QY 299 CTCGAAAGACATCTGAGAGGCAAAACGGTGAAGGTGCCAGCTATGATTTGTGACAC 358  
 Db 201 -----GlyTrpAlaLeuAlaGlyTrp-----Asn 209  
 QY 359 ACTCAAGTTTACACAGACCAACGGGTGTCTACCTGCGACGTGTTCTGTGAGGCGCA 418  
 Db 209 lsser-----\*\*His---LeuAspPro-AsnThrTrp-----ThrGln 220  
 QY 419 TCTTGGTGTCTACAG-----CCAGAGATCCGGACATGTTCCACTGGGCTCT 469  
 Db 221 LysTrpThrGly-GluSerProAlaProGlyGlnGly---ValAlaProAlaPro-- 238  
 QY 470 TCGTGACACCGACT----- 484  
 Db 239 -ArgGly--ProThrAlaGluHisGlyHisCysGluLeuThrThrGluSerGlnTySer 257  
 QY 484 ----- 484  
 Db 258 AsnAsnValProIleLeuPheGlnAsnProSerGlyValAlaLeuArgSerArgThrGlu 277  
 QY 485 -----CCG 487  
 Db 278 ProAlaGlyTrpValProProThrArgHisGln\*\*\*AspAspGly\*\*\*ThrAlaAlaPro 297  
 QY 488 ACGTCAGGCTGTCTCGAAGAGTTCTCCGGAGCGTCCGCGAGGAGGACCTGAGCAGA 547  
 Db 298 AlaserGly-----GlyAlaProValSerThrPro-----ThrTrpAla-- 310  
 QY 548 TTTCGACGAGTACACACCACTTGCGTGAAGCC----- 578  
 Db 311 -----GlyThrPro-LeuAsnAlaSerLeuGlyProThrAspProGlnGlySPx 327  
 QY 578 ----- 578  
 Db 327 ogIlyCysArgProProCysAlaLeuProIlyProAlaGlyProGluArgSerAla\*\*\*G 347  
 QY 579 -----GGCCTTCGAGAGGTTCTGCTGCCGAC----- 605  
 Db 347 yGlySerLeuGlyCysArgSerMetLeuProAlaSerSerGlyProProProAlaProG 367  
 QY 606 -----AAAGAAATATCCCGATGTGATCCAC 634  
 Db 367 yProArgArgLeuAlaAlaGlyAlaHisThrSerAlaSerAlaArgGlySProProAlaAl 387  
 QY 635 GAGAGTGCACATATGTGTGTCATCACTGATCT----- 671  
 Db 387 aalaAlaGly---Trp-----GlnProArgArgProGlyPheAlaGlyArgAlaAl 403  
 QY 671 ----- 671  
 Db 403 aleuProGlyProProHisProProSerSer\*\*\*ArgGluLeuGlyGlyLeuProGlyPr 423  
 QY 672 -----GCAGACATCCGACATCTGATGTGACATCT 706  
 Db 423 ogIlyTrp\*\*\*ThrLeuAspProLeuProAlaHisProAlaHisProPro-GlySerAlaP 443  
 QY 707 GCAATGCAACCGAGAGGTCGAAATGGCGGAGCTCAAGCGGACCTTTTTCAGGCCAG 766  
 Db 443 ropProTrpGlyAlaLeuGlyGly--TrpAlaAlaAlaArgAlaSerIle----- 458  
 QY 767 GGAACACCTGGGATGCTGACCTCTGGCAAGAGGTGACATTTGGAGTCCAGACGAC 826

```

Db      459 -----ProTirSerProSerLeu-----CysLeuSerPhe-----ProAlaVal-Th 472
Qy      827 CCCACTG 833
Db      472 rProval 474

RESULT 39
US-09-488-725A-3209
/ Sequence 3209, Application US/09488725A
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq Inc
/ TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
/ FILE REFERENCE: 784FLPCT
/ CURRENT APPLICATION NUMBER: US/09/488, 725A
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US/09/488, 725
/ PRIOR FILING DATE: 2000-01-21
/ PRIOR APPLICATION NUMBER: US09/552,317
/ PRIOR FILING DATE: 2000-04-25
/ PRIOR APPLICATION NUMBER: US09/598, 042
/ PRIOR FILING DATE: 2000-06-20
/ PRIOR APPLICATION NUMBER: US09/620, 312
/ PRIOR FILING DATE: 2000-07-19
/ PRIOR APPLICATION NUMBER: US09/653, 450
/ PRIOR FILING DATE: 2000-08-31
/ PRIOR APPLICATION NUMBER: US09/662, 191
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: US09/693, 036
/ PRIOR FILING DATE: 2000-10-19
/ PRIOR APPLICATION NUMBER: US09/727, 344
/ PRIOR FILING DATE: 2000-11-29
/ NUMBER OF SEQ ID NOS: 7144
/ SOFTWARE: Pf_Fl_genes_b Versions 1.0
/ SEQ ID NO 3209
/ LENGTH: 2064
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-488-725A-3209

Alignment Scores:
Pred. No.: 942 Length: 2063
Score: 258.60 Matches: 114
Percent Similarity: 21.95% Conservative: 37
Best Local Similarity: 16.57% Mismatches: 64
Query Match: 16.60% Indels: 474
DB: 1 Gaps: 16

us-09-486-522-3 (1-834) x US-09-488-725A-3209 (1-2063)
Qy      828 GGGTCGCTGCTGAGATCCAAATGTGACCGTTCAGAGGTACGATCCAGGGTGTGTC 769
Db      760 GYGImeSerGly---GImet-----LeuPro-----GInGInGlyP 772
Qy      768 CCCTG-----GCTCAAAAGATCGCTTGAGTCCG 756
Db      772 roValnsnnsnserProserGlnValmeGlyllegIn---GlyGlnValLeuArgPro 790
Qy      735 CCCATTGAACCTCTCGTGGTCCATTG----- 708
Db      791 Pro---GlyProserPro---HiMeValagInGInHiGlyAspProAlaThrAl 808
Qy      707 -----CAGATGTCACCATTCAGAAATGCTCGATGTGCTGCAC 670
Db      808 aasnnsnAspValSerLeuSerGImetMetPro-----AspValSerIle 823
Qy      669 GATCAGATTGAT-----GGC 655
Db      824 GInGInThAsnMeValProproHiSValGlnAlaMeGInGInIysnSerAlaSerGly 843
Qy      654 AACCATATTGT-----644
Db      844 AsnHiAsPheSerGlyHiGlyMeSerPheAsnAlaProPheSerGlyAlaProAsnGly 863

```

```

Qy      644 ----- 644
Db      864 AsnGImeSerGlyGlnAsnProGlyPheProValAsnIysAspValThrLeuThr 883
Qy      643 -----CACTCTCTCGT-----GGATGATCAGATCCGAT 614
Db      884 SerProLeuValAsnLeuLeuGlnSerAspIleSerAlaGly---HisheGlyVa 902
Qy      613 ACTTCTTTGTCGACAGCAGAACTCTCGAAGCC----- 579
Db      902 1-----AsnAsnIysGlnAsnAsnThrAsnAlaAsnIysProIlyIyIyAspProp 920
Qy      579 ----- 579
Db      920 roAlGlyIyIyAsnSerGlnGlnAspLeuAsnThrProAspThrArgProAlaGlyL 940
Qy      578 -----GGCTTCAGAAAGTGTGATCTGCGTCAGAA 548
Db      940 euGInGlnAlaAspGlnProProLeuProGly-----GInGInGlyIleSerLeuAspAs 956
Qy      547 TCTGCTCAGAGTCCCTCCCTCGGCGACGTCGGAAGAACTTTGAGACAGAGCTGACGT 488
Db      958 n-----SerGlyProIyIyLeu-----ProGInPheSerAsnArgProPro----- 971
Qy      487 CGGAGTCGCTGTCAGAAAGAGCGCAG----- 460
Db      972 -GlyIyIy---Pro-----SerGInProValGlnGlnArgProLeuGlnGlnMetPr 987
Qy      459 -----GTGGAACATGTCGCGATCTCTGCTGTAGAACACCAAGATCCCTCAA 410
Db      987 oProGInLeuMeGInHiSVal-----AlaPro-----ProProGInProProGIn 1002
Qy      409 ACAGAACACAGTCCGAGGATAGCA----- 383
Db      1003 GInGInProGInProGIn---LeuProGInGInGlnGlnProProProSerGlnPro 1021
Qy      383 ----- 383
Db      1022 GInSerGInGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 1041
Qy      382 ---CCGTGCTCTGTGTAACCTTGAGTGTGTCACAAAT---CATAGTCCGACCTCCA 329
Db      1042 AspProIySer---ValArgLeuProValSerGlnAsnValHis-----ProPro 1057
Qy      328 ---CCGTTTGCCTTCACAGATGTTCTTCAGAGTCTGTGATCAATCATTTATCA 275
Db      1058 ArgGlyProLeuAsnPro---AspSerGlnArgMetPrometGlnGln-----Se 1073
Qy      274 AGGCATCTGAGATGCTCAAAATTTGACTGCTTTCAAGGCTTTGGCTTGTGCTGCGG 215
Db      1073 rGly-----SerValProValMetValSerLeuGlnGly---ProAlaSerValPro 1089
Qy      214 TCAGACCTTGAGAACCTGCTGCTGCTGAGATGACCACTTCGCGCTCGCGCTG----- 160
Db      1090 ProSerProAspIySerIn-----ArgMet-----PrometProValAsnTh 1103
Qy      160 ----- 160
Db      1103 rProLeuGlySerAsnSerArgIyIyMetValTyrgInGlnIySerProGlnAsnProSerSe 1123
Qy      160 ----- 160
Db      1123 rSerProLeuAlaGlnMetAlaSerLeuProGlnAlaSerGlySerGlnAlaProSerVa 1143
Qy      159 -----TTCACTCGTGTGCTGCTCCAGACATCCATGATCT 125
Db      1143 lProGlyGlyProAsnAsnMeCProSerHiSValValIyLeu-ProGlnAsnGlnLeuMeC 1163
Qy      124 TC----- 123
Db      1163 eThrGlyProIyAspProGlyProSerProLeuSerAlaThrGlnGlnIyAlaThrProGln 1183

```

```

Qy 122 -----TCACACAGCTGCACTTCCG---CTGGCAGTGC 92
Db 1183 InProProValaSerLeuProSerSerHisGlyHisPheProAsnValAlaAlaIar 1203
Qy 91 CG-----CCGCTCACCCCTATCAGAAAGGCGCTGTGCGAGCGTGG 47
Db 1203 roThrlGlnThrSerArgProIysThrProAsnArg-----AlaSerProArg 1218
Qy 46 CCT-----44
Db 1219 ProIyTrProGlnThrProAsnAsnArgProProSerThrGluProSerGluIleSer 1238
Qy 43 -----CCGGCGCGGGCTCTCGCAGTCTTCCG-----17
Db 1239 LeuSerProGluThrGluLeuAsnAlaSerIleAlaGlyLeuPheProGlnIleAsnIle 1258
Qy 16 ----CTCCCGCCGAGCCCA 2
Db 1259 ProIeuProProArgPro 1264

RESULT 40
US-09-488-725A-3457
; Sequence 3457, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLEPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc fl_genes_b Versions 1.0
; SEQ ID NO 3457
; LENGTH: 1410
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-3457

Alignment Scores:
Pred. No.: 547 Length: 1409
Score: 258.20 Matches: 108
Percent Similarity: 23.45% Conservative: 28
Best Local Similarity: 18.62% Mismatches: 76
Query Match: 16.58% Indels: 368
DB: 1 Gaps: 15

us-09-896-522-3 (1-834) x US-09-488-725A-3457 (1-1409)
Qy 830 TGGGGTCTGCTGCTGAGCTCCAAATGTGACCGTTTGCAGAGCTCAGCATCCAGGGTGG 771
Db 705 TyrGlyLeuArgLeuGluArgGluAla-----GlyTyr 717
Qy 770 TCCCTGCTGCTGAGAAAGGTCCGCTTGTAGCTCCGCCGATTGAGACCTT-----723
Db 718 AlaSerGluAlaGlyLys--ProIeu-----LeuHisProValArgProGlyHisProIeu 735
Qy 722 -----CCTCGGTGC--CATTTCAGATGTACCAATTCAGATGTCCT-----683

```

```

Db 736 ProIeuLeuProAlaCysGlyHis-----HisHisAlaProMetProAspTyr 752
Qy 682 -----GGATGTGCT-----674
Db 752 rSerCysLeuLysProProLysAlaGlyGluGluHisGlyGlyCysSerTyrThre 772
Qy 673 -----GCACGATCAGGTGATGACGACA-----650
Db 772 tCysProGluGlyArgTyrGly-----HisProGlyTyrProAlaLeuValThrTyrSe 790
Qy 649 -----TATTGTCCACTCTCTGCGGATGATTCATCGCATC 612
Db 790 rTyrGlyGlyAlaValProSerTyrCysProAlaTyr--GlyArgValPro-----HisSe 808
Qy 611 T-----611
Db 808 rCysGlySerProGlyGlyGlyArgGlyTyrProSerProGlyAlaHisSerProArgAl 828
Qy 610 -----TCTTTGTCCGAGCAGACACTCTCGAGAGCGCGCTTCAAGAG-----566
Db 828 aglySerIleSerProGly--SerProProTyrProGlnSerArgLysLeuSerTyrGly 847
Qy 566 -----566
Db 847 uIleProThrGluGluGlyGlyAspArgTyrProIeuProGlyHisLeuAlaSerAlaGly 867
Qy 565 -----TGG-----563
Db 867 yProIeuAlaSerAlaGluSerLeuGluProValSerThrPArgGluGlyProSerGlyHis 887
Qy 562 -----TGTACTCGCTCAGAAATCTGCTCAGG 537
Db 887 sSerThrIeuProArgSerProArgAspAlaProCysSerAlaSerSerGluLeuSerGly 907
Qy 536 TCCCTCCCTCGGCGACGCTCCG-----GAAACTCTT 504
Db 907 yProSer-----ThProIeuHisThrSerSerProValGlnGlyLysGluSerT 924
Qy 503 CGAGACAGCTGACGTCGAGTGGTGTCCAGAAAGAGCGGAGGAAATGTCGCCGG 444
Db 924 hrArgArgGlnAsp-----ThrArgSerPro--ThrSerAlaProThrGlnArgLeu-----940
Qy 443 ATCTCTGTGC-----TGTAGAACACCAAGATCCCTCAAAAC 408
Db 941 -SerProGlyGluAlaIeuProProValaSerGlnAlaGlyThrGlyLysAlaProGluLe 960
Qy 407 AGAACACAGTCCGAGGAGTAAACCACTGCTCTGTGTAACCTTGAGTGTCAAAA 348
Db 960 u-----ProSerGlySerGlyProGluProIeuAlaProSerProValaSer-----975
Qy 347 TCATAGTCCGACACTCCACCGCTTTTGCCTCCACAGATGTTCTCAGAGTCCGTGCATC 288
Db 976 -----ProThrPhe--ProPro-----SerSerPro--Se 984
Qy 287 AAATCATTTATCAAGG-----CATCTGATGATGATTAATTTGATCTGCT 243
Db 984 rAspTyrProGlnGluArgSerProGlyGlyHisSerAspGlyAlaSer-----Pro 1001
Qy 242 TTCAGGCTGTGGCTTGTGCTGTGCTGCG-----TCAGACCTTG 204
Db 1002 -ArgSerProValaProThrThrIeuProGlyLeuArgHisAlaProTrpGlnGlyPro--1020
Qy 203 TAGAACCTGTCTCCGCTCAGAGATGACACACTTCGCGG-----166
Db 1021 -ArgGlyProProAspSer--ProAspGlySerProIeuThrProValaProSerGlnMetP 1040
Qy 165 -----CCGCTGTTCCACTCGTCTGTGCTCCAGCACTCATGATCTTC 123
Db 1040 rotTyrLeuValAlaSerPro--GluProProGlnSerSerPro--ThrPro-----1055
Qy 122 TCACACAGGTGCACTTCCGCTGCGAGTG-----CCG 90
Db 1056 -----AlaPheProIeuAlaAlaSerTyrAspThrAsnGlyLeuSerGlnPro 1071

```

```

QY      89 CCGCTCACCC-----TATCAAGAAAGCCGCTGATGC 57
      |||||
Db      1072 Probu---ProgluylsarghlsbleuProgluylProgluylnglnProgluylPro-TTP--- 1088
QY      56 GGACGCTGCGCTCCGCGCGGAGCTCTCGCAGCTTTCGCTCCGCC 9
      |||
Db      1090 -----glnProgluGlnAlaSerProAla 1098

RESULT 41
US-09-488-725A-2369
; Sequence 2369, Application US/09488725A
; GENERAL INFORMATION:
;   APPLICANT: HySeq Inc
;   TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
;   FILE REFERENCE: 784PLPCT
;   CURRENT APPLICATION NUMBER: US/09/488, 725A
;   PRIOR FILING DATE: 2000-12-22
;   PRIOR APPLICATION NUMBER: US/09/488, 725
;   PRIOR FILING DATE: 2000-01-21
;   PRIOR APPLICATION NUMBER: US09/552, 317
;   PRIOR FILING DATE: 2000-04-25
;   PRIOR APPLICATION NUMBER: US09/558, 042
;   PRIOR FILING DATE: 2000-06-20
;   PRIOR APPLICATION NUMBER: US09/620, 312
;   PRIOR FILING DATE: 2000-07-19
;   PRIOR APPLICATION NUMBER: US09/653, 450
;   PRIOR FILING DATE: 2000-08-31
;   PRIOR APPLICATION NUMBER: US09/662, 191
;   PRIOR FILING DATE: 2000-09-14
;   PRIOR APPLICATION NUMBER: US09/693, 036
;   PRIOR FILING DATE: 2000-10-19
;   PRIOR APPLICATION NUMBER: US09/727, 344
;   PRIOR FILING DATE: 2000-11-29
;   NUMBER OF SEQ ID NOS: 7144
;   SOFTWARE: pc_fl_genes_b Versions 1.0
;   SEQ ID NO 2369
;   LENGTH: 2044
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-488-725A-2369

Alignment Scores:
Pred. No.:          970          Length:          2044
Score:              257.60        Matches:          121
Percent Similarity: 14.83%        Conservative:      22
Best Local Similarity: 12.55%      Mismatches:        67
Query Match:        16.56%        Indels:            754
DB:                  1            Gaps:              18

us-09-896-522-3 (1-834) x US-09-488-725A-2369 (1-2044)
QY      2  TGGCTTCGGCGGAGCGCAAGACTGCGAAGCCCGCGCGGAGCCGACCGTCCGACC 61
      |||
Db      45  TTP-----Glygin---Cys-AenAlaProgluTTPleuProPheAlaArg-Pr 59
QY      62  AGCGGCCCTTCCTGATAGGGGTGAGCGCGGCGGACCTCCAGCGGGAAGT----- 109
      |||
Db      59  cThraSleuThrPheGlnPheGln-----PheProIleGlyThrTrieuAenTyr 76
QY      110 -----CGACCG----- 115
Db      77  GluCySArgProGlyTyrSerGlyThrArgProPheSerIleIleCySleuLysAenSerVal 96
QY      116 -----TGTGTGAAGAATCA----- 130
Db      97  TrpThrGlyAlaLysAspArgCySArgArgLysSerCySArgAsnProProAspProVal 116
QY      131 -----TGAGATTGC----- 139
Db      117  AsnGlyMetValHisValIleLeuSgIlyIleGlnPheGlySerGlnIleLeuTyrSerCyS 136
QY      139 ----- 139

```

Db	137	ThrIysGlyTyrArgLeuIleGlySerSerSerAlaThrCysIleIleSerGlyAspThr	156
QY	140	-----TGGGACAGAACG-----	151
Db	157	ValIleTyrAspAsnGluThrProIleCysAspArgIleProCysGlyLeuProProThr	176
QY	151	-----	151
Db	177	IleThrAsnGlyAspPheIleSerThrAsnArgGluAsnPheHisTyrGlySerValVal	196
QY	152	-----AGGTGGAAACAGCGGACGGCA-----	172
Db	197	ThrTyrArgCysAsnProGlySerGlyGlyArgGlyValPheGluLeuValGlyGlyPro	216
QY	172	-----	172
Db	217	SerIleTyrCysThrSerAsnAspArgValGlyIleTyrSerGlyProAlaProGln	236
QY	172	-----	172
Db	237	CysIleIleIleProAsnLysCysThrProProAsnValGluAsnGlyTleLeuValSerAsp	256
QY	172	-----	172
Db	257	AsnArgSerLeuPheSerLeuAsnGluValValGluPheArgCysGlnProGlyPheVal	276
QY	173	-----AGGTGGTCATCTGAGCCA-----	191
Db	277	MethySgIlyProArgArgValLysCysGlnAlaLeuAsnLysTyr-----GluProGly	294
QY	191	-----	191
Db	294	uLeuProSerCysSerArgValCysGlnProProAspValLeuHisAlaGluArgTh	314
QY	191	-----	191
Db	314	rGlnArgAspLysAspAsnPheSerProGlyGlnGluValPheTyrSerCysGluProGly	334
QY	191	-----	191
Db	334	YTyraSrpLeuArgIleAlaAlaSerMetArgCysThrProGlnGlyAspTrpSerProAl	354
QY	192	-----GGACAGGTTCTTCAAGGT-----	209
Db	354	aAlaProThrCysGluValLysSerCysAspAspPheMetGlyGlnLeuLeuAsnGlyAr	374
QY	209	-----	209
Db	374	gValLeuPheProValAsnLeuGlnLeuGlyAlaLysValAspPheValCysAspGluGly	394
QY	209	-----	209
Db	394	yPheGlnLeuLysGlySerSerAlaSerTyrCysValLeuAlaGlyMetGluSerLeuTr	414
QY	210	-----CCTGA-----	214
Db	414	pAsnSerSerValProValCysGluGlnIlePheCysProSerProProValIleProAs	434
QY	215	CGGACAGACAGAGCCCAAGCCTTGAA-----AGACAGTACCAATTTT-----	258
Db	434	ngIlyArgHisThrGlyLysProLeuGluValPheProPheGlyLysThrVal-----AanTyr	454
QY	259	-----GACATCCAGAT-----GCCTTGATTAATGATT-----	286
Db	454	hrCysAspProHisProAspArgIleThrSerPheAsp-----LeuIleGlyLeuSerThrIle	473
QY	287	TGATGACACAGACTCTGAAGAACAATCGGAGGCGCAAAACGGTGG-----	331
Db	474	ArgCysThr-----SerAspProGlnGlyAsnGlyVal-----TrpSerSerProAlaPro	490
QY	332	AGGTGCCGACCTATGATTTGTGTGACACACTCAAGGTTACAGAGACCAAGTGGTCTAC-----	390

```

Db 491 ArgCysGly-----IleLeuGlyHisCysGlnAla--Pro--AspHis--PheLeuPheA 507
QY 390 ----- 390
Db 507 IalysLeuLysThrGlnThrAsnAlaSerAspPheProIleGlyThrSerLeuLysTyrG 527
QY 390 ----- 390
Db 527 IuCyAsArgProGlnTyrTyrGlyArgProPheSerIleThrCysLeuAspAsnLeuValT 547
QY 391 -----CCTGGAGAGCGTGGTCTGTTTGAAGGCATCTGGTGTCTTACAGCCAGAGA 442
Db 547 rpsSerSerProLysAspVal---CysLysArgLysSer---CysLysThr--ProProAs 564
QY 443 TCCG----- 446
Db 564 pProValAsnGlyMetValHisValIleThrAspIleGlnValGlySerArgIleAsnTyr 584
QY 447 -----GGACATGTTCCACCTGGCCCTCTTGAGACACCGATCCGACGTCA 493
Db 584 rSerCysThrThrGlyHis-----ArgLeuIle--GlyHis-----SerSerAla 598
QY 494 GGCCTGCTCGAAGAATTCTCCGGACGTGCGCCGAGGAGGAGACCTGGAGAGATTCGA 553
Db 599 GluCyAsile-----LeuSerGlyAsnAlaIleHis-----TrpSer----- 610
QY 554 CGCAGTACACCACTTCCGTGTAAGCCGCGCTTCGAGAGATTGCTGCTGCCCAAGAAAGT 613
Db 611 ---ThrLysProPro-----IleCys-----GlnArg--- 618
QY 614 ATGCCAGATGATCATCCACGAGAGATGACAAATATGTTGCCATCACTGATCGTC 673
Db 619 -----IleProCysGly-----LeuProProThr----- 626
QY 674 AGCAGATCCAGACATTCGATGATGTCGATC----- 705
Db 627 -----IleAlaAsnGlyAspPheIleSerThrAsnArgGluAsnPheHisT 642
QY 706 -----TGCMAATGGCACCGAGAGAGGTCCAAATGGCGGAGCT 742
Db 642 YrGlySerValValThrTyrArgCys--Asn---Pro---GlySerGlyValArgLysV 659
QY 743 ACAAGCGGACCTTTCTGAGCCGAGGAGCAC----- 774
Db 659 alpHeGluLeuValGlyGluProSerIleTyrCysThrSerAsnAspAspGlnValGlyI 679
QY 774 ----- 774
Db 679 IeTrpSerGlyProAlaProGlnCysIleIleProAsnLysCysThrProAsnValG 699
QY 774 ----- 774
Db 699 IuAsnGlyIleLeuValSerAspAsnArgSerLeuPheSerLeuAsnGluValValGluP 719
QY 775 -----CCTGGAGTGCAGACCTCTGGCAAAACGTCACATT----- 808
Db 719 heArgCysGlnProGlyPheValMetLysGlyProArg--ArgValLysCysGlnAlaLeu 738
QY 808 ----- 808
Db 739 AsnLysTrpGluProGluLeuProSerCysSerArgValCysGlnProProAspVal 758
QY 808 ----- 808
Db 759 LeuHisAlaGluArgThrGlnArgAspLysAspAsnPheSerProGlyGlnGluValPhe 778
QY 808 ----- 808
Db 779 TyrSerCysGluProGlyTyrAspLeuArgGlyAlaAlaSerMetArgCysThrProGln 798
QY 809 -----TGAGTCCAGCAGACAGACCCCACT 832
Db 799 GlyAspTrpSerProAlaAla---ProThr 807

```

```

RESULT 42
US-09-488-725A-5690
; Sequence 5690, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784P/CT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US/09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US/09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US/09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US/09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US/09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US/09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US/09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_Fl_genes_b Versions 1.0
; SEQ ID NO 5690
; LENGTH: 498
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)..(490)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-5690

Alignment Scores:
Pred. No.: 65.2          Length: 490
Score: 257.20          Matches: 108
Percent Similarity: 19.63%          Conservative: 20
Best Local Similarity: 16.56%          Mismatches: 66
Query Match: 16.54%          Indels: 458
DB: 1                  Gaps: 12

us-09-896-522-3 (1-834) x US-09-488-725A-5690 (1-490)
QY 10 GCGGAGGCGAAGACTGCGAGAGCCCGCGAGGCGGACCGTCGACAGCGGCC 69
Db 5 Alagly-----ValCysAlaAlaProAlaPro-----LeuProLeuLeuAlaLeuAla 21
QY 70 TTCCTGATAGGGGTGAGCGCGGCACTGCCAGCGGAGATCGACCGTGTGTG----- 121
Db 21 rgarAspArg-----ArgProCysSerProGlyAl 31
QY 122 -----AGAGATCATG 132
Db 31 agLAlaAlaProTrpGlnThrGlyGlyProAlaIleAspGlyAlaTrpArgThrSer-- 50
QY 133 GAGTTCGGAGACGAGACGAGTGGAGACAGCGCA----- 167
Db 51 --ValSerAlaLeuArgArgGlyAlaThrGlyAlaProCysSerProGlyAlaGluAla 70
QY 167 ----- 167
Db 70 IapProTrpGlnThrGlyGlyProAlaIleAspGlyAspGlyGluLeuPro**ValArgS 90
QY 168 -----GCGAAGTGTCTACTCCAGACGACGAGTTC 201
Db 90 ergLgluAlaProArgGlyCysGlyAlaGluGlyGlyProGlySerGlyProVala 110
QY 202 TACAGGTCTCGACGCGAGACGAGAAAGCCCTTGAAGACAGTCAATTTTGAC 261
Db --- 261

```

```

Db      110 rGaTgProGlyAlaGlyArgGly-----AlaHisAlaGlyGlnGlyArgGlnGlnAspPro 128
QY      262 CATCCAGATGCGCTTTGATATGATTTGATGACAGACCTGTGAAGAACATCGGAGCGC 321
Db      129 GluProAspGly-----LeuArgHisArg-----GlnHis----- 138
QY      322 AAAACGGTGAGGTCGCCAGCTATGATTTGTGACACACTCAAGGTATACAGAGACAC- 380
Db      139 -----GlyAla-----AlaSerHisAlaArg-----HisAla 147
QY      380 ----- 380
Db      147 rGleuGlnArgLeuArgProGlyHisHisGlnAsnArgHisValArgArgAspProGlnA 167
QY      381 -----GGTGGTCACCGCTGGGACGCGTTCGTGTTGAGGGCATCTT----- 422
Db      167 laProProGlyGly-----ProAlaPro-----GlyHisAlaAlaLeuP 181
QY      423 -----GGTGTCTCAAGCCA----- 437
Db      181 rGluArgThrArgGlyValAlaGlnProProAlaThrAlaHisAlaGlySerAspAlaT 201
QY      437 ----- 437
Db      201 rPaArgAlaArgArg***SerGlnArgThr**GluArgAlaArgProArgHisProThrP 221
QY      438 -----GGAGATCCGGGAGACATGTTCCACCTGGCGCTTCCTGGGAGAC 477
Db      221 heGlnGlyArgAlaGlySerGlyGlnProGlyArgGlnProAsnPro-----His 238
QY      478 ACCGACTCCGACGTCAGCTGTCTCGAAGAGTCTCCGAGGA----- 518
Db      238 sProGlyProSerSer-----ProProAlaAlaProGlyProAlaGlyAla***GlyA 256
QY      519 -----CGTGGCGCCGAG----- 530
Db      256 snProGlnLeuGlyValAlaProArgSerAspArgAsnProSerGlnGlyLeuArgThrA 276
QY      531 -----GAGGACCTGGAGACAGATTCTGACGACAGATACACCATTCCTGGAG 576
Db      276 rG1LeArgArgProGlyThrPro-----AspCys-GlyProProSer----- 289
QY      577 CCGGCTTCGAGAGTTCGCTGCGCCGACAAAGAGATGACCGATGATCATCCAGCA 636
Db      290 -----ProAlaGlySerSer-----AlaSerAlaSerThrPheArgCys-----Ths 304
QY      637 GGAGT-----GGAACATATGTTGCCATCACTGATCCGTGAGCAGCATCCAG 684
Db      304 eSerLeuSerLeuLeuGlyProProGlyAlaHisAsnLeuAspThrAlaPro-----Gln 322
QY      685 GACATTCGTAAGGTGACATCTGCAATGACCGGAGAGGTCGAATGGGC----- 736
Db      322 Asp-----Arg***His-----GlyPro**GlyAspIysAsr 333
QY      737 -GGAGCT----- 742
Db      333 gG1yAlaProGlyValAlaGlyGlyAspProArgProPro**GlyAsnPheValArg** 353
QY      743 -----ACAGCGGACCTTTCTGAGCCA 765
Db      353 *LeuLeuLeuMetProGlyValAla**ArgHisGlyThrSer-----ProPheLeu----- 370
QY      766 GGGAGACA-----CCCTGGAGTGTGACCTTGGC----- 795
Db      371 --GlyProSerLeuGlyGlyAsnGlyGlyGlnThrAsp-----SerGlyAsnLeuPhe 387
QY      795 ----- 795
Db      388 GlyThrProIysGly***SerHisProAlaPheThrIysSerThr***SerMetGlyAla 407
QY      796 AAACGGTCACATTTGGAGTCCAGACAGACAGACCCAC 831
Db      408 GluIysSerTyr-Tyr-----AsnHisProHis 416

```

```

RESULT 43
US-09-488-725A-5651
; Sequence 5651, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488,725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488,725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_fl_genes_b Versions 1.0
; SEQ ID NO 5651
; LENGTH: 410
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(408)
; OTHER INFORMATION: Xaa = any amino acid or nothing
US-09-488-725A-5651

Alignment Scores:
Pred. No.: 43.9 Length: 408
Score: 257.10 Matches: 105
Percent Similarity: 23.62% Conservative: 28
Best Local Similarity: 18.65% Mismatches: 71
Query Match: 16.51% Indels: 359
DB: 1 Gaps: 11

us-09-896-522-3 (1-834) x US-09-488-725A-5651 (1-408)
QY      828 GGGTCTGCTGGAGTCCGAATGTCACCGTTTGCAGAGTCAGCATCC----- 779
Db      47 GlyGluGlyAlaGlyIle-----Arg***AlaSerGlyLeuThrA 60
QY      778 -----CAGGCTGCTCCCTGGCTC 760
Db      60 laAlaGlyAlaAlaSerAlaAlaAlaAlaProProProThrArgGlyGlyProAlaPro- 79
QY      759 AGAAAGATCCGCTGTAGCTCCGCCATTTGACCTCC-----TCGGTCCATTTGCA 706
Db      80 ---AlaGlyCysGlyArgAlaProPro-Tyr-ProAlaProLeuArgValPro----- 95
QY      705 GATGTCACATTCAGAAATGCTCGATGTCGTCAGACGATGATGCAACATATT 646
Db      96 -----ThrHisGlyArgAlaProAlaProArgSerArgAlaAla-----ProArgA 111
QY      645 GTCACATCTCGTGGAGATGATCACAATCGGCATATCTTTGTGCGAGGACAGAACTCTTC 586
Db      111 laProAlaLeu-----SerHis-Gly-----ThrAlaAlaAlaAlaLeuSerProA 126
QY      585 GAAGCCGGCT----- 575
Db      126 laSerProAlaGlyProAlaAspPro***LeuProGlyHisSerSerGlnSerProProA 146
QY      574 --TCAAGAAAGGAGGTACTGCGTCAGAATCTGCTCCAGGTCCTCCCTCGGCGGACGTC 517

```

```

Db      146  rgGly***ArgTrp---GlyArgSerArgSerAlaProAlaPro-----AlaHis--- 161
QY      516  CCGGAG-----AAGCTTCGAGACG-----CCT 493
Db      162  ProGluHisProAlaProAlaGlySerAlaSerAlaSerGlnGlnThrProGlyTrpPro 181
QY      492  GAGCTCGAGGCGGCTG----- 476
Db      182  Gly-----SerCysCysLeuAlaGlnGlyTrpGlnAlaGluProLeuGlyAlaProGlyA 200
QY      475  -----CCAGAGAGAGC----- 464
Db      200  laGluAspGlyProValProProGlnArgGlyPheProLeuGlyThrLeuGlySerProA 220
QY      463  -----GACGTGGAGACATGCTCCGATCTCTGCTGCTGGAACAC 424
Db      220  laGlySerTrpAlaGlyLeuAlaGlyTrpGly***AlaGlyAlaProGlyThrGlnAla- 239
QY      423  CAAGATGCCCTCAAGAGAACACGTCGCGAGGAGAGACACGCTGGTCTGTGTAACCT 364
Db      240  -----ThrAlaProArgAlaAlaGlyGlnThrPro--ValAlaAlaAlaPr 254
QY      363  TGAAGTGTGCAGAAATCATAGTGCAGACCTCCAGCGTTTGGCTTCACGATGTTCTT 304
Db      254  oAsnCys-----ArgVal**Gly--SerAlaPro-----AlaLeuHis----- 266
QY      303  CAGAGTCTCTGTGCATCAAAATCATTAATCAAGGACCTTGAGATGTCAAAATGTGCTCC 244
Db      267  ArgAlaPro-----AlaAlaAlaAspProGlySerProLeuGlnAlaPr 281
QY      243  TTTCAAGGCTTGGCCTTGTGCTGCGCGTCAGACCC----- 206
Db      281  o-ProArgAlaTrpAlaSerProAlaAlaAlaGlyProGlyLeuSerSerSerAspTyrC 301
QY      206  ----- 206
Db      301  ysGlyGlyLeuGlyAlaGlyTrpArgAlaGlyIleSerProGluLeuGlyAlaAlaG 321
QY      206  ----- 206
Db      321  lLeuSerAspAsnTrpAlaArgCysProGlyProGlyProAlaGlu**GlyGlyGlnP 341
QY      205  -----TGAAGAACCTGTCCTGAGATGACACACCTTCGCGCGCTGTCCACCTC 151
Db      341  roGlyCysArgThrIleProAlaSerAlaCysMetProSer-----ProPro- 356
QY      150  GTT-----CTGTCCAGCACTCCATGATCTTCACACACAGGTGCACTT 106
Db      357  ValGluGlySerLeuGlyLeuSerArgLys-----GlyHisGlyAspLeu 371
QY      105  CCGCCTGGCAG-----TGCGCGCGCTCA----- 83
Db      372  ProSer--GlnAlaArg**GlyTrpHisGlyCysArgArgAlaArgHisLeuValProL 391
QY      82  -----CCCTATACAGAGAGGCGCGCTGAGCGGACGTCGCGCTCCGG 40
Db      391  euProAlaGluLeuGlyPro-----ArgGlyArg-----ThrGlyArgPro----- 404
QY      39  CGCGGCGCTTCGCACTTCCTCGCCT 15
Db      405  -----SerSerPro 407

RESULT 44
US-09-488-725A-2391
; Sequence 2391, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OR INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCE: 784FLPCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21

```

```

; PRIOR APPLICATION NUMBER: US09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598,042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620,312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653,450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662,191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693,036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727,344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc_flt_genes_b Versions 1.0
; SEQ ID NO 2391
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2391

Alignment Scores:
Pred. No.: 33.2 Length: 355
Score: 256.70 Matches: 105
Percent Similarity: 24.44% Conservative: 26
Best Local Similarity: 19.59% Mismatches: 74
Query Match: 16.50% Indels: 332
DB: 1 Gaps: 10

us-09-896-522-3 (1-834) x US-09-488-725A-2391 (1-355)
QY      3  GCGTTCGCGCGGAGCGGAGCACTGGCA-----GAGCCCGCGGCC 41
Db      6  GlyPheProGlyAsnArgGlyLeuMetGlyGlnGlyGluIleGlyProProGlyGln 25
QY      42  GAGAGCGGACCGTCGCGGACGAGCGGCGCTTCGATGAGGAGTGAAGCGCGACCTGCGCAG 101
Db      26  GlnGlyLeuGlySerGlyAlaPro---GlyMetPro---GlyLeuMetGlySerAsnGlyse 43
QY      102  CGGAGATCGACCGCTGTGTGAAGAAATCATGAGTTGCTGGACAGAACAGGTGAAACA 161
Db      43  r-----Pro-----GlyGln-----ProGlyThr 49
QY      162  GCGGACGCGAAGGTGTCTATCTGAGCGCAGACAGGTTCACAGGTCTCGACGCGACA 221
Db      50  ProGlySerIysGlySerIysGlyGluProGly-----IleGlnGlyMetProGly--- 66
QY      222  GCAAGAGCGCAAGGCTTGAAGAGACAGTACAAATTTGACCATTCAGATGCTTTGATTA 281
Db      67  -----AlaSerGlyLeuGlyGlyGlu-----ProGlyAla----- 76
QY      282  TGATTGATGACAGACGACTTGAAGAACATCTGGA----- 317
Db      77  -----ThrGly--SerProGlyGluProGlyIlyrMetGlyLeuProGlyIleGln 92
QY      318  -----GGGCAA 323
Db      93  GlyLeuGlyGlyAspIysGlyAsnGlnGlyGluGlyGlyIleGlnGlyGlnGlyGlu 112
QY      324  AACGGT-----GAGAGTGCAGACCTATGATTTGTGACACACTCAAGTTACAGAGAC 377
Db      113  AsnGlyArgGlnGly-IleProGlyGlnGlnGlyIle-----GlnGlyHis----- 127
QY      378  CACGGT-----GGTCTACCTGCGGACGCTGCTGTTTGA 413
Db      128  HisGlyAlaGlyGlyAlaGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 146
QY      414  GGCATCTGTGTTCTA-----CAG 434
Db      147  GlySerIysGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGlyGly 166
QY      435  CAGGAGATCGGAGACATGTTCCACCTGCGCGCTCTGTGGAACACGACTCCGACGTGAG 494

```



```

Db      167  |||||ProGlnGlyPro-----ProGlnGlyPro-----Pro-----G 177
QY      495  GCTGCTCCGAAGATTTCCTCCGAGCTGCCCGAGGAGGACCTGGAGCAATTCTGAC 554
Db      177  |||||LeuAsp-GlyLysProGlyArg-----GluPheSer-----GluGlnPheLeu 192
QY      555  GCAGTACACACCTGCTGTAAGCCGCGCTTCGAGAACTTCGCTGCGC-----GAC 605
Db      192  gGlnValCysThrAspVal-----IleArgAlaGlnLeuProValLeuLeuGlnSer 209
QY      606  AAGAAGATATGCCGATGATGATC-----GACGAGAGTGGACAAATATGTTGCCATCAAC 663
Db      210  GAlaArgIleArgAsnCysAspHisCysLeuSerGlnHisGlySerProGlyIleProGly 229
QY      631  -----CCACGAGAGTGGACAAATATGTTGCCATCAAC 663
Db      230  ProProGlyProIleGlyProGlnGlyProArgGlyLeuProGlyLeu-----P 246
QY      664  CTGATCGTCGACGACATCCAGACATTCG-----GAGGTCGCAATGGCGGAGC 741
Db      246  rooIyArGAspGlyValProGly-----LeuValGlyValProGlyArGProGlyValArg 264
QY      694  -----AATGTGACATCTGCAATGCAACCGAG----- 721
Db      265  GlyLeuLysGlyLeuProGlyArGAsnGlyGlu-----LysGlySerGlnGlyPheGly 282
QY      722  -----GAGGTCGCAATGGCGGAGC 741
Db      282  yTyProGlyGlnGlnGlyProProGlyProProGlyProGlnGlyProProGlyIleSe 302
QY      742  TACAAGCGACCTTTCTGTGAGGACACCCCTGGGATGCTGACCTTGCAAA--- 798
Db      302  LysGlnGlyGlyPro-----ProGlyAsp---ProGlyLeu---Pro---GlyLysAsp 316
QY      799  -----CGGTCACATTTGGAGTCCAGACGACGACGCC 828
Db      317  GlyAspHisGlyLysPro-----GlyIleGlnGlyGln-Pro 328

```

```

RESULT 45
US-09-488-725A-2343
; Sequence 2343, Application US/09488725A
; GENERAL INFORMATION:
; APPLICANT: Hyseq Inc
; TITLE OF INVENTION: Novel Nucleic Acid and Polypeptides
; FILE REFERENCES: 784F1PCT
; CURRENT APPLICATION NUMBER: US/09/488, 725A
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US/09/488, 725
; PRIOR FILING DATE: 2000-01-21
; PRIOR APPLICATION NUMBER: US09/552, 317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: US09/598, 042
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: US09/620, 312
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: US09/653, 450
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: US09/662, 191
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: US09/693, 036
; PRIOR FILING DATE: 2000-10-19
; PRIOR APPLICATION NUMBER: US09/727, 344
; PRIOR FILING DATE: 2000-11-29
; NUMBER OF SEQ ID NOS: 7144
; SOFTWARE: pc fl_genes_b Versions 1.0
; SEQ ID NO 2343
; LENGTH: 1056
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-488-725A-2343
Alignment Scores:

```

```

Pred. No.: 343
Score: 256.60
Percent Similarity: 15.77%
Best Local Similarity: 12.60%
Query Match: 16.47%
DB: 1
us-09-896-522-3 (1-834) x US-09-488-725A-2343 (1-1055)
QY      827  GGTCTGCTGTGAGTCCAAATGTACCGTTTCCGAGAGTACG----- 783
Db      122  GlyPheLeuAla-----ArgLeuProAlaAlaSerGlyAlaValAlaGly 136
QY      782  -----ATCCGAGGTGTGTCCTCCGCGTCA----- 759
Db      137  LysTrpProCysLeuValProGly-----SerProGlyThrGlnLeuProGlnGlnAlaArg 155
QY      758  -----GAAAAGTCCGCTTG 744
Db      156  AlaLeuArgProSerSerThrLeuSerGlySerAlaGlnLeuProGlnGlnAlaArg--- 174
QY      743  TAGCTCCGCGCATTTGACCCCTCTCGGTGCAATTTCAGATGTACACCATTCAGAAATGTC 684
Db      175  -----AlaLeuGlyProSerSer---ThrLeuSerGlyCys---ThraSpCys--- 188
QY      683  TGGATGTGCTGCACGATCAGTTGATGAGCAGCATATTTCCACTCTCTGCGGAGATGATC 624
Db      189  -AlaCysGlnGlyArgAlaGly-----GlnAlaProLeuGlyValAla 202
QY      624  ----- 624
Db      203  PheGlyLysLysLeuProAlaPheAlaThrIleProIleHisGlnLeuGlnHisGlyLys 222
QY      623  ---ACATCGGACATTACTTTCTTTCGCGC-----AGCGAAGATCCTCTG 585
Db      223  LysTyAspIleTyThrAlaSerGlyLysValTyAlaLeuTyArgGln---LeuLeuG 242
QY      584  AA----- 583
Db      242  LniHisGlyCysProArgCysProGlnLeuProProPheSerLeuPheGlyAspLeuGlnG 262
QY      582  ---GCGCGGCTTCAGGAAGGTGAGTACTGCGTCAAGATTCG----- 543
Db      262  LniHisMetArgAlaGlnHisGln---LeuPheCysCysArgLeuCysLeuGlnHisLeu 280
QY      543  ----- 543
Db      281  GlnIlePheThrTyGlnArgLysTrpTyTrSerArgLysAspLeuAlaArgHisArgMet 300
QY      543  ----- 543
Db      301  GlnGlyAspProAspAspThrSerHisArgGlnHisProLeuCysLysPheCysAspGln 320
QY      543  ----- 543
Db      321  ArgTyTrLeuAspAsnAspGlnLeuLeuLysHisLeuArgArgAspHisTyTrPheCysHis 340
QY      543  ----- 543
Db      341  PheCysAspSerAspGlyValaGlnAspTyTrTyTrSerAspTyAlaTyTrLeuArgLniHis 360
QY      543  ----- 543
Db      361  PheArgGlnLysHisPheLeuCysGlnGlnGlyArgCysSerThrGlnGlnPheThrHis 380
QY      542  -----TCCAGTCC----- 534
Db      381  AlaPheArgThrGlnIleAspLeuLysAlaHisArgThrAlaCysHisSerArgSerArg 400
QY      533  -----CTCCCTGCGCGCAGC 519
Db      401  AlaGlnAlaArgGlnAsnArgHisIleAspLeuGlnPheSerTyTrAlaProArgHisSer 420

```

```

QY 518 TCCCGAGAACTCT----- 505
Db 421 ArgArg--AsnGluGluGlnAlaProGlyLeuAspAlaProArgProValProProI 440
QY 505 ----- 505
Db 440 IeValValProGlySerArgGluValThrGlyCysLeuLeuAlaAlaGlyValValGlyG 460
QY 504 ----- 474
Db 460 IyGluAspTyrGluGluValAspArgTyrSerArgGlnGly--ArgValAlaArgAlaG 479
QY 473 ACGAAGAGGGCA----- 461
Db 479 yThrArgGlyAlaGlnGlnSerArgArgGlySerTPrArgTyrIysArgGluGluAs 499
QY 461 ----- 461
Db 499 pArgGluValAlaAlaAlaValaLargAlaSerValAlaAlaGlnGlnGlnGluAlaAr 519
QY 460 ----- 455
Db 519 gArgSerGluAspGlnGlnGlnGlyArgProIyGlyGluGluAlaAlaAlaArgG 539
QY 455 ----- 455
Db 539 yProGluAspProArgGlyProArgArgSerProArgThrGlnGlnGlyProGlyPr 559
QY 454 ----- 444
Db 559 oIyGluThrSerThrAenglyProValSerGlnGluAlaPheSerValThrGlyProAl 579
QY 443 ATCTCCGCGCTGTGAACACCAAGATGCCCTCAACAGAA----- 404
Db 579 aAlaProGlyAlaLeuProProSerProIyLeuIyAspGluAspPheProSerLe 599
QY 404 ----- 404
Db 599 uSerAlaSerThrSerSerSerCysSerThrAlaAlaThrProGlyProValGlyLeuAl 619
QY 404 ----- 404
Db 619 aLeuProTyrAlaIleProAlaArgGlyArgSerAlaPheGlnGlnGluAspPheProAl 639
QY 403 ----- 365
Db 639 aLeuValSerSerValProIyPro--GlyThrAlaProThrSerLeuValSerAlaTr 658
QY 364 ----- 356
Db 658 pAsnSerSerSerSerSerIySlyValAlaGlnProProLeuSerAlaGlnAlaThrG 678
QY 355 ----- 330
Db 678 ySerGlyGlnProThrArgIySAlaGlyIySArgGlyGlyArgIySArgGlyGlyPr 698
QY 329 ACCGTTT----- 323
Db 698 oProPheThrGlnGlnGlnGluGluAspGlyGlyProAlaLeuGlnGlnLeuLeuSerTh 718
QY 323 ----- 323
Db 718 rArgProThrGlySerValSerSerThrLeuGlyLeuAlaSerIleGlnProSerIySv 738
QY 323 ----- 323
Db 738 IGlYIySlySlySlyValGlySerGlyIySProGlyThrThrLeuProGlnProProPr 758
QY 322 ----- 298
Db 758 oAlaThrCysProPro--GlyAlaLeuGlnAlaProGluAlaProAlaSerArgAlaG 778
QY 297 --CGTGCAATCAATCATTAACAAGCATCTGATGTGTAATAATTGACTGTCTTTC 240

```

```

Db 778 IyProValAlaValValVal----- 790
QY 239 AAGCCTTGCCCTTCTGCTCTGCGGCAGACCTTGAACCTTGCCTGGCTCAGAGT 180
Db 791 ---ProAlaProAlaArg-----SerAlaPro-IySgluPro-ProGly----- 803
QY 179 ACCACCTTCGCGTGCCTGCTTCACCTCGTTC--TGTCCAGCAACTCCATGATCTTC 123
Db 804 ---LeuProArgProLeu---GlySerPheProCysPro---ThrPro----- 816
QY 122 TCACACAGGTGCACTTCGCGTGCAGTGCAGTCCGCCCTCAACCTTATCAAGAAAGGCC 63
Db 817 ---GlnGluAspPhePro---AlaLeu-----Gly-GlyPro- 826
QY 62 TGGTGCAGACGTCGCGCTCCGCGCGGGGCTCTCCGACGTCCTTCGCGCGCGAAGCC 3
Db 827 ---Cys-----ProPro-----ArgMetProProProPr 835
QY 2 A 2
Db 835 O 835

```

Search completed: December 12, 2003, 10:47:49  
 Job time : 49 secs